

Dietary regulation of microRNA expression in colorectal cells

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List of Abbreviations

Ac acetylation

ACTB beta actin

ACVR2 activin type 2 receptors

AGO2 argonaute-2

AKT (PKB) v-akt murine thymoma viral oncogene homolog 1

ANOVA analysis of variance

APC adenomatous polyposis coli

APS ammonium persulfate

Arg arginine

BAX BCL2-associated X protein

BCL2L11 (Bim) BCL2-like 11 (apoptosis facilitator)

BR butyrate-resistant

BRAF v-Raf murine sarcoma viral oncogene homolog B1

C13ORF25 C13 open reading frame 25

CAS cellular apoptosis susceptibility

CCDC88A coiled-coil domain containing 88A

CCND1 cyclin D1
CCNE1 cyclin E1

CDK19 (CDC2L6) cyclin-dependent kinase 19 CDK8 cyclin-dependent kinase 8

CDKN1A (p21) cyclin-dependent kinase inhibitor 1A cyclin-dependent kinase inhibitor 2A

cDNA complementary DNA

CDX2 caudal type homeobox 2

ChIP chromatin immunoprecipitation

CHX cycloheximide

CIMP CpG island methylator phenotype

CIN chromosomal instability

CRC colorectal cancer

CSIRO Commonwealth Scientific and Industrial Research Organisation

CTGF connective tissue growth factor

CTNNB1 catenin (cadherin-associated protein), beta 1

DALY disability-adjusted life year

DGCR8 DiGeorge syndrome critical region gene 8

DMSO dimethyl sulfoxide

DNA deoxyribonucleic acid

DNMT1 DNA (cytosine-5-)-methyltransferase 1

DNMT3A DNA (cytosine-5-)-methyltransferase 3 alpha
DNMT3B DNA (cytosine-5-)-methyltransferase 3 beta

dsRNA double stranded RNA

DTT dithiothreitol

E2F transcription factor family

E2F1 E2F transcription factor 1

E2F2 E2F transcription factor 2

E2F3 E2F transcription factor 3

ECL enhanced chemiluminescence

EDTA ethylenediaminetetraacetic acid

EGR2 early growth response 2

EMAST elevated microsatellite instability at selected tetranucleotide

repeats

EPIC European Prospective Investigation into Cancer and Nutrition

ESR1 estrogen receptor 1

FAP familial adenomatous polyposis

FBXW7 F-box and WD repeat domain containing 7, E3 ubiquitin protein

ligase

FDA US Food and Drug Administration

FOS v-fos FBJ murine osteosarcoma viral oncogene homolog

FSANZ Food Standards Australia New Zealand

GAB1 GRB2-associated binding protein 1
GAB2 GRB2-associated binding protein 2

GADD45A growth arrest and DNA-damage-inducible, alpha

H1/H5 histone 1/ histone 5 H2A and 2B histone 2A and 2B

H3 histone 3 H4 histone 4

HAT histone acetyltransferase

HER2 (ERBB2) human epidermal growth factor receptor 2

HDAC histone deacetylase

HDI histone deacetylase inhibitor

HDM histone demethylases

His histidine

HMT histone methyltransferase

HNPCC hereditary nonpolyposis colorectal cancer hnRNPA1 heterogeneous nuclear ribonucleoprotein A1

HRAS v-Ha-ras Harvey rat sarcoma viral oncogene homolog

IgG immunoglobulin G
IP immunoprecipitation

IPA Ingenuity Pathway Analysis

JARID1B histone demethylase jumonji, AT rich interactive domain 1B

K lysine

KRAS v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog

LIN28A lin-28 homolog A

Lys lysine

MAP mitogen-activated protein

MAPK7 (ERK5) mitogen-activated protein kinase 7

MAPK12 mitogen-activated protein kinase 12

MCC mutated in colorectal cancers

me methylation
me2 di-methylation
me3 tri-methylation

MGMT O6-methylguanine-DNA methyltransferase

MIR17HG miR-17-92 cluster host gene

miRNA microRNA

MLH1 DNA mismatch repair protein MLH1 (MutL protein homolog 1)

MLH2 DNA mismatch repair protein MLH2 (MutL protein homolog 2)

MSH2 mutS homolog 2
MSH3 mutS homolog 3
MSH6 mutS homolog 6

MSI microsatellite instability
MSS microsatellite stable

MYB v-myb myeloblastosis viral oncogene homolog

MYC (C-MYC) myelocytomatosis oncogene

NC negative control

NEDD9 (HEF1) neural precursor cell expressed, developmentally down-regulated

9

NF-μB nuclear factor kappa-light-chain-enhancer of activated B cells

NHMRC National Health and Medical Research Council

NR not reported

NRAS neuroblastoma RAS viral (v-ras) oncogene homolog

NRM normal rectal mucosa

NSP non-starch polysaccharide
O6CMG O6-carboxymethylguanine

O6MeG O6-methyl-2-deoxyguanosine

PACT protein activator of PKR
PBS phosphate buffered saline

PcG polycomb group

PDCD4 programmed cell death 4

RHOB ras homolog family member B PI3K phosphatidylinositol 3-kinases

PIC protease inhibitor cocktail

PIK3CA phosphoinositide-3-kinase, catalytic, alpha polypeptide

PMS2 postmeiotic segregation increased 2

PMSF phenylmethylsulfonyl fluoride

pre-miRNA pri-miRNA primary miRNA

PTEN phosphatase and tensin homolog RISC RNA-induced silencing complex

RM red meat

RNA ribonucleic acid RNAi RNA interference

RNU6B U6B small nuclear RNA RPL30 ribosomal protein L30

RS resistant starch

RTCA real-time cell analysis

RT-PCR reverse transcription polymerase chain reaction

SDS-PAGE sodium dodecyl sulfate polyacrylamide gel electrophoresis

SAHA suberoylanilide hydroxamic acid

SCFA short-chain fatty acid SD standard deviation

SEM standard error of the mean

shRNA short hairpin RNA

siRNA small interfering RNA

SIS (PDGFB) platelet-derived growth factor beta polypeptide

SMAD2 SMAD family member 2
SMAD3 SMAD family member 3
SMAD4 SMAD family member 4
SP1 Sp1 transcription factor

SP3 Sp3 transcription factor

TBS tris-buffered saline
TCF4 transcription factor 4

TEMED tetramethylethylenediamine

TGFBIIR transforming growth factor beta, receptor type II

TNM Tumour Node Metastasis (TNM) Classification of Malignant

Tumours

TP target protector

TP53 tumour protein p53

TPM1 tropomyosin 1

TRBP human immunodeficiency virus transactivating response RNA-

binding protein

TRxG trithorax group

TS thymidylate synthase

TSA trichostatin A

TSP1 thrombospondin-1

TSS transcription start site

TXNIP thioredoxin-interacting protein

UTR untranslated region

WCRF World Cancer Research Fund

WNT wnt signalling protein

XPO5 exportin 5

YLL years of life lost

Summary

Colorectal cancer (CRC) development is associated with epigenetic modifications, including DNA methylation changes, altered histone modification patterns, and dysregulated microRNA (miRNA) expression. While some dietary compounds can alter colorectal cell behaviour through epigenetic mechanisms, their role in modifying miRNA expression in CRC cells and normal colorectal tissue has been less studied. The diet-derived compound butyrate, with its known role in histone modification, is a plausible candidate for altering miRNA expression. This study examined dietary regulation of miRNA expression in colorectal cells, and explored the role of butyrate and other histone deacetylase inhibitors (HDIs) in modulating CRC risk through altered miRNA expression. The down-stream consequences of these miRNA changes, and the roles of miRNAs in the context of the anti-proliferative effects of HDIs, were determined. In addition to exploring the action of butyrate, a potentially protective dietary component, the study also investigated whether factors that possibly increase CRC risk, such as high red meat intake, alter miRNA expression.

In vitro, butyrate and other HDIs altered levels of some miRNAs that are dysregulated in CRC, including the oncogenic miR-17-92 miRNA cluster which is over-expressed in CRC. Butyrate decreased miR-17-92 miRNA levels in CRC cells, with a corresponding increase in expression of miR-17-92 targets, including cell cycle inhibitors and proapoptotic genes. Mechanisms for this decrease included changes in regulators of miR-17-92 host gene transcription, and altered histone acetylation and methylation patterns centred around the transcription start site and promoter of the miR-17-92 host gene. Decreased miR-17-92 expression may be partly responsible for the anti-proliferative effects of HDIs, with introduction of miR-17-92 cluster miRNA mimics reversing this effect and decreasing target gene transcript levels. Of the cluster members, miR-19a and miR-19b were primarily responsible for promoting proliferation, while in a novel finding, miR-18a acted in opposition to other members to decrease growth. Two proproliferative genes, NEDD9 and CDK19, were identified as novel miR-18a targets. This study presents the first evidence of competing roles for miR-17-92 cluster members, in the context of HDI-induced changes in CRC. miR-18a may play a homeostatic role in containing the oncogenic effects of the entire cluster, but may be selectively decreased in CRC compared with other cluster members.

SUMMARY

In addition to the capacity of butyrate to reverse the dysregulation of miR-17-92 miRNAs in CRC cells *in vitro*, this action was demonstrated with resistant starch supplementation *in vivo*, in rectal biopsies from healthy human volunteers exposed to high red meat levels. High red meat intake raised levels of miRNAs with oncogenic potential, particularly miR-17-92 cluster miRNAs and miR-21. Resistant starch supplementation raised faecal butyrate concentrations, and decreased miR-17-92 cluster miRNAs to baseline levels. *In vivo* modulation of miRNAs in colorectal cells by dietary compounds has not previously been demonstrated in humans. Regulation of miRNA expression demonstrates a plausible mechanism to explain some of the chemoprotective effects of butyrate, and potentially carcinogenic properties of other dietary components. Understanding how dietary compounds alter miRNA expression, and how miRNAs modulate the action of HDIs, may provide new opportunities for CRC therapies and prevention strategies.

DECLARATION

Declaration

I certify that this thesis does not incorporate without acknowledgment any material previously submitted for a degree or diploma in any university; and that to the best of my knowledge and belief it does not contain any material previously published or written by another person except where due reference is made in the text.

Karen J Humphreys

Publications and Presentations

Peer-reviewed Publications

Humphreys KJ, Cobiac L, Le Leu RK, Van der Hoek MB, Michael MZ. Histone deacetylase inhibition in colorectal cancer cells reveals competing roles for members of the oncogenic miR-17-92 cluster. *Molecular Carcinogenesis*. 5 February 2012. [Epub ahead of print].

Poster Presentations

Humphreys KJ, Le Leu RK, Cobiac L, Michael MZ. Butyrate alters microRNA expression in colorectal cells. 31st Lorne Genome Conference, Mantra Erskine Resort, Lorne, Victoria, Australia, 14 – 16 February 2010.

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