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Differences in the expression of microRNAs implicated in colorectal carcinogenesis and involved in the WNT signalling pathway in the macroscopically-normal epithelium of people at higher-risk of colorectal cancer

F. C. Malcomson¹, N. D. Willis¹, I. McCallum¹, L. Xie¹, S. Kelly¹, M. Bradburn¹, N. J. Belshaw², I. T. Johnson² and J. C. Mathers¹

¹Human Nutrition Research Centre, Institute for Ageing and Health, Newcastle University, Newcastle upon Tyne NE4 5PL, UK and ²Institute of Food Research, Norwich Research Park, Norfolk NR4 7UA, UK

People with ulcerative colitis (UC) or adenomatous polyps (adenomas) are at increased risk of colorectal cancer (CRC)(1). Altered expression of microRNAs (miRNAs), small non-coding RNAs that regulate gene expression post-transcriptionally, has been observed in those with UC⁽²⁾ and adenomas⁽³⁾. Importantly, abnormally-expressed miRNAs contribute to the initiation and progression of CRC and are potential biomarkers for diagnosis and prognosis of this cancer⁽⁴⁾. This study aimed to investigate differences in the expression of a panel of miRNAs in the macroscopically-normal mucosa of people at higher-risk of CRC.

We quantified expression of 8 miRNAs that are (i) implicated in CRC, (ii) regulators of WNT signalling, a pathway frequently aberrantly activated in $CRC^{(5)}$, and/or (iii) whose expression is altered by butyrate treatment in healthy participants (n = 56) and in patients at higher CRC risk with quiescent UC (n = 26) or history of adenomatous polyps (n = 12). RNA was isolated from mucosal biopsies of macroscopically-normal tissue collected at 10 cm from the anal verge, cDNA was synthesised by reverse transcription and used to quantify the expression of miR-17, miR-19a, miR-19b, miR-20a, miR-25, miR-93, miR-106b and miR-424 by quantitative PCR. For normally distributed data, the ANOVA General Linear Model was used to compare miRNA expression between the 3 risk groups, adjusting for age, sex and endoscopy procedure as covariates. Where data were not normally distributed, the nonparametric Kruskal-Wallis test was used.

Table 1. Median and range values for miRNA expression expressed as adjusted copies (2^{-\Delta ct} × 1,000) relative to the geometric mean of RNU6 and SNORD68 controls.

miRNA	Healthy Participants		Polyp Patients		UC Patients	
	Median	Range	Median	Range	Median	Range
miR-17	129	69-401	125	52-179	118	75–153
miR-19a	97	17–1728	156	19–751	89	29-464
miR-19b	69	15-3809	91	16-437	82	25-279
miR-20a	333*	107–1550	308*	152-424	279*	181-379
miR-25	116	13-9987	69	34–129	78	50-153
miR-93	77	10-1102	70	32–125	68	47-114
miR-106b	164	61–5548	162	77–242	144	109-180
miR-424	32**	9–1145	24**	7–50	69**	17–137

^{**} p < 0.01 and *p < 0.1 for differences between risk groups (Kruskal-Wallis test).

We observed significantly higher miR-424 expression (p < 0.01), a miRNA reported to be increased in CRCs⁽⁶⁾, and reduced miR-20a expression (p = 0.055) in participants with quiescent UC (Table 1). miR-20a expression also appears to be reduced in polyp patients. Alterations in miRNA expression may be detected in the healthy tissue of people at higher-risk of CRC and may represent very early molecular changes contributing to the progression from normal mucosa to carcinoma.

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