EPIGENETICALLY ALTERED CIRCULATING NUCLEOSOMES
AS BLOOD MARKERS OF COLORECTAL CANCER

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With thanks to the Gastroenterology Unit & Oncology Unit and the Biobank
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SUMMARY

BACKGROUND: Genome wide epigenetic signals including methylated DNA, histone modifications and histone variants are altered in cancer cells. Circulating DNA in cancer patients displays epigenetic changes that match those found in cancer tissue. This circulating DNA is nucleosome bound and is thought to be of tumor origin.

We have developed ELISA tests for circulating nucleosomes that contain specific epigenetic signals and used these to measure global epigenetic changes in the serum and plasma of colorectal cancer patients.

METHODS: Serum and plasma samples taken from subjects referred for colonoscopy, were assayed for circulating nucleosomes containing methylated DNA, H4K16Ac, H3K9(Me)3, H3K27(Me)3, macroH2A1.1 and H2AZ. The assays were conducted using NuQ® ELISA kits developed for this purpose and the results were compared with colonoscopy and histological findings.

RESULTS: A single NuQ® assay for nucleosome associated methylated DNA in plasma detected more than 70% of subjects with colorectal cancer and distinguished these from both healthy subjects or subjects with benign colon disorders with specificities above 70%. A combination of two NuQ® assays (nucleosome associated methylated DNA in combination with either a nucleosome associated histone modification or variant) expressed as a ratio was able to detect more than 80% of colorectal cancers with a greater than 80% specificity and also detected more than 50% of precancerous polyps.

39 subjects referred for colonoscopy
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No findings on colonoscopy 7
Colorectal cancer 7
Pre-cancerous polyps 8
Other colon diseases 14
Rectocolitis 4
Crohn’s disease 5
Diverticulosis 8

CONCLUSIONS

Simple ELISA blood tests for epigenetically modified circulating nucleosomes offer a promising new avenue for biomarker research in colorectal cancer.