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Combining omics to find new targets of aspirin in colorectal cancer

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Colorectal cancer (CRC) is the second leading cause of cancer deaths both in the UK and Europe and is a major public health concern as it accounts for the third highest number of cancer cases in the world. One approach that has been gaining a lot of interest is the repurposing of drugs used for other treatments of which aspirin is one. Plenty of epidemiological studies have shown that aspirin is beneficial in primary, secondary and tertiary prevention of colorectal cancer. Colorectal adenoma cells (RG/C2s) were treated with 0 mM, 2 mM and 4 mM aspirin for 24 hours before protein was collected for a SILAC approach and DNA was collected for methylation micro-array analysis. Changes in methylation were identified using the Infinium HumanMethylation450 BeadChip array. We used previously published transcriptomic data Sabates-Bellver et al. (2007) comparing normal and adenoma colons and combined the proteomic, transcriptomic and methylomic results to identify novel aspirin targets. Our results show that in general, aspirin decreases the expression of proteins in adenoma cells. After setting a threshold, our SILAC approach identified 129 proteins affected by aspirin treatment. After combining with methylomic and transcriptomic data, information of aspirins effect was available for 114 proteins. We set a threshold to identify the number of proteins consistently down-regulated with aspirin and identified 7 proteins. We have potentially identified 7 novel targets of aspirin and these may be useful in trying to understand the alternative mechanisms of its action.

Biography

Aayah Nounu has obtained first class honors in Bachelor of Science in Cancer Biology and Immunology from The University of Bristol, UK. She is currently pursuing PhD, looking at the effect of aspirin on colorectal cancer using both epidemiological methods and traditional laboratory methods.

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