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Mass spectrometry identification and quantification of N-oxalylglycinein: An inhibitor for 2-oxoglutarate oxygenase in spinach leaves

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Background: 2-Oxoglutarate and ferrous iron dependent oxygenases are involved in a variety of biological processes in aerobic organisms ranging from humans to bacteria. Synthetic N-oxalylglycine has been identified as a broad-spectrum 2OG oxygenase inhibitor. We report the identification of NOG as a natural product present in spinach leaves.

Method: To investigate whether NOG and related derivatives naturally occur in spinach leaves, we first developed an analytical method using reversed-phase liquid chromatography mass spectrometry (RP-LC/MS) and an NOG standard. The detection of NOG provided a linear response with concentration in the range 10-1000 μM with a correlation coefficient R^2>0.998. The detection limits for NOG were 5 μM and the limit of quantification was13 μM.

Results: The LC-MS, LC-MS/MS, NMR, and ESI accurate mass analyses provide positive evidence for the presence of NOG in spinach leaves. The amount of NOG at natural abundance in the spinach leaves sample was calculated to be 0.1681 mg per 3g dry weight of spinach leaves.

Conclusions: The results presented here demonstrate that NOG is present as natural products in plant tissues known to contain high levels of oxalic acid, i.e. spinach. We did not detect NOG in E. coli, or human tissue culture cells. Thus, whilst we cannot rule out the possibility that NOG is present in animal cells, there is no evidence for its presence at currently detectable levels. Whether or not the amount of NOG present in spinach leaves is bioavailable in sufficient quantity to elicit a physiological effect upon ingestion remains to be investigated.

Biography

Khalid Al-Qahtani has completed his PhD at the age of 32 years from University Oxford. He was awarded the delegate's choice prize for best young person's poster presentation at the BMSS annual meeting, April 2014. He has published more than 9 papers in peer reviewed journals and is focussing on building a database for cancer metabolomics linking this with changes in metabolic pathways for studying regulation in cancer cells.

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