Proceedings of the Nutrition Society (2012), **71 (OCE2)**, E122 doi:10.1017/S0029665112001796

Summer Meeting hosted by the Irish Section, 16–19 July 2012, Translational nutrition: integrating research, practice and policy

Application of metabolomics to mining effects of milk peptides on cellular metabolism

H. Whelan[1], A. Nongonierma[2], R. J. Fitzgerald[2] and L. Brennan[1]
[1]*UCD Institute of Food and Health, UCD Conway Institute, Food for Health Ireland, Belfield, Dublin 4,*
[2]*Department of Life Sciences, University of Limerick, Limerick, Republic of Ireland*

Type 2 diabetes mellitus (T2DM) is a complex metabolic disorder, which is characterised by insulin resistance and pancreatic β-cell dysfunction. Biologically active food components with the potential to increase life expectancy and prevent diseases such as T2DM, heart disease and cancer are currently being investigated, with particular attention being paid to bioactives of dairy origin[(1–3)]. The objective of this study was to combine GC-MS and NMR based metabolomics with functional assays to investigate the effect of a bovine milk derived bioactive peptide on pancreatic beta cell function and metabolism. The BRIN-BD11 and INS-1E pancreatic beta cell lines were cultured with 1 mg/ml of "Bioactive A" for 24 hours. Insulin secretion was measured and the changes in mitochondrial membrane potential and intracellular calcium following glucose stimulation were determined. Metabolic extractions were performed using a chloroform methanol extraction procedure. Fatty acid analysis was performed on GC-MS and aqueous metabolites were analysed using NMR. Treatment of BRIN-BD11 cells with "Bioactive A" caused a significant increase in glucose and alanine-stimulated insulin secretion ($p<0.01$ *vs.* 1.1 mM glucose). Metabolomic analysis revealed a significant decrease in saturated fatty acids (palmitic, stearic and palmitoleic, $p<0.05$), as well as changes in numerous amino acids (lactate, alanine and aspartate) in beta cells treated with "Bioactive A" when compared to cells cultured under control conditions. Overall the results indicate that a decrease in saturated fatty acids in combination with alterations to TCA cycle amino acids and intermediates are responsible for the induction of glucose stimulated insulin secretion in the beta cell. Future work will focus on translation of this work into humans with emphasis on the development of novel functional foods.

1. Zimecki M & Kruzel ML (2007) *Experimental Therapeutics & Oncology* **6**, 89–106.
2. Nakamura T *et al*. (2011) *Atherosclerosis* **219**, 298–303.
3. Ehlers PI *et al*. (2011) *Life Sciences* **88**, 206–2011.