*Proceedings of the Nutrition Society* (2010), **69 (OCE8)**, E586 doi:10.1017/S0029665110004805

*Winter Meeting, 2 December 2010, Functional genomic biomarkers, nutrition and disease susceptibility*

# Peripheral blood mononuclear cell gene expression and plasma protein profiles are differentially affected by glucose and lipid tolerance tests

C. O. Grada, E. Dillon, C. Morris, R. McBride, M. Ryan, M. Walsh, L. Brennan, M. J. Gibney and H. M. Roche

*UCD Conway Institute and Institute of Food and Health, School of Public Health and Population Science, University College Dublin, Belfield, Dublin 4, Ireland*

Peripheral blood mononuclear cells (PBMC) are an easily accessed tissue type that show differential gene expression following nutritional stimulus *in vivo*[1]. This study addressed the hypothesis that the PBMC transcriptomic signature and the associated metabolic phenotype would be differentially regulated by lipid *v*. carbohydrate nutritional challenges[2].

An oral lipid tolerance test (OLTT) and a glucose tolerance test (OGTT) were completed in a 'lean' cohort of ten individuals selected from a representative sample of 200 healthy Irish adults aged 18–60 years (age: 24.6 SD 3.84 years, BMI: 24.5 SD 2.2 $kg.m^2$). Fasting and postprandial peak plasma and PBMC samples were taken at 1 and 4 h post-OGTT and -OLTT, respectively. RNA was hybridised to Affymetrix Human Gene ST 1.0 arrays. Microarray data were normalised using RMA and R/BioConductor determined differentially expressed genes. The metabolic profile of volunteers was characterised including plasma TAG, NEFA, glucose, insulin and inflammatory profiles were determined.

A total of 2292 genes were differentially expressed following OLTT. No single genes were significantly differentially expressed following OGTT. The genes showing greatest changes in expression post-OLTT include *CENPK*, *CLC*, *OCLN*, *TMEM176A*, *FOLR3*, *ANKRD22*, *VNN1* and *PGA5* (all log Fc $> \pm 1.3$). Key genes involved in lipid metabolism (*LPL*, *LRP1*, *PLIN3*) and inflammation (*IKBKG*, *NLRP3*) were increased following the OLTT, but not OGTT. The KEGG pathway showing greatest enrichment, *Fc gamma R-mediated phagocytosis*, also contains genes related to inflammation. Most notably, the ERK-activated *cPLA2* gene is present, which modulates arachidonic acid (AA) and EPA release from DAG. Given the central role of AA/EPA, this may affect downstream eicosanoid, prostaglandin, leukotriene or resolvin production.

The transcriptomic signature will be related to the metabolic phenotype, which included an increase in plasma glucose following the OGTT ($P < 0.0001$), elevated plasma TAG post-OLTT ($P = 0.0354$) and lower NEFA concentration following both OGTT ($P < 0.0001$) and OLTT ($P = 0.001$). Interestingly the increase in inflammatory gene expression was associated with greater postprandial plasma IL-6 ($P = 0.0091$) and EGF ($P = 0.0053$) and a decrease in IFNG ($P = 0.104$) concentrations post-OLTT, with no such changes post-OGTT.

In conclusion, the OLTT induced a pro-inflammatory state in the PBMC transcriptome and plasma protein markers implicated in insulin resistance, the Metabolic Syndrome and T2DM, with no such response following OGTT.

This work was funded under the Food for Health Research Initiative (NDP 2007–2013; 07FHRIUCD1) of the Irish Department of Agriculture, Fisheries and Food, the Health Research Board and the Department of Health and Children. Samples collected as part of a registered clinical trial (NLM identifier: NCT01172951). H. M. R. was supported by Science Foundation Ireland Principal Investigator Programme (06/IM.1/B105).

1. Bouwens M, Afman LA & Müller M (2007) *Am J Clin Nutr* **86**(5), 1515–1523.
2. Mohanlal N & Holman RR (2004) *Diabetes Care* **27**(1), 89–94.

https://doi.org/10.1017/S0029665110004805 Published online by Cambridge University Press