Proceedings of the Nutrition Society (2008), **67 (OCE)**, E187 doi:10.1017/S0029665108008197

Joint meeting of the Société Française de Nutrition and The Nutrition Society, 6–7 December 2007

Do single nucleotide polymorphisms in β-carotene dioxygenase-2 (*BCDO2*) gene affect the postprandial response?

F. Tourniaire[1], A. M. Minihane[2], J. Hesketh[1] and G. Lietz[1]
[1]*School of Clinical Medical Sciences, University of Newcastle, Newcastle upon Tyne, UK and* [2]*University of Reading, Hugh Sinclair Human Nutrition Group, School of Food Biosciences, Reading, UK*

Many studies have highlighted the benefits of a carotenoid-rich diet on health[(1)]. However, it is not clear to date whether carotenoids and/or their breakdown products are responsible for the observed health benefits. Currently, two human enzymes have been identified and cloned, which catalyse the centric (β-carotene monooxygenase-1; BCMO1) and eccentric (BCDO2) cleavage of carotenes[(2)]. *BCMO1*- or *BCDO2*-knock-out mice develop an obese phenotype independent of the type of diet (standard or high-fat), suggesting that these enzymes play a major role in lipid homeostasis[(3)]. Previous studies have identified several single nucleotide polymorphisms (SNP) in the coding region of *BCMO1* that are common in the UK population, leading to a reduced catalytic activity of the corresponding enzyme *in vitro*[(4)]. Here, an investigation was conducted into whether genetic variations exist in the *BCDO2* gene as well, and whether these variations could influence the postprandial response in human volunteers.

Primers were designed to cover each of the twelve exons of the *BCDO2* gene and were used to amplify DNA using a high-fidelity polymerase. Resulting PCR products were then screened for the presence of SNP by denaturing HPLC and identified by sequencing. Allelic frequency of the SNP were determined and analysed in relation to biological variables and β-carotene absorption through an on-going collaboration with the University of Reading.

Table 1. Biological variables for the total population and in the different groups according to the genotype

	All		WT		HET		MUT	
	Mean	95% CI	Mean	95% CI	Mean	95% CI	Mean	95% CI
BMI (kg/m^2)	26.2	25.7, 26.8	25.8	24.8, 26.8	26.7	25.9, 27.4	25.5	24.5, 26.6
Total C (mM)	5.48	5.30, 5.65	5.53	5.19, 5.87	5.53	5.29, 5.77	5.17	4.83, 5.50
HDL-C (mM)	1.35	1.28, 1.42	1.48	1.33, 1.62	1.33	1.23, 1.42	1.17*	1.06, 1.27
LDL-C (mM)	3.44	3.28, 3.60	3.42	3.08, 3.76	3.50	3.28, 3.72	3.28	2.97, 3.58
HDL-C:LDL-C	2.81	2.61, 3.02	2.66	2.25, 3.06	2.88	2.60, 3.17	2.92	2.55, 3.30
TAG (mM)	1.35	1.25, 1.46	1.24	1.07, 1.44	1.44	1.30, 1.59	1.36	1.07, 1.74
TAG AUC (mmol.h/l)	122	113, 133	123	95, 129	129	115, 144	129	105, 15
NEFA (mM)	0.49	0.46, 0.52	0.48	0.42, 0.53	0.47	0.43, 0.51	0.56	0.48, 0.65
NEFA AUC (mmol.h/l)	22.8	21.7, 24.0	22.9	21.0, 25.0	22.9	21.1, 24.8	22.5	20.7, 24.4

WT, wild type; HET, heterozygote; MUT, mutant; C, cholesterol; AUC, 8 h postprandial area under the curve.
Mean value was significantly different from that for the wild type group: $*P<0.05$.

The data in the Table show that women carrying a specific mutant allele in the *BCDO2* gene display reduced fasting HDL-cholesterol and elevated TAG compared with the wild type. Functionality of the identified SNP is currently under investigation. These data need to be confirmed in other populations, and mechanistic studies in animal models such as knock-out mice are warranted to understand the metabolic pathways involved in these observations.

1. Amiot-Carlin MJ, Babot-Laurent C & Tourniaire F (2008) Plant pigments as bioactive substances. In *Food Colorants: Chemical and Functional Properties*, pp. 127–146 [C Socaciu, editor]. Boca Raton, FL: CRC Press.
2. Kiefer C, Hessel S, Lampert JM, Ledere MO, Breithaubt DE & von Lintig J (2001) *J Biol Chem* **276**, 14110–14116.
3. Hessel S, Eichinger A, Isken A *et al*. (2007) *J Biol Chem* **282**, 33553–33561.
4. Leung W, Méplan C, Hesketh J & Lietz G (2005) *Biochim Biophys Acta* **1740**, 93–317.