Concurrent Session 8: Lipids in human health

**Omega-3 during pregnancy: balance between risks and benefits**

DS Sinikovic¹, H Yeatman¹, D Cameron², BJ Meyer¹

¹School of Health Sciences, University of Wollongong, NSW 2522
²Northern Illawarra Maternal and Paediatric Services, Illawarra Area Health Service, NSW 2500

**Background** – Pregnant women and their babies are a priority public health target group. Long Chain Omega-3 Polynsaturated Fatty Acids (LC n-3 PUFA) and their importance during pregnancy have been studied extensively over the years. It is not known if adequate amount of information is available to pregnant women from their health professionals in relation to risks and benefits of omega-3 (n-3).

**Objective** – To determine communication strategies between health professionals and pregnant women using a series of interviews and surveys to understand health professionals’ attitudes regarding risks and benefits of omega-3 and subsequent information flow.

**Design** – A total of 16 health professionals were recruited and interviewed (7 midwives, 7 dietitians, 2 general practitioners). Interviews were transcribed and content analysis was performed in order to generate both qualitative and quantitative data. Interviews examined the extent to which information is being delivered to pregnant women. Pregnant women are currently being surveyed to determine information flow of LC n-3 PUFA.

**Outcomes** – Only four of 16 interviewed health professionals have a wide knowledge of n-3, two of which are midwives who are involved in educating other midwives and the other two are long term practising dietitians. Five of seven midwives provide no advice about n-3. Dietitians see pregnant women only if there are underlying nutritional disorders and hence have limited access. General practitioners interviewed were not involved in the management of pregnant women as they are referred to ante-natal clinics. Survey data collection and analysis are still pending.

**Conclusions** – Preliminary results show there is limited knowledge about n-3 and the health professionals that do know about n-3 have limited contact with the pregnant women. Therefore more strategic information flow about n-3 to pregnant women is warranted.

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**Differential effects of dietary fatty acids on genes associated with liver fat metabolism**

M McGlynn¹ and P Lewandowski²

¹The Office of the D.V.C. of Research Deakin University, ²School of Biomedical Science Victoria University

**Background** – It has been recognized that specific fatty acids have the ability to directly influence the abundance of gene transcripts in organs such as the liver. However little comparison has been made between the effects of common dietary of fatty acids and there influence on gene expression.

**Objectives** – To determine the effect of diets rich saturated, monounsaturated and polyunsaturated on gene transcripts associated with liver fat metabolism. Specifically how these three classes of fatty acids influence mRNA levels of key transcriptional regulators (PGC1α, PPARα, PPARδ, SREBP1C & ChREBP), fat oxidative (ACO, L-CPT1, HMG-CoA lyase & UCP-2) and fat synthetic (ACC, MCD, GPAT & malic enzyme) genes were investigated.

**Design** - Rats (n=32) were evenly divided into four groups; a saturated fat diet, a monounsaturated fat diet, a polyunsaturated fat diet (each diet contained 23% fat) and standard rat chow (7% fat) diet and fed for 12 weeks. Real-time PCR analysis was performed on liver tissue.

**Outcomes** – PGC1α and SREBP1C increased 1.9 fold or greater in all groups. Conversely, PPARα, PPARδ and ChREBP demonstrated variable changes with diet composition. Monounsaturated and polyunsaturated fat increased HMG-CoA lyase 2.8 fold, a response that was absent in the saturated fat fed animals. UCP-2 was decrease 3.0 fold by all dietary treatments. Malic enzyme was increased 2.8 and 2.4 fold with saturated and polyunsaturated diets respectively, yet was unaltered by the monounsaturated fat diet.

**Conclusion** – Modifications in common dietary fat composition initiated divergent gene responses in liver. These alterations were complex, with no uniform alteration in transcription factors with closely related functions (PPAR-family) and genes encoding proteins within the same metabolic pathway (fat oxidation or fat synthesis). Further studies are necessary to identify the predominant mechanisms regulating these differences in gene expression.