**2023 Boden Research Conference Abstract Guidelines**

**Please read the guidelines below and then add your formatted abstract to the box. Once completed, save this word document as “Surname\_Firstname\_Boden abstract” and return via email to** [**nc@science.org.au**](mailto:nc@science.org.au)

**Theme**: Abstracts should be on research related to personalised or precision nutrition. Quantitative and qualitative research and reviews will be considered.

**Format**: One single 250-word paragraph structured abstract under the following headings: background and aim, methods, results, and conclusion (include these headings only). This must be written in full sentences. Do not include citations, tables, or figures. The title, authors and headings are excluded from the word count.

**Title:** Should be in sentence case and centre justified. Use bold font.

**Authors:** Include all authors and asterisk the presenting author and use numeric superscripts for identifying all authors’ affiliations. These are not included in the word count.

**Body of the abstract**: the following sections should be included.

**Background and aim**: Provide 1 or 2 sentences that explain the context of the study and state the aim.

**Methods**: Describe the study design and identify specific methods such as animal models or human participants. Describe any intervention and control group if used. Include the measurements of outcomes. Include statistical analyses conducted.

**Results**: Report the most important findings, including results of statistical analyses. For quantitative research, include summary estimates such as mean or median with standard error of the mean, confidence intervals or interquartile range as appropriate. Measures of association should include 95% confidence intervals. Levels of significance should be provided.

**Conclusion**: Summarise in 1 or 2 sentences the primary outcomes of the research, including their relevance to personalised or precision nutrition research.

**General rules**

* Use the Times Roman 11-point font
* Left justify the abstract and centre and bold the title
* Allow one line space after title and another after authors and affiliation
* Number of participants with n (lower case), space between the letter and number e.g. n = 5678
* Significance written with p (lower case) and space between p and the value e.g. p< 0.001
* Space between a number and the unit or value e.g. 58 kg; 28 years; 20 ± 2
* No space between a percent value and sign e.g. 90%

**Example abstract (adapted from DOI: 10.1016/j.clnu.2020.08.024)**

**Blunted nutrient-response pathways in adipose tissue following high fat meals in men with metabolic syndrome: A randomized postprandial transcriptomic study**

Aimee L Dordevic1\*, Susan L Coort2, Chris T Evelo2, Chiara Murgia3, Andrew J Sinclair4, Maxine P Bonham5, Amy E Larsen6, Petra Gran7, David Cameron-Smith8

1. Department of Nutrition, Dietetics & Food, Monash University, Melbourne, Australia. Electronic address: aimee.dordevic@monash.edu.

2. Department of Bioinformatics - BiGCaT, NUTRIM School of Nutrition and Metabolism in Translational Research, Maastricht University, Maastricht, the Netherlands.

3. School of Agriculture and Food, University of Melbourne, Melbourne, Australia.

4. Department of Nutrition, Dietetics & Food, Monash University, Melbourne, Australia; Faculty of Health, Deakin University, Melbourne, Australia.

5. Department of Nutrition, Dietetics & Food, Monash University, Melbourne, Australia.

6. Department of Physiology, Anatomy, and Microbiology, La Trobe University, Melbourne, Australia.

7. Faculty of Health, Deakin University, Melbourne, Australia.

8. Liggins Institute, University of Auckland, Auckland, New Zealand; The Riddet Institute, Massey University, Palmerston North, New Zealand; Singapore Institute for Clinical Sciences, Agency for Science, Technology and Research, Singapore.

**Background and aim:** Excessive adipose tissue is central to disease burden posed by the Metabolic Syndrome (MetS). Whilst much is known of the altered transcriptomic regulation of adipose tissue under fasting conditions, little is known of the responses to high-fat meals.

**Methods:** Nineteen middle-aged males (mean ± SD; 52.0 ± 4.6 years), consumed two isocaloric high-fat, predominately dairy-based or soy-based, breakfast meals. Abdominal subcutaneous adipose biopsies were collected after overnight fast (0 h) and 4 h following each meal. Global gene expression profiling was performed by microarray (Illumina Human WG-6 v3).

**Results:** In the fasted state, 13 genes were differently expressed between control and MetS adipose tissue (≥ 1.2 fold-difference, p < 0.05). In response to the meals, the control participants had widespread increases in genes related to cellular nutrient responses (≥ 1.2 fold-change, p < 0.05; 2444 & 2367 genes; dairy & soy, respectively). There was blunted response in the MetS group (≥ 1.2 fold-change, p < 0.05; 332 & 336 genes; dairy & soy, respectively).

**Conclusion:** In middle-aged males with MetS, a widespread suppression of the subcutaneous adipose tissue nutrient responsive gene expression suggests an inflexibility in the transcriptomic responsiveness to both high-fat meals. These findings identify tissue-level mechanisms of disordered metabolism that can be targeted using precision nutrition interventions to improve health.

**Enter your abstract into the box below**