13th European Nutrition Conference

FENS 2019 | Malnutrition in an Obese World: European Perspectives

The Convention Centre Dublin, Ireland
15 - 18 October 2019

Hosted by

How to Use the Online Abstract Submission System for 13th European Nutrition Conference (FENS) 2019

Important Information

- Abstracts are submitted via an online submission system. Register with the abstract submission website and establish your user name and password.
- If you are submitting more than one abstract you **must** use the same login for each abstract.
- The maximum length of an abstract is **400 words**. **Please ensure that research findings are described to a level sufficient for reviewers to make an informed decision on scientific quality. Abstracts that fail to meet these criteria will be rejected.**
- Do not include author names in the title or body of your abstract – these are entered online during the submission process.
- You can alter your abstract at any time up to the submission deadline of **5th April 2019 – after this date changes will not be possible**.
- Abstracts will be reviewed and any abstract that was submitted for oral presentation, but was unsuccessful in that regard, will be considered for poster presentation.
- Each author may present **a maximum of two presentations, either oral or poster,** at the Conference.
- Please note that at least one author **must** register in full to attend and present the abstract at the Conference, with the presenting author registered by **16th August 2019**.

1. The Submission Process

Submitting an abstract is a **3-step process**. We strongly recommend that you complete your submission at one time.

Step 1: Register on the system

We are using a dedicated website for abstract submission and you must first register on the system. https://app.oxfordabstracts.com

The website is accessible by username and password. Please note that you will need to create your own username and password to access the system. You only need to register once - each subsequent time that you visit this page, you will log in with your e-mail and chosen password.

Step 2: Submit your abstract

- Once you have registered and created your profile, you must log in to the dedicated submission webpage, https://app.oxfordabstracts.com/stages/798/submission when you have prepared your abstract - enter your email address and the password you chose when you registered.

- The maximum length for an abstract is 400 words and it should include the following content: introduction, materials and methods, results and discussion. Please ensure that research findings are described to a level sufficient for reviewers to make an informed decision on scientific quality. Authors are also responsible for ensuring that the abstract is free of typographical errors, mistakes in grammar, style and spelling. Abstracts that do not meet these criteria may be rejected.
- Submitting an abstract requires that you complete a questionnaire for each abstract. Some questions are mandatory (marked with an asterisk) and you will not be able to complete your submission until these questions have been answered. You will be required to provide the names, affiliations and e-mail addresses of all authors, confirmation that all authors have approved the submission and the Theme and Strand to which you are submitting your abstract. Please also indicate whether you wish your abstract to be considered for oral presentation.
- As part of the submission process, you must also indicate if there are any commercial interests and associations that may pose a conflict of interest. Additionally, you must confirm your willingness to allow your abstract, if accepted, to be published in the conference programme. It may also be published in Proceedings of the Nutrition Society subject to selection by the Scientific Committee.
- It is strongly recommended that you complete your submission once started. However, if you decide to start your submission for completion at a later point, you must ensure to "Submit" your incomplete abstract. It will then be available for you to finish at a later stage. Failure to "Submit" your incomplete abstract will result in it being lost and you will have to start again.

Step 3: Confirmation e-mail

You will receive an e-mail confirming that your submission has been received. The subject of the mail will indicate if your submission is complete or incomplete. **An incomplete submission may have an answer that is unfinished, or you may have exceeded the word limit for the abstract. Incomplete submissions will not go for review.** You must log back into the submission system, click on the title of the abstract and complete it. Once complete you will receive the confirmation e-mail stating that your abstract is complete and will go for review.

If you wish to make another submission, please click on New Submission and a new blank submission form will open.

2. Amending a Submission

You may wish to change your submission. You can do this at any time up to the deadline of **5th April 2019 – after this date changes will not be possible.**

- Log in to the abstract submission system.
- You will see the abstract(s) that you have submitted. Click on the abstract title to open the file.

- Amending an abstract is just the same as the original submission process except that the online form will be automatically filled in with the answers that you gave previously. You don't have to change an answer if you don't want to.
- Once you click "Submit", your changes will be saved and you will be sent an email confirming that your abstract has been amended. **Your changes will not be recorded if you fail to click "Submit".** You will also receive an e-mail confirming that an amendment has been made to your abstract.

3. Conference Themes and Strands

Authors are welcome to submit under the following conference Themes and Strands:

Theme 1: Determinants and drivers across the lifecycle
Theme 2: Assessment and novel technologies
Theme 3: Current metabolic perspectives
Theme 4: The food environment
Theme 5: Hot topics/emerging issues

Each theme has 4 potential strands associated with it.

Strand A: Genetic, molecular, cellular
Strand B: Metabolism, physiology
Strand C: Epidemiology, population
Strand D: Policy, practice, risk assessment, behaviour

Should your abstract not fit within any strand, please select 'Other'.

4. Queries

If you have any queries about the submission process or you want to withdraw an abstract, please contact the conference administrator at abstracts@fens2019.org

5. Sample Abstracts

These are for information only – you must not enter your abstract as below as the abstract system captures the abstract in a series of steps. However, the output will be similar to the following.

Nutritional responses of cellular defence systems to different fats with or without phytochemical rich extracts: molecular markers of health status

J.E. Drew[1], Garry Duthie[1], A.J. Farquharson[1], Graham Horgan[2]
[1]The Rowett Institute, University of Aberdeen, [2]Biomathematics and Statistics Scotland, Foresterhill, ABERDEEN, AB25 2ZD, UK.

Maintenance of homeostatic regulation in response to nutritional challenges is an indicator of health status. Cell defence systems, immunity, inflammation, redox regulation, metabolism and DNA repair are essential to maintain homeostatic regulation and are impacted by nutrition. This study used human whole blood to assess cell defence system status in humans and identify potential food formulations that may impact on health status. Males 21 to 60 years (n= 16) provided fasted baseline blood samples (0h). Meal formulations, 50% unsaturated fat, 50% saturated fat, 50% unsaturated fat, 10g/100g beetroot extract and 50% saturated fat, 10g/100g beetroot extract were consumed by each subject on consecutive visits at least 1 week apart. Plasma insulin, leptin, IL6, IL1β and TNFα were measured by immunoassay using a MILLIPLEX®MAP Human Adipokine Magnetic Bead Panel 2 (Millipore Corporation, Billerica, MA, USA) according to the manufacturer's instructions. Total RNA was extracted from postprandial blood collected at 0h, 1h, 2h, 4h, 6h and 24h in PAXgene® blood RNA tubes (PreAnalytiX GmbH) using a Blood RNA Kit (Qiagen, Crawley, UK). Total RNA quality assessed by Agilent Bioanalyser (Agilent Technologies, Bracknell, UK) was >RIN 7. Analysis of gene expression was conducted using the GenomeLab System and an in-house designed multiplex assay, the hCellDSPlex. The hCellDSPlex incorporated cell defence system markers of immunity (*CD54*, *CD62E*, *CEACAM5*, *CD69*, *CD106*), redox (*SOD2*, *NOS2*, *GPX1*, *HO1*, *NRF2*, P22PHOX, GSS), inflammation (*PTGS2*, *IL1B*, *IL10*, *IL6*, *TNFA*, *CRP*), metabolism (*SIRT1*, *UCP2*, *SOCS3*, *COX6C*, *COQ2*) and DNA damage and repair (*TP53*, *P16INK4A*, *GADD45A*, *APE1*), red blood cell marker (*EPB42*) and reference genes (*PPIA*, *PSMB6* and *Kan(r)*). Principal component analysis (PCA) revealed characteristic gene expression patterns within the group of study subjects. One-way ANOVA blocked for subject identified cell defence system gene markers associated with differences in individual volunteers, meal formulation and time. *SIRT 1*, *UCP2*, *HO1*, *GSS*, *PTGS2*, *TP53*, *CDKN2A*, *PPIA*, *SOCS3* and *APE1* expression profiles characterised distinct stratified sub-groups associated with plasma high density lipoproteins, TNFα and postprandial responses of *SOCS3* and *PPIA*. Leptin, IL6 and DNA strand breaks revealed differing responses to fat type consumed. This study demonstrates postprandial immune, inflammatory, redox, metabolic and DNA repair responses that are largely independent of fat type consumed (unsaturated/saturated) or addition of beetroot extract, in apparently healthy individuals. However, postprandial responses were characterised by regulation of gene expression associated with markers linked to health status and are subject to inter-individual variation that may influence postprandial responses.

Sex specific differences on glycaemia and insulinaemia in response to white rice-based meals combined with chicken, fat and vegetable

M. Sayegh[1], L. Sun[2], M.K. Leow[2], C.J. Henry[2] J.E. Drew[1], V. Ranawana[1]
[1]*The Rowett Institute, University of Aberdeen, Foresterhill, Aberdeen, AB25 2ZD, UK.* [2]*Clinical Nutrition Research Centre, Singapore Institute for Clinical Sciences, Brenner Centre for Molecular Medicine, Singapore 117609*

Consumption of high glycaemic index (GI) carbohydrate foods can result in blood glucose fluctuations and postprandial hyperglycemia. Postprandial hyperglycaemia is the result of an excessive glucose production, which can increase the risk of cardiovascular disease (CVD), even in non-diabetic individuals. Evidence suggests that postprandial glucose homeostasis can be improved if high GI foods are co-ingested with protein, fat or vegetables, either singly or in combination, with the potential to reduce CVD risk. However, inter-individual variations in metabolic responses preclude conclusive evidence, particularly in women. Using data from an acute randomised controlled crossover study (The Singapore Study), secondary data analysis was conducted to determine the contribution of sex specific effects to observed inter-individual variation in postprandial glucose responses to white rice-based meals combined with chicken, fat and vegetable. The Singapore study recruited males (n=8) and females (n=6) and concluded that co-ingesting protein, fat, or vegetable with white rice, attenuated postprandial glycaemic responses (GR), measured postprandially at 15, 30 45, 60, 90, 120, 150 and 180 minutes, to varying degrees. Factors such as age, health and hormonal status were not controlled in the Singapore Study. Secondary data analysis was conducted using principal component analysis (PCA) (UMETRICS SIMCA-P+ 12.0 software) to assess patterns between male and female GR at different time points following the consumption of each meal. ANOVA (ver. 24.0; SPSS Inc., Chicago, IL, USA) was used to compare mean male and female GR. PCA revealed that sex specific variation between male and female responses following the consumption of all meals, accounted for approximately 38% of variation in the data. Comparison of mean blood GR for males and females revealed significantly higher blood glucose in females at postprandial time points 120, 150 and 180 minutes following consumption of white rice with vegetables. A repeated measures ANOVA determined that the overall mean of postprandial glucose following vegetable consumption was significantly different between males and females (P=0.02). However, when individual participant postprandial GR were investigated, high heterogeneity was also evident within the male and female cohorts. Collectively, these findings highlighted both sex specific and within sex inter-individual variations, suggesting that there are also additional factors which modulate these variations, potentially age, hormonal and health status. Future nutrition research studies should assess and report on sex specific effects and responses.