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Up front

Competition for publication in Diabetologia continues to grow, and less than 20% of papers are accepted. Of all the high-quality papers that appear in this month's issue I want to draw your attention to four articles that I think are particularly interesting. The articles are summarised here. Our publisher, Springer, has kindly made the full text of each of these papers freely available. I hope you enjoy reading them!

Sally M. Marshall, Editor

Exercise training response heterogeneity: physiological and molecular insights

Lauren M. Sparks

There is considerable variation in the magnitude of exercise training responses. In a review in this issue (https://doi.org/10.1007/s00125-017-4461-6), Lauren Sparks explains that selecting a response variable a priori is critical and its analytical rigour paramount. Furthermore, the statistical power of the chosen outcome should be assessed prior to classifying exercise responses to ensure that even the subtlest differences in a biologically meaningful outcome can be detected with confidence and investigated more thoroughly to determine mechanisms. The author discusses how both endogenous (inherent and potentially a predictor of the response) and exogenous (environmental and can be manipulated) factors contribute to exercise response heterogeneity and can be exploited to achieve maximal beneficial responses on an individual basis. It is hoped that, as the field of exercise metabolism continues to combine the plethora of -omics data with deep clinical phenotyping of participants in clinical exercise trials, the paradigm will be shifted by allowing exercise prescriptions to be targeted to those most likely to benefit and by identifying novel approaches to treat those who do not.

Chylomicrons stimulate incretin secretion in mouse and human cells

Arianna Psichas, Pierre F. Larraufie, Deborah A. Goldspink, Fiona M. Gribble, Frank Reimann

Glucagon-like peptide-1 (GLP-1) is a gut hormone that is released in response to food ingestion, to enhance insulin secretion and suppress appetite. In this issue (https://doi.org/10.1007/s00125-017-4420-2), Psichas and colleagues show that gut endocrine cells producing GLP-1 respond to chylomicrons, which are formed and released by the intestinal epithelium into the lymph after fat absorption. In a cell line model, chylomicron detection involved partial lipolysis by lipoprotein lipase and subsequent activation of the free fatty acid receptor FFA1, although other, yet to be identified mechanisms were involved in mixed epithelial primary cultures. Whatever the mechanisms prove to be, this research highlights that, in addition to detecting the presence of nutrients in the intestinal lumen, the gut also generates hormonal signals in response to the arrival of nutrients in the bloodstream. These time- and nutrient-dependent signals activate a variety of target cells to optimise the utilisation and storage of absorbed nutrients.

Application of white blood cell SPECT/CT to predict remission after a 6 or 12 week course of antibiotic treatment for diabetic foot osteomyelitis

Julien Vouillarmet, Myriam Moret, Isabelle Morelec, Paul Michon, Julien Dubreuil

Foot osteomyelitis is a frequent condition in patients with diabetes and is associated with an increased risk of amputation. There is a wide disparity in remission rates after medical treatment alone, which may be explained by the absence of a specific marker of remission and the lack of consensus as to the optimal duration of treatment. In this issue (https://doi.org/10.1007/s00125-017-4417-x), Vouillarmet et al report the results of a prospective study that investigated the remission rate of foot osteomyelitis treated medically in 45 people with diabetes, using white blood cell (WBC)-single photon emission computed tomography (SPECT)/computed tomography (CT) to guide the duration of antibiotic treatment (6 or 12 weeks). Twenty-four patients were treated for 6 weeks and 22 patients treated for 12 weeks; the overall remission rate after at least 1 year of follow-up was 84%. These results suggest that WBC-SPECT/CT may help predict remission of osteomyelitis and thereby assist in clinical decision making regarding the duration of antibiotic treatment. This article is the subject of a commentary in this issue by William J. Jeffcoate.

Transethnic insight into the genetics of glycaemic traits: fine-mapping results from the Population Architecture using Genomics and Epidemiology (PAGE) consortium

Stephanie A. Bien, James S. Pankow, Jeffrey Haessler, Yinchang Lu, Nathan Pankratz, Rebecca R. Rohde, Alfred Tamuno, Christopher S. Carlson, Fredrick R. Schumacher, Petra Bůžková, Martha L. Daviglus, Unhee Lim, Myriam Fornage, Lindsay Fernandez-Rhodes, Larissa Avilés-Santa, Steven Buyske, Myron D. Gross, Mariaelisa Graff, Carmen R. Isasi, Lewis H. Kuller, JoAnn E. Manson, Tara C. Matise, Ross L. Prentice, Lynne R. Wilkens, Sachiko Yoneyama, Ruth J. F. Loos, Lucia A. Hindorff, Loic Le Marchand, Kari E. North, Christopher A. Haiman, Ulrike Peters, Charles Kooperberg

Genomic studies have had tremendous success identifying variants associated with type 2 diabetes and underlying biomarkers. However, these findings have been almost exclusively discovered in homogenous populations of European ancestry. In this issue, Bien et al (https://doi.org/10.1007/s00125-017-4405-1) present the results of their investigation into associations between genetic variation and glycaemic traits in a multiethnic study of nearly 30,000 individuals without diabetes. Their results suggest that although the effects of glycaemic trait variants discovered in Europeans often generalise to other populations, transethnic research is imperative for a full understanding of the genetic influences. The authors report three independent variant associations in known genetic regions, of which one variant was ancestry-specific. In addition, a novel association with fasting insulin was discovered for a variant near *SLC17A2*. Genomic discoveries may eventually be used to inform personalised screening and therapeutic decisions. As such, these findings highlight the importance of including diverse ancestral backgrounds in future genomic studies.