

Approach Bias in Obesity Management: A Proposed Solution

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There is no argument that caloric manipulation holds an indisputable importance in weight loss management programs. The scientific community, however, would agree that mounting evidence on other non-calorie related weight lowering potentials of foods have not been used as much as they merit in current obesity clinical trials. For example, intestinal microbiota balance manipulation has been proposed as an auxiliary method to weight loss diets in addition to calorie restriction or manipulation [1]. In planning a diet, imagine that we just focus on calorie content of, let us say an apple and forget about its high satiety index or its high polyphenol content that might help weight loss irrespective of caloric considerations.

In a recent review, Feinman and Fine discuss that “A calorie is a calorie” violates the second law of thermodynamics and that some diets have metabolic advantages over some other isocaloric diets [2]. One could argue that multiple factors, such as interactions between nutrients-hormones [3], nutrients-neurotransmitters [4], nutrients-personalities [5,6], nutrients-appetite [7,8] and an enormous number of other influential connections, has not been taken into account in the second law of thermodynamics. Consequently, considering that these parameters would promise great auxiliary advantages in obesity management, especially if dietary regimens are planned based on a deep knowledge of unique nutritional properties that some foods, fruits, vegetables or herbs have. Different nutrients, foods, and herbs have different effects on thermoregulation, absorption, intestinal microbiota, anabolism, catabolism etc and we are only focusing on caloric contents of foods or caloric balance of diets.

We have produced a huge amount of data and information, yet the process of translation of this information into applicable diets has been sadly slow. For instance, despite a solid literature body of evidence, there is still a rather limited use of “aging” markers in clinical practice. It would be then advisable for physicians and health professionals to routinely rely on markers of systemic inflammation and endothelial dysfunction, i.e. overall cellular aging factors and which are now available and feasible at the doctor’s desk (CAF-panel, Natrix, Reggio Emilia, Italy) as dietary-response predictors as recently presented (C. Conti, Personal communication, International Age-Management Symposium, Sept 30-Oct 3, 2011, Warsaw, Poland). The recent evidence also suggests that in addition to the marked decreases in body weight associated, a calorie-restricted diet may contribute to the redistribution of fats within the body. This is also what we observed in concomitance with improved cellular membrane potential by using a novel body composition analytical device (Phosa, Rilevo, Piacenza, Italy) [9]. The calorie has been the pivot of dietary regimens and management programs traditionally, and this has led to an approach bias in nutrition intervention policies globally. An integrated discipline is urgently needed to translate data and information to produce feasible, sensible and applicable understanding of results obtained from obesity clinical trials. Building the bridges to bioinformatics in nutrition research should be the most urgent action in the coming

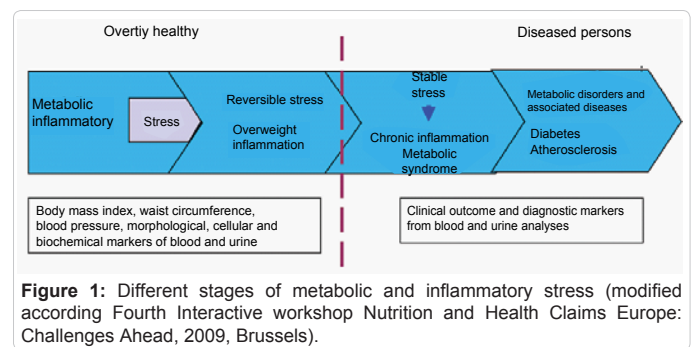


Figure 1: Different stages of metabolic and inflammatory stress (modified according Fourth Interactive workshop Nutrition and Health Claims Europe: Challenges Ahead, 2009, Brussels).

decade and so let us call for a scientific discussion to investigate the possibility and requirements of establishing such a new discipline, in coming proceedings and congresses of nutrition. For example, on the nutrigenetics viewpoint, recent genome-wide association studies (GWAS) have identified several single nucleotide polymorphisms associated with fasting glucose and insulin concentrations in individuals free of diabetes. Indeed, a meta-analysis of data from 14 cohorts comprising about 48,000 caucasians studying the interactions of whole-grain intake with loci previously associated in GWAS with fasting glucose and/or insulin concentrations confirmed such beneficial association and a potential interaction between variation in GCKR and whole-grain intake in influencing fasting insulin concentrations with a smaller reduction in fasting insulin concentrations in those with the insulin-raising allele [10]. In this regard, pilot ongoing studies targeting specific metabolic pro-inflammatory polymorphisms clusters (Metabolic panel, NextGenomics, Prato, Italy) are preliminarily proving to be useful predictor to help physicians identifying those subjects with a more consistent clinical response (Marotta F, Personal communication-Study in progress, International Symposium on “Innovations in age-management medicine”, Dec. 2-3, 2011, Warsaw, Poland).

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