Novel multiplex technology platform to assess gene expression signatures in blood: predicting health benefits in response to diet
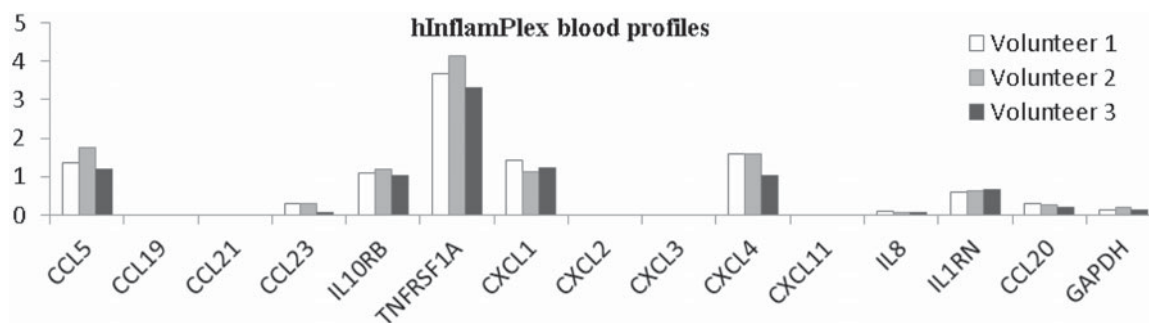
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Diet is critical for maintenance of optimal health and reduced disease risk. Assessment of dietary modulation of health and disease status in humans has been limited to date as a consequence of difficulties in accessing target tissues and observed inter-individual responses to nutrition. The use of human peripheral blood as a means of assessing health and disease status of non-hematologic tissue and organ systems in the human body is gaining momentum. Together with recent innovations in gene expression technologies it is now clear that gene expression profiling of human blood to determine predictive markers associated with health status and modulation by diet is now a feasible prospect to investigate diet-gene interactions.

Paxgene blood kits were assessed in collection of human whole blood samples ($n = 10$). Gene expression profiles of cellular defence systems associated with inflammation and metabolism were assessed using a novel gene expression technology platform, the GenomeLab System (Beckman) and in-house custom designed GeXP multiplex assays[1,2]. The in-house custom designed GeXP multiplex assays consist of a series of inflammatory gene targets, the hInflamPlex, associated with early events in colon cancer[1,2] and endocannabinoid signalling, the hECSPlex, associated with appetite and energy regulation.

The PAXgene system yielded total RNA of consistent quantity (1.6–3.6 ug/ml of whole blood) and quality (rRNA ratio 1.8–2.0) and proved practical for use in human intervention studies, permitting collection and storage at room temperature prior to frozen storage, and later processing to extract total RNA. Human whole blood total RNA (100 ng) was used to establish inflammatory (14 gene targets) and metabolic (25 gene target) gene expression profiles using the hInfamPlex[1,2] and hECSPlex GeXP assays.

Human blood and the dynamic cell population is a useful biological indicator to determine predictive signatures indicating health status and the impact of exposure to diet. Predictive gene signatures will require functional and biological validation to generate confidence in prediction of health status. However, the data presented indicates that this approach is feasible in monitoring and surveying the impact of diet-gene interactions to generate evidence for effective translation of research on food, drink and health.

1. Drew JE, Mayer C-D, Farquharson AJ *et al*. (2011) J Mol Diagn **13**, 233–242.
2. Farquharson AJ, Steele RJ, Carey FA, Drew JE. Mol Biol Reports Epub 23 Dec 2011.