

Gene Expression

Description

Subjects' peripheral blood mononuclear cells were analyzed to examine global gene expression. This molecular approach was used to distinguish between CFS cases, subjects who meet the CFS research case definition except that a major depressive disorder with melancholic features was identified (CFS-MDDm), chronically fatigued but not meeting the CFS research case definition due to insufficient number of symptoms or fatigue severity (ISF), chronically fatigued but with ISF and a major depressive disorder with melancholic features (ISF-MDDm), and non-fatigued (NF) controls.

Study Sample

169 participants

Data Collection Methods

Subjects had blood specimens collected in the morning on Day 1, prior to breakfast. Four 6-mL tubes of blood were collected in vacutainers containing citric acid (yellow top tubes). The peripheral blood mononuclear cells (PBMCs) were isolated on lymphocyte separation medium (Organon Teknika, Durham, NC) and stored in liquid nitrogen under conditions designed to maintain viability. Prior to storage, each vial was labeled with the appropriate identifiers. A technician from the CDC Molecular Epidemiology Program who was experienced in the collection, processing and storing of PBMCs in this manner trained the laboratory technician at the clinic.

RNA extraction and microarray hybridization were performed as described in the paper [Ojaniemi 2003].

The total RNA isolation protocol used the first guanidinium method described and only the MWG A array was used for data generation.

Reference

Ojaniemi H, Evengard B, Lee DR, Unger ER, Vernon SD.(2003). Impact of RNA extraction from limited samples on microarray results. *Biotechniques*. Nov;35(5):968-73

Data file headings

Column headings	Interpretation
Spot labels	Probe annotation (Gene-Bank IDs (2002)) and MWG control annotations
ARM Dens - Levels	Signal no correction
% Removed (ARM - Levels)	RLS signal correction for non-specific staining
MAD - Levels	Mean density
SD - Levels	Standard deviation
Pos X - μm	Probe position X
Pos Y - μm	Probe position Y
Area - μm^2	Probe spot area
Bkgd	Background
sARMDens	Background corrected data
S/N	Signal to Noise estimate
Flag	Flag
% At Floor	% RLS signal at background
% At Ceiling	% RLS signal at maximum
% At Floor - Bkgd	% RLS background signal at background
% At Ceiling - Bkgd	% RLS background signal at maximum