Gene expression profiling in persons with multiple chemical sensitivity before and after a controlled n-butanol exposure session

To investigate the pathophysiological pathways leading to symptoms elicitation in multiple chemical sensitivity (MCS) by comparing gene expression in MCS participants and healthy controls before and after a chemical exposure optimised to cause symptoms among MCS participants. The first hypothesis was that unexposed and symptom-free MCS participants have similar gene expression patterns to controls and a second hypothesis that MCS participants can be separated from controls based on differential gene expression upon a controlled n-butanol exposure. Participants were exposed to 3.7 ppm n-butanol while seated in a windowed exposure chamber for 60 min. A total of 26 genes involved in biochemical pathways found in the literature have been proposed to play a role in the pathogenesis of MCS and other functional somatic syndromes were selected. Expression levels were compared between MCS and controls before, within 15 min after being exposed to and 4 hours after the exposure. Participants suffering from MCS and healthy controls were recruited through advertisement at public places and in a local newspaper. 36 participants who considered themselves sensitive were prescreened for eligibility. 18 sensitive persons fulfilling the criteria for MCS were enrolled together with 18 healthy controls. 17 genes showed sufficient transcriptional level for analysis. Group comparisons were conducted for each gene at the 3 times points and for the computed AUC expression levels. MCS participants and controls displayed similar gene expression levels both at baseline and after the exposure and the computed AUC values were likewise comparable between the 2 groups. The intragroup variation in expression levels among MCS participants was noticeably greater than the controls. MCS participants and controls have similar gene expression levels at baseline and it was not possible to separate MCS participants from controls based on gene expression measured after the exposure.