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Expression of ROS related transcripts in Egyptian children with ASD

Marwa K Ibrahim, Nagwa Abdel Meguid, Reham M Dawood, Noha G Badr el Din, Mona Anwar, Adel Hashish and Mostafa Awady
National Research Center, Egypt

Autism Spectrum Disorders (ASDs) have become more spread wide over recent years. In the present study we attempt to unveil the association between ASD and mediators of oxidative stress pathway at molecular level. We used pathway focused PCR array to analyze gene expression pattern of 84 oxidative stress transcripts in peripheral blood mononuclear cell (PBMC) pools isolated from a total 28 patients with mild/ moderate or severe autism and 16 non-autistic healthy subjects (each sample is a pool from 4 autistic patients or 4 controls). All the participants were diagnosed using; Text Revision (DSM-IV-TR), Childhood Autism Rating Scale (CARS) and Autism Diagnosis Intervention- Revised (ADI-R). Only 8 genes showed differential regulation over 1.5 fold change accompanied by statistical significance ($p < 0.05$) when compared the autistic group to the non-autistic one. The transcriptional profile revealed down regulation of 7 transcripts: Ferritin heavy polypeptide1, Glutamate-cysteine ligase modifier subunit, Neutrophil cytosolic factor2, Prostaglandin-endoperoxide synthase 2, Prion Protein, Superoxide dismutase2 mitochondrial and Thioredoxin and up regulation of one gene Glutathione peroxidase 7 in the PBMCs of autistic patients (either mild or severe) compared to controls ($p < 0.05$ for all). These results suggested that ASD is accompanied by dysregulation of the molecular signals involved in oxidative stress pathway. The current data form the basis for focused studies using single gene expression or custom arrays on a larger number of cases to get the most statistically regulated factors.

khalilm@livemail.uthscsa.edu

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