EPP0920

The RNA editing patterns are different in blood of euthymic and depressed bipolar patients

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Introduction: Bipolar disorder (BD) is a severe mental disorder associated with functional impairment, high disability and premature mortality. Modifications of editing in mRNA of serotonin receptor subtype 2C (5-HTR2c) was reported by us in depressed suicide decedents. We have also identified a panel of RNA editing-based blood biomarkers for the diagnosis of BD, which also allowed to discriminate unipolar depression from BD with high sensivity and specificity.
Objectives: Herein, aiming to confirm the diagnostic value of this panel, a new cohort of BD patients was recruited in Brazil.
Methods: This study is based on the analysis of 47 control patients (CTRL) compared to 40 patients with bipolar disorder (BD). BD patients (BP) were classified into 4 subgroups: euthymic (BP_EUT, n = 17), depressive (BP_DEP, n = 11), manic/hypomanic (BP_HM, n = 7) and mixed (BP_MIX, n = 5). The diagnostic value of a panel of RNA editing-based blood biomarkers for the diagnosis of BD, which includes a set of eight genes, namely PDE8A, CAMK1D (calcium/calmodulin-dependent protein kinase type 1D); GAB2 (growth factor receptor bound protein 2-associated protein 2); IFNAR1 (interferon alpha/beta receptor 1); KCNJ15 (ATP-sensitive inward rectifier potassium channel 15); LYN (tyrosine-protein kinase Lyn); MDM2 (E3 ubiquitin-protein ligase Mdm2); PRKCB (protein kinase C beta type), which was able to discriminate unipolar depression from BD with high sensivity and specificity, was confirmed here by testing an independent cohort of patients suffering from BD recruited in a well-known genetic admixed ancestry population, which is typical in South America, more specifically in Brazil.
Results: We identified new combinations allowing a clear discrimination of euthymic versus depressed bipolar patients, and euthymic versus healthy controls, confirming that RNA editing is a key mechanism in the physiopathology of mental disorders, in particular in BD.
Conclusions: In conclusion of this study, we confirm that RNA editing is a key mechanism in the physiopathology of mental disorders in general, and in BD in particular, and that measuring changes in this mechanism at the peripheral level allowed us to stratify BD patients not only with respect to their symptomatology, but also with respect to the pathophysiology, thus paving the way for personalised medicine in psychiatry.

Disclosure of Interest: None Declared

EPP0921

A healthy dietary pattern is associated with microbiome diversity in bipolar patients: the Bipolar Netherlands Cohort (BINCO) study

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Introduction: The gut microbiome is one of our most prominent surfaces interacting with the outside world through the food we eat. It is influenced in terms of composition and diversity by our diets and life style habits and, in turn, affects us through the 'gut-brain axis'. Cardiovascular risk, which is one of the main causes of death in Bipolar Disorder (BD), is affected by diet. The association between diet and microbiome in BD patients has not been studied.
Objectives: We aimed to assess whether [1] dietary quality is associated with the microbiome's diversity, and [2] what changes and interactions occur during in both the dietary quality and microbiome diversity during the subsequent year of onset BD.
Methods: 39 recently diagnosed patients with BD of the 'Bipolair Nederlands Cohort' (BINCO) (mean age 36 years, 61.5% female) were included. Food Frequency Questionnaires (FFQ) and corresponding Dutch Healthy index (DHD-15) were analyzed at baseline and one year follow-up. Feces samples corresponding to the FFQ were analyzed using 16S rDNA gene amplicon sequencing to attain the Shannon Diversity index and the Chao1 diversity index. Multivariate regression analyses were performed.
Results: The Shannon diversity index significantly correlated to the DHD-15 total score after adjusting for sex and age (beta = 0.451; P = 0.004). The Chao1 index showed the same trend, but did not reach significance (beta = 0.264; P = 0.11). These positive correlations seemed to be driven by the positive effect of fish, beans, coffee, fruits and nuts. There was neither a significant change in DHD-15 index nor in the diversity measures after one year.
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