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dysregulation as well as hyperactive and inattentive symptoms have been linked to altered gut-microbial composition in different psychiatric disorders, mostly acting on the dopamine metabolism or inflammation. In this study, we aim to investigate the role of gut microbes in ADHD for reactive aggression and link the abundance of specific genera to markers of brain functioning.

Methods: Therefore, we assessed reactive aggression with the reactive and proactive aggression questionnaire and acquired functional MRI during the presentation of angry, happy and fearful faces in a dynamic facial expression task in 78 adults with ADHD and 78 control subjects. We analyzed the associations of whole-brain activity with levels of reactive aggression as well as hyperactive and inattentive symptoms in an interaction of the general linear model. Furthermore we analyzed the gut-microbial composition by sequencing the fecal samples in the 16S rRNA gene. A prevalence cut-off of 10% for genera and samples was applied before analyzing the group differences and investigating associations with reactive aggression scores. Additionally, we will implement a linked ICA to integrate the multivariate neuroimaging findings of functional activity and connectivity together with the microbial composition to investigate potential components implying biological mechanisms such as neurotransmitter routes or inflammation.

Results: Reactive aggression scores were associated with ADHD diagnoses, but no brain activation patterns indicated generally altered emotion processing in ADHD. However, investigating the brain activities associated with reactive aggression in people with and without ADHD showed an interaction of diagnosis and reactive aggression scores. We found high levels of activity in the right Insula, the limbic system and middle and superior frontal area to be particularly associated with high reactive aggression ($p < .05$ cluster extent threshold corrected). In the microbiome analysis we found nominal differences in the gut-microbial composition of 20 taxa on the genus level between adults with ADHD and controls of which eight genera were correlated with reactive aggression scores ($p < 0.05$). Results on gut-microbiome-brain interactions follow. Conclusion: Differential brain functioning during emotional processing as well as gut-microbiome compositional differences between subjects with and without ADHD seem to be associated with emotion dysregulation such as reactive aggression. The interplay of the gut-microbiome and the brain activity is an interesting viewpoint to understand more about the etiology and biological mechanisms underlying emotion dysregulation in adult ADHD.

No conflict of interest

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CLINICAL PROFILE OF PATIENTS ATTENDING THE EMERGENCY DEPARTMENT IN DIFFERENT PHASES OF COVID-19 PANDEMIC

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Introduction: The COVID-19 pandemic had a significant impact worldwide [1,2]. Consultations in the Emergency Service of the Hospital Clínic of Barcelona varied in terms of reasons for consultations, psychopathology, and other aspects, before and during the pandemic.

Objectives: To examine changes in the profile of patients admitted before the COVID-19 pandemic, during the lockdown, and after the strict lockdown to the Psychiatric Emergency Service of a third-level hospital, in order to assess variations in the period of lockdown in the number of patients, clinical characteristics, diagnoses, and the severity of cases, and also to study the tendency of these variations in the first period of time after the strict lockdown.

Methods: All adult psychiatric inpatients admitted from December 13th to June 14th to the Psychiatric Emergency Service of Hospital Clínic of Barcelona, Spain, were retrospectively included for analysis and divided into three groups –T0, T1, and T2- depending on the time they attended the Emergency Service, including T0 those patients admitted before lockdown, T1 those who attended during the strict lockdown and T2 those visited just after that period. SPSS v25.0 was used in order to compare the differences between groups.

Results: A total of 1991 patients were included -1224 in T0, 546 in T1, and 221 in T2. The majority of patients were male (52.08%), with a mean age of 41.21 years (SD 16.53). Significant differences in the proportion of males and females were found comparing groups, with a proportion significantly higher of females in T0 (50.3%) compared with T1 (43.6%) and T2 (45.2%; $p < 0.05$). No significant differences in mean age were found between groups. The ratio of the

number of patients per day was significantly higher in T0 than in T1 and T2 ($p < 0.05$). A significant difference was found in the proportion of patients consulting with substance use disorders, being significantly lower in T0 than in T1 and T2 (12.2% vs 15.9% and 15.4%, respectively; $p < 0.05$). Patients visited during lockdown (T1) showed a significantly higher proportion of admissions in an acute unit (38.1% vs 24.1% in T0 and 27.1% in T2), a significantly higher proportion of patients consulting with dementia (1.5% in T1 vs 0.5% in T0 and 0.9% in T2), and a lower proportion of patients consulting with anxiety (13.9% in T1 vs 25.2% in T0 and 23.5% in T2).

Conclusions: The COVID-19 pandemic and the situation of lockdown lead to a significant reduction in the overall consultations to the Emergency Service [3], showing a higher proportion of severe cases and patients with a longer duration of symptoms before the consultation. The increase in the proportion of patients visited with dementia might be explained by cohabitation with their relatives due to lockdown and teleworking, and also the lack of availability of caregivers. This study also suggests that patients with anxiety might have avoided Emergency consultations during the initial period of the pandemic [4], even though visits had more tendency to be telematic and anxiety disorders have been prevalent during the lockdown.

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EPIGENETIC MODULATION OF OXYTOCIN RECEPTOR GENE IN OBSESSIVE COMPULSIVE DISORDER: A LINK WITH MICROBIOTA-HOST AXIS

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Background: Obsessive-compulsive disorder (OCD) is a psychiatric condition responsible for a significant impairment of daily functioning and reduction in quality of life. Robust literature evidence suggests a genetic by environment interplay in the etiopathogenesis of OCD, yet the underlying molecular clues remain only partially understood [1, 2]. In order to further deepen our knowledge about OCD, it is essential to better understand how genes interact with environmental risk factors, a cross-talk that is thought to be mediated by epigenetic mechanisms. The human microbiota may be a key player, because bacterial metabolites can act as epigenetic modulators [3].

Objective: The aim of this study was to further investigate the role of epigenetic regulation of OXTR in OCD by analyzing its transcriptional regulation in both blood and saliva samples, evaluating in the latter also the distribution of the major phyla. In particular, we explored the role of gene DNA methylation and of