Self-rating anxiety scale (SAS). Associations among CLBP, demographics, psychosocial or sleep disorders parameters and clinical outcomes were analyzed using multivariate models.
Results: People with CLBP exhibited a substantially greater prevalence of depressive, insomnia and obstructive sleep apnea (OSA) symptoms than controls ($p < 0.05$). CLBP diagnosis was independently correlated with female gender, older age, as well as worse physical and mental health outcomes measured by (i) higher level of sleep symptoms such as sleepiness, OSA and insomnia symptoms and (ii) higher prevalence of physician-diagnosed depression, and moderate to severe depressive symptoms. The level of functional disability for CBLP patients (based on Quebec score) was independently associated with age, physician diagnosed depression, lower educational status, moderate to severe depressive symptoms and OSA symptoms. The combination of moderate to severe depressive symptoms with OSA or insomnia symptoms was the most important predictive factor for functional disability for CBLP patients (OR 13.686, 95% CI 4.581-40.885; p<0.001).
Conclusions: Depressive symptoms and subjective sleep disorders appear to relate to greater CLBP-intensity and/or CLBP-related disability in people with CLBP. To achieve the desired outcomes when treating patients with chronic CLBP, it is essential to employ a holistic approach, involving assessment and management of their psychological comorbidities, and sleep issues, that may improve quality of life in these patients.

Disclosure of Interest: None Declared

Genetics and Molecular Neurobiology

O0064

Gene expression of protein synthesis, immunity and brain pathways specifically altered in Anorexia Nervosa

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Introduction: Anorexia nervosa (AN) is a severe and chronic psychiatric disorder, resulting from a voluntary food restriction, vomiting, use of laxatives and excessive exercises, leading in dramatic weight loss and high mortality. AN is a multifactorial disease involving genetic and epigenetic factors supporting that AN is a metabo-psychiatric disorder. The molecular mechanisms involved in the etiology of AN remain unclear. One work reported gene expression by RNA sequencing in peripheral blood before and after weight restoration in 6 AN patients (Kim 2013), and one RNA sequencing in human iiPSC-derived neurons from 4 patients and 4 controls (Negraes 2017). To date, the profile of expression of genes and proteins in AN is undetermined.
Objectives: In this study, our goal is to identify specific gene expression signatures from circulating blood nuclear cells to decipher the pathophysiology of AN and characterize biomarkers that can be used for diagnostic or prognostic of AN.
Methods: All consented participants are recruited at Sainte-Anne Hospital, Paris, France, using DSM5 criteria. They had a blood draw in Paxgene tube for the collection of RNAs. Total RNA was extracted from peripheral blood mononuclear cells of 15 patients suffering of AN and 15 healthy controls. All messenger RNAs are sequenced on a Novaseq plateform. Reads are aligned to the human genome 19 and statistical analyses on the read counts for differentially expressed genes are computed with DESeq2.
Results: The total RNA sequencing allows us to identify 673 dysregulates genes (p adjusted value <0.01, fold change >1,5). Among them, 248 are down-regulated and 425 are up-regulated genes in AN patients compared to controls. From them, 151 transcripts are annotated as pseudogene and 45 are referenced as antisense RNA. Of the 522 remaining transcripts, 424 correspond to a transcript or protein annotated by HGNC and ENSEMBL and 93 are known pseudogenes. A large number of proteins resulting from the expression of deregulated genes interact with each other and form a statistically enriched network impacting biological processes. They are mainly increased and acting in the cellular machinery allowing protein synthesis (biological process: transcription, ribosome, spliceosome and mitochondria). In contrast, down-regulated genes present an enrichment in genes involved in immunity pathways. Finally, several genes are also expressed in the brain. We observed a significant enrichment of genes expressed in the blood and brain tissues.
Conclusions: We identify specific profiles of gene expression in AN. Several genes are both blood and brain tissue expression. Some genes are good candidates for biomarker of the diagnostic in AN that need to be investigated in a longitudinal study to evaluate their useful as prognostic biomarker of AN.
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Disclosure of Interest: None Declared

O0065

Crosstalk between Anxiety and Depression and Inflammatory bowel diseases: preliminary data on circulating miRNAs

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Introduction: Numerous studies have established a heightened prevalence of anxiety and depression (A&D) in individuals diagnosed with Inflammatory Bowel Diseases (IBD) when compared to the general population. Research indicates that patients with active IBD exhibit a higher frequency of anxiety symptoms and depression symptoms compared to those with inactive disease. In patients with IBD, anxiety was linked to reduced medication adherence and an increased likelihood of undergoing surgery. Furthermore, associations were identified between depression and an elevated risk of disease relapse, as well as a poorer response to treatment in IBD

patients. In both IBD and depression, there is evidence of disruptions in circulating miRNAs.
Objectives: One facet of the ongoing project titled "The brain-gut axis linking inflammatory bowel disease with anxiety and depression: the inflammation-microbiome network" (CRP/ROU21-01) involves the exploration of circulating miRNA profiles in various patient groups.
Methods: These groups encompass IBD patients with symptoms of anxiety and/or depression (IBD+A&D+), patients lacking anxiety and depression symptoms (IBD+A&D-), a cohort of individuals without IBD but experiencing depressive and anxiety symptoms (IBD-A&D+), and a control group (IBD-A&D-). Thus far, our investigation has entailed screening a comprehensive panel of 179 miRNAs in the plasma of six IBD patients and 12 non-IBD patients (CTRL) to identify a subset of highly dysregulated miRNAs. MiRNA isolation was achieved using the miRNeasy Serum/Plasma Kit, and miRNA expression levels were assessed via quantitative reverse transcription-polymerase chain reaction (qRT-PCR) utilizing the Human serum/plasma focus, MIRCURY LNA miRNA Focus PCR panel (Qiagen).
Results: Our statistical analysis revealed significant differential expression in 45 miRNAs ($p<0.05$). Specifically, we identified 29 miRNAs with elevated expression and seven miRNAs with reduced expression. Among these dysregulated miRNAs, 15 (miR-223-3p, miR-143-3p, let-7f-5p, miR-30b-5p, miR-26a-5p, let-7a-5p, miR-339-5p, let-7d-5p, miR-221-3p, miR-191-5p, let-7g-5p, miR-24-3p, miR-107, miR-26b-5p, miR-320b) were associated with depression and/or anxiety and were previously identified as dysregulated in the plasma of patients in other studies. These miRNAs will soon undergo evaluation in the plasma of IBD-A&D+ and IBD+A&D+ patients.
Conclusions: These initial findings provide us with a panel of circulating miRNAs that warrant further investigation in the aforementioned patient groups. The miRNA profile we obtained may either be unique to IBD or linked to the intricate phenotypes of IBD occurring concurrently with anxiety and depression. A more profound comprehension of these mechanisms will aid in the development of enhanced
diagnostic tools and disease monitoring strategies, as well as the exploration of innovative therapeutic approaches.

Disclosure of Interest: None Declared

Neuroimaging

O0068

Longitudinal amygdala resting state functional connectivity develops differently in adolescents with internalising disorders compared to healthy peers

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Introduction: Longitudinal neuroimaging studies focused on adolescents with internalising psychopathology (i.e. with clinical anxiety and/or depression) are scarce, even though anxiety and depression are highly prevalent mental illnesses in adolescence. Often linked to comorbidity with anxiety disorders, a large proportion of depressed adolescents displays more severe symptoms and poorer response to treatment. Previous longitudinal resting-state fMRI (RS-fMRI) studies of intrinsic functional connectivity (iFC) in depressed adolescents point to dysregulation of underlying neural networks such as the corticolimbic network, including among others the amygdala and frontal regions, which are involved in emotion processing and regulation.
Objectives: This naturalistic study investigates longitudinal changes in resting-state iFC in adolescents with internalising disorders, compared with healthy peers.
Methods: 23 treatment naïve adolescent patients with clinical depression and comorbid anxiety (INT) and 24 healthy controls (HC) participated in RS-fMRI scans at baseline and after three months. Questionnaires measuring anxiety and depression were completed at both timepoints. Imaging analyses were conducted using independent component analysis (ICA) to extract 7 networks, being the default mode, frontoparietal (bilateral), affective, salience, executive control and dorsal attention network. Additional iFC of amygdala subregions, being laterobasal (LB) and centromedial (CM), was investigated using seed-based analyses. To investigate changes over time between groups, voxelwise analyses were conducted using FSL's PALM.
Results: No significant results within ICA defined networks were found. iFC between the left LB amygdala and left frontal pole significantly increased over time in patients and decreased in HC. iFC between the right LB amygdala and right pre- and post-central gyrus also significantly increased over time in patients and decreased in HC, and was significantly associated with reduction in depressive symptoms within patients.
Conclusions: This study provides initial evidence that iFC between the laterobasal amygdala and frontal regions develops differently over time in adolescents with internalising disorders compared to healthy peers and that it is associated with reduction in depressive symptoms.

Disclosure of Interest: None Declared

O0069

Abnormal Neural Activation in Attention-Deficit/Hyperactivity Disorder: A Meta-Analysis of Functional Magnetic Resonance Imaging Studies

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