with the brain cortex, as it has been described in densely granulomated somatotropinomas (2). In one case with T2 hyperintensity, the pituitary mass presented the same imaging characters as multiple brain metastases from a bronchial carcinoïd. In one case, T2 signal was isointense. In 3 cases, tiny millimetric T2 hyperintense images were disseminated within pituitary hyperplasia. In several cases where pituitary MRI was considered as normal, correlation of the patient'age with pituitary size could make suspect an enlarged gland. In a case labeled empty sella, T2MRI signal of the pituitary remnant was hypointense. When coupling T2 and T1 gadolinium enhanced sequences, no pituitary adenoma was visualized and normal pituitary tissue was never identified along with pituitary hyperplasia.
In conclusion, T2 MRI hypointense signal of the pituitary gland is a better hallmark than pituitary hyperplasia for the diagnosis of acromegaly due to
GHRH ectopic secretion. Analysis of T2 MR signal in these cases is essential to avoid unnecessary interventions to the pituitary.
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Genetics and Development (including Gene Regulation)

GENETICS AND DEVELOPMENT AND NON-STEROID HORMONE SIGNALING II

Cross-Species Glucocorticoid-Sensitive Posterior Dentate Gyrus Gene Network: Developing a Polygenic Score Associated to Susceptibility to Depression After Early Life Adversity Exposure in Humans

Danusa Mar Arcego, PhD[1], Nick O'Toole, PhD[1], Jan-Paul Buschdorf, PhD[2], Nirmala Arul Rayan, PhD[2], Barbara Barth, Msc[1], Irina Pokhvisneva, PhD[1], Zihan Wang, Msc[1], Sachin Patel, Msc[1], Euclides José de Mendonça Filho, Msc[3], Randriely Merscher Sobreira de Lima, Ph.D. student[3], Carla Dalmaz, PhD[3], Patricia Pelufo Silveira, MD,PHD[4], Michael Joseph Meaney, PHD[4].
[1]MCGILL UNIV, Montreal, QC, Canada, [2]Singapore Institute for Clinical Genetics, Singapore, Singapore, [3]Universidade Federal do Rio Grande do Sul, Porto Alegre, Brazil, [4]McGill Univ, Montreal, QC, Canada.

MON-722

Exposure to stress during the life-course has consistently been associated with neuropsychological disorders, but the precise role of stress released glucocorticoids remains unclear in this context. We aimed at using hippocampal gene expression data from macaques to identify clusters of genes sensible to glucocorticoid exposure and create a biologically relevant polygenic score to investigate emotional disorders in a child and adult humans exposed to early adversity. RNA-sequencing data from the posterior dentate gyrus (pDG) of adult *Macaca fascicularis* females treated with Betamethasone (glucocorticoid) or saline injections for 8 consecutive days were analyzed from two cohorts: Singapore (reference) and Vietnam (replication) with N=12/each. Weighted gene co-expression network analysis (WGCNA) was used to identify clusters (modules) of co-expressed genes associated with betamethasone. In Singaporean animals, genes were clustered in 52 modules, in which 5 were associated with betamethasone. Two modules were preserved in a replication dataset (Vietnam) and in data from female rats treated with corticosterone for 6 weeks, being the black module (557 genes, P=0.01, r=0.7) the one having the highest correlation with glucocorticoid exposure. Gene ontology analysis (FDR<0.05, Metacore®) revealed that this module is associated with transcription processes. The SNPs derived from genes within the module were used to calculate an expression-based polygenic risk score (ePRS) in the human samples, weighing each SNP by the slope of the association between genotype and gene expression (GTex). Linear regression analysis showed a significant interaction between ePRS and early adversity on the Dominique - major depressive disorder domain (β=1304; P=0.003; N=65) in girls aged 6 years (MAVAN), in which a higher ePRS was associated with more symptoms as the adversity scores increases (simple slope analysis,P=0.004). A comparable interaction between the ePRS and postnatal adversity was also observed in adult women (UK Biobank), in which there was an increased risk for early depression onset (β= -424.3, P=0.04; N=13899). In the adult cohort, whole brain gray matter volume was also associated with differences in the expression of the genes that composed the ePRS-black network (main ePRS effect, β=1865776, P=0.03, N=10902). Glucocorticoid exposure affects a specific group of genes in pDG of adult female macaques and rats, influencing transcriptional processes. Variations in the expression of this gene network sensible to glucocorticoids were associated with susceptibility for the development of depression in girls and adult women exposed to early life adversity. These show the importance of glucocorticoids on the development of depressive symptoms. The gene network affected by glucocorticoids can guide future pharmacological or mechanistic studies in other samples or species.

Reproductive Endocrinology

BASIC MECHANISMS IN REPRODUCTION: FROM BEGINNING TO END

Kisspeptin as a Biomarker for Pregnancy Complications

Maria Phylactou, Dr, MBBS[1], Ali Abbara, MBBS, BSC, PhD[1], Maya Al-Memar, Dr, MBBS, PhD[1], Pei Chia Eng, Dr, MBBS, BSc[1], Alexander N. Comninos, MBBS, BSc, MRCP, PhD[1], Chioma Izzi-Engbeaya, PhD MBBS MRCP (UK)[1], Sophie A. Clarke, MBBS, PhD[1], Edouard Mills, Dr, MBBS, MRes[1], Rans Nadir, BSc[1], Mark Sykes, Dr, MBBS[1], Pacuszka Ewa, BSc[1], Lisa Yang, MBBS[1], Hanine Fourie, MBBS[1], Paul Bech, BSc, PhD[1], Tom Kelsey, BSc, PhD[2], Tom Bourne, MBBS, BSC, PhD[1], Waljit Singh Dhillo, BSc, MBBS, PhD, FRCP, FRCPath, FRCPath[1].
[1]Imperial College London, London, United Kingdom, [2]University of St Andrews, St Andrews, United Kingdom.

OR20-06

Kisspeptin as a biomarker for pregnancy complications
Background:
Placentation (invasion of the placenta into the maternal endometrium) is hypothesised to be critical for healthy placental function and is abnormal in two thirds of miscarriage. Kisspeptin has emerged as a putative regulator