bioactive peptides and exhibit a wide spectrum of tumor behavior from relatively indolent to rapidly progressive. Pituitary tumors represent 20% of intracranial tumors and share some features of NET histo-pathologic morphology, their excess hormone production and some have proposed re-naming pituitary tumors as PitNETs. However there has been no precise cell type composition comparison at the whole genome level in these two types of tumors. To explore intratumoral heterogeneity at a single cell resolution in pituitary and pancreatic NETs, we employed single cell RNA sequencing (scRNA-seq) to analyze in parallel cell populations from surgically resected pituitary tumors (n=4) and pancreatic NETs (pNET, n=2) using a 10x Genomics platform (v3). Using Cell Ranger pipeline for alignment and mapping, we obtained an average of 8,306±2,519 cells/sample with 1,516±822 genes/cell (mean reads/cell 67.9±30K). Seurat v3 was then used for read pre-filtering, normalization, and cluster identification. We identified 5 genes commonly expressed in both pNET and pituitary tumor populations, namely CALY (clathrin light chain binding GO:0032051), SPINT (peptidase inhibitor activity GO:0030414), CHGB (hormone activity GO:0005179), SCG5 (GTP binding GO:0005525) and SEZ6L2. As proof of their oral epidermal embryonic origin, the commonly expressed genes in 4 pituitary tumor samples include pituitary tissue restricted transcription factors (POU1F1, BEX1/2 GO:0033613), GNAS (G-protein beta/gamma-subunit complex binding GO:0031683), NLRP1 (peptidase activator activity involved in apoptotic process GO:0016505), PTN (protein phosphatase regulator activity GO:0019888) and ATP6V1G1 (ATPase binding GO:0051117). In parallel, 71 genes were present at high levels in pNET and involved in molecular functions such as calcium ion binding (HSPA5; ENPP2; C2CD4B; CALR; HSP90B1 GO:0005509) and endopeptidase inhibitor activity (PCSK1N; WFDC2 GO:0004866). Although our exploratory findings are limited to 6 samples, the robust commonly expressed genes within each tumor type clearly separated pituitary and pancreatic neuroendocrine tumors into distinct entities. We did observe conservation of chromogranins and prohormone convertases in these two tumor types, but it only represented a very small portion of overlap in transcriptome in pNETs. In summary, our findings suggest that pituitary and neuroendocrine tumors have only limited common molecular features, and by and large they stand as separate biologic populations. Our observations may begin to provide insight into the differences in tumor progression that are encountered clinically between pituitary tumors and pancreatic NETs.

Diabetes Mellitus and Glucose Metabolism

CLINICAL STUDIES IN OBESITY, DIABETES RISK, AND CARDIOVASCULAR OUTCOMES

Left Ventricular Myocardial Deformation in T2DM Is Associated with Chronic Hyperglycemia but Not Myocardial Perfusion: A Study Based on Magnetic Resonance Imaging

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SAT-620

Background: Diabetic cardiomyopathy is accompanied by left ventricular diastolic dysfunction. Abnormal glucose metabolism plays an important role in the pathogenesis of diabetic cardiomyopathy. However, it's still not clear whether the influence of hyperglycemia on LV dysfunction is directly affects cardiomyocytes or is related to impaired myocardial perfusion. In this work, we focus on investigating the association between HbA1c and myocardial dysfunction, and if it is independent of myocardial perfusion reserve.
Materials and Methods: 64 type 2 diabetic patients were recruited at the endocrine clinic. They are divided into two group, well blood glucose-controlled group (HbA1c<7) and poor glucose-controlled group (HbA1c≥7) T2DM group, according to their HbA1c level. All of the T2DM patients and age-matched healthy volunteers (normal glucose metabolism group, NGM group) underwent CMR to acquire normal values for myocardial strain and perfusion reserve.
Results: Well blood glucose-controlled group owned lower global circumferential PSSR than NGM group (p=0.037). Global circumferential PS (p=0.011), global longitudinal PS (p=0.004), global radial PDSR (p=0.005), circumferential PDSR (p=0.001), longitudinal PDSR (p=0.001), global circumferential PSSR (p=0.049), longitudinal PSSR (p=0.041) were significantly lower in the poor glucose-controlled group compared to the NGM group. In the multivariable linear regression analysis, HbA1c existed in all equations except the global circumferential PSSR equation and $p<0.05$, and Slope, Max SI and Tpeak did not show dependent association with longitudinal and circumferential strain parameters.
Conclusion: In subclinical cardiac dysfunction T2DM patients, diastolic dysfunction is more common, but systolic dysfunction is still exist. Poor blood glucose control which is defined as HbA1c ≥ 7% is an independent risk factor for LV deformation for T2DM patients. Subclinical myocardial dysfunction is not triggered by myocardial perfusion reserve.

Pediatric Endocrinology

PEDIATRIC OBESITY, THYROID, AND CANCER

Diabetic Ketoacidosis at Type 1 Diabetes Diagnosis in Children from a Large Centre (Hangzhou, China)

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MON-107

Objective: To review the clinical symptoms and biochemical parameters associated with diabetic ketoacidosis (DKA) in children newly diagnosed with type 1 diabetes (T1D) in our single medical centre over 10 years. **Methods:** Participants were children aged <16 years diagnosed with T1D between 1 January 2009 and 31 December 2018 at the Children's Hospital, at Zhejiang University School of Medicine (Hangzhou, China). DKA occurrence was assessed by blood gases using pH and bicarbonate. The severity of DKA was categorized according to ISPAD 2014