MON-200
Objective: Aldosterone- and cortisol-producing adrenal tumors (A/CPTs) are considered to be a subtype of primary aldosteronism (PA). The clinical characterizations of these tumors are still unclear, and they are often neglected by clinicians. The aim of this study was to summarize the clinical characterizations of these tumors to reduce the missed diagnosis.

Methods: The clinical, imaging and pathological data of patients with PA admitted to our hospital from January 1, 2013 to December 31, 2016 was reviewed. All the PA patients with a combination of a positive aldosterone-to-renin ratio (ARR) and a positive captopril challenge test (CCT), in whom the dexamethasone inhibition test was performed as well, were included in our study. These patients were divided into two groups, A/CPTs group and simple PA group, according to the function of cortisol secretion. The data of the two groups were compared and analyzed with SPSS 23.0. P<0.05 was statistically significant.

Results: There were 87 patients with PA included in our study, 32 of whom (36.8%) were diagnosed with A/CPTs. In these 32 A/CPTs patients, 31 patients (96.9%) were combined with subclinical Cushing syndrome. Compared to these in simple PA group (n=55), the patients in A/CPTs group (n=32) were elder (53.81±10.70 ys vs 48.42±10.17 ys, P=0.022), with larger diameter of adrenal tumors (1.50cm vs 1.15cm, P=0.001), higher fasting plasma glucose (5.33mmol/L vs 4.99mmol/L, P=0.047), higher serum cortisol levels and lower serum ACTH levels (all P<0.05). 24 patients in A/CPTs group and 23 patients in simple PA group underwent adrenalectomy. 6 patients (25.0%) in A/CPTs group and 3 patients (13.0%) in simple PA group received glucocorticoid replacement therapy after adrenalectomy.

Conclusions: The prevalence of A/CPTs in PA is high. The patients with A/CPTs are mainly combined with subclinical Cushing syndrome, and prone to need glucocorticoid replacement therapy. Therefore, we recommend that all patients with PA should evaluate the function of cortisol secretion, and all patients with A/CPTs should be followed up closely after adrenalectomy to reduce the morbidity of adrenal insufficiency.

Diabetes Mellitus and Glucose Metabolism
CLINICAL AND TRANSLATIONAL STUDIES IN DIABETES
Chronic Unpredictable Environmental Stress May Induce Predisposition to Diabetes Mellitus
Alok Raghuve, Ph.D.
Aligarh Muslim University, Aligarh, India.

MON-648
Title: Chronic Unpredictable Environmental Stress may induce predisposition to diabetes mellitus Objective: Chronic unpredictable environmental stress (CUES) may induce predisposition to diabetes mellitus. Material & Methods: This study investigates the role of CUES on impaired homeostasis. Stressed group mice (n=20) were exposed to CUES for 16 weeks. Weekly body weight, feed consumption, feed efficiency ratio, fasting blood glucose were monitored. Plasma HbA1c, plasma cortisol, plasma epinephrine and plasma insulin, serum lipids, antioxidants and carbohydrate metabolizing enzymes activity were assessed along with DNA damage and histopathological examination of liver, kidney, pancreas, spleen and skeletal muscles. Semi-quantitative expression of IL-4, IL-6 and β-actin was also assessed. Results: Fasting blood
glucose levels & HbA1c in the stressed were significantly higher compared to control (p<0.001). Serum lipids were found insignificantly higher in stressed mice compared to control. Body weights of the stressed mice and feed efficiency ratio were found significant (p<0.001). Plasma corticosterone, plasma epinephrine, HOMA-IR was found to be significantly higher in the stressed group (p<0.001). Plasma insulin level was found to be significantly lower in the stressed group (p< 0.001). Significant changes were observed in antioxidants level, carbohydrate metabolizing enzymes activity, peripheral tissues and DNA integrity. Expression of IL-4, IL-6 was found significantly higher in the stressed group. **Conclusions**: CUES initiates pathogenesis of diabetes.

**Reproductive Endocrinology**

**FEMALE REPRODUCTION: BASIC MECHANISMS**

**Dynamics of the Transcriptome in Rat Granulosa Cells Exposed to Different Follicle-Stimulating Hormone (FSH) Glycosylation Variants as Revealed by RNA-Seq/New Generation Sequencing (NGS).**

Jesús Espinal-Enriquez, Ph.D.1, Guillermo De-Anda-Jáuregui, Ph.D.2, Georgina Hernández-Montes, Ph.D.3, Saúl Lira-Albarrán, M.D., D.Sc.4, Teresa Zarikhán, M.Sc.5, Rubén Gutiérrez-Sagal, Ph.D.2, Rosa G. Reboliar-Vega, Ph.D.3, George Russell Bousfield, Ph.D.4, Viktor Y. Butnev, Ph.D.4, Enrique Hernández-Lemus, PhD4, Alfredo Ulloa-Aguirre, M.D., D.Sc.4.

1. Instituto Nacional de Medicina Genómica. Mexico City, Mexico, 2. National University of Mexico (UNAM), Mexico City, Mexico, 3. Instituto Nacional de Ciencias Médicas y Nutrición “S. L. C.,” Mexico City, Mexico, 4. Wichita State University, Wichita, KS, USA.

**MON-023**

Follicle-stimulating hormone exists as different major glycoforms defined by distinct glycosylation patterns of the hormone-specific β-subunit. It has been documented that variations in glycosylation confer differential biological effects to the glycoforms when multiple in vitro biochemical readings are analyzed. We here applied Next Generation Sequencing (NGS) to explore changes in the transcriptome of rat granulosa cells exposed for 0, 6, and 12 h to 100 ng/ml of four highly purified FSH glycoforms, each exhibiting distinctly different glycosylation patterns: human pituitary FSH21 and equine FSH (eFSH) (hypoglycosylated), and human FSH24 and CHO cell-derived human recombinant FSH (rFSH) (fully-glycosylated). Total RNA from triplicate incubations was prepared from FSH glycoform-exposed cultured granulosa cells obtained from DES-pretreated immature female rats, and total RNA libraries were sequenced in a HighSeq 2500 sequencer (2 x 125 bp paired-end format, 10–15 x 10^6 reads/sample). The computational workflow was focused on investigating differences among the four FSH glycoforms at three levels: gene expression (Salmon and DESeq2 bioinformatic tools), enriched biological processes (DAVID tool), and perturbed pathways (GAGE tool). Among the top 200 differentially expressed genes, only 4 (0.6%) were shared by all 4 glycoforms at 6 h, whereas 118 genes (40%) were shared at 12 h. At 6 h, up-regulated genes in rFSH were associated with cell response, angiogenesis, extracellular matrix organization, and mitosis; eFSH with sex hormones (shared with FSH23); FSH21 with cellular response and response to drugs (shared with rFSH); and FSH24 with cAMP-related processes. There were more shared biological processes at...