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.

Neuroendocrinology and Pituitary

CASE REPORTS IN UNUSUAL PATHOLOGIES IN THE PITUITARY

A Rare Case of Atypical Rhaboid Teratoid Tumour with Germinoma Differentiation in a 59 Year Old Woman

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Atypical teratoid/rhabdoid tumours (ATRT) are a rare class of central nervous system malignant tumours which are comprised of elements of ectoderm and mesoderm germ-cell layers, but exhibit microscopic similarity to skeletal muscle. These tumours are more commonly seen in pediatric patients, with few case reports recently describing adult patients with this condition, in particular middle-aged women.[1–3] We present the case of a previously healthy 59-year-old woman who was found incidentally to have a pituitary mass on CT head, with retrospective symptoms of headaches, polyuria, polydipsia, diplopia, and low blood pressure. At presentation, she was found biochemically to have pan-hypopituitarism with a left cranial nerve six deficit, with an MRI depicting a 19.5 x 22 x 11 mm suprasellar mass extending into the infundibulum and hypothalamus, with displacement of the optic chiasm; repeat imaging ruled out apoplexy. She was started on supplemental levothyroxine and hydrocortisone replacement therapy, and sent for urgent transsphenoidal resection, which was complicated afterwards by hypernatremia from diabetes insipidus. Preliminary reports were suggestive of germinoma given the diffuse presence of Oct 3/4 and C-kit, with a proliferation index of 99%; further cytology of lumbar puncture revealed no malignant cells. However, upon further pathological analysis, her tumour demonstrated loss of INI-1 expression, which is diagnostic of ATRT. Given the mixed features on immunohistochemistry, the final diagnosis was concluded as an atypical teratoid/rhabdoid tumour of the sella turcica with germinoma differentiation. A multidisciplinary approach consisted of initial radiotherapy, with chemotherapy targeted towards a germinoma-type tumour, and pituitary hormone replacement including treatment for central diabetes insipidus. This represents a unique case of a rare tumour with germinoma differentiation in an older patient that has not been previously reported.

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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).

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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 FSH^{21} and equine FSH (*e*FSH) (hypoglycosylated), and human FSH^{24} and CHO cell-derived human recombinant FSH (*rec*FSH) (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 *rec*FSH were associated with cell response, angiogenesis, extracellular matrix organization, and mitosis; *e*FSH with sex hormones (shared with FSH^{21}); FSH^{21} with cellular response and response to drugs (shared with *rec*FSH); and FSH^{24} with cAMP-related processes. There were more shared biological processes at