Conclusion: Melatonin could effectively reduce inflammation and apoptosis leading to improve the ovaries transplantation in mice.

Keywords: Apoptosis, Inflammation, Melatoin, Ovary, Autotransplantation

O26: New insight into the molecular diagnosis of male infertility

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Background: Spermatogenesis is a complex process of proliferation and differentiation of male germ cells which regulated by many genes in transcription and post transcription level. MicroRNAs (miRNAs) are small non-coding RNA molecule function as post-transcriptional regulators of gene expression. They play a key role in regulation of early and late spermatogenesis, and reproduction. In this study, we investigate the role of miRNAs in infertile males.

Methods: The patients were assigned to five groups based on semen analysis (n=55), normozoospermic patients (N), moderate oligoasthenoteratozoospermic (MOAT), severe oligoasthenoteratozoospermic patients (SOAT), obstructive azoospermia (OA) and nonobstructive azoospermia (NOA). The expression of miR-34c and target gene P53 (tumor suppressor) was investigated using quantitative RT-PCR. In addition, Malondialdehyde (MDA) and DNA fragmentation were measured. Network analysis was performed using Pathway Studio web tool (Elsevier). Databased of gene, protein, microRNA, and small molecule interaction of Pathway Studio were constructed using Medscan language programming to highlight the possible role of miR- 34c and P53 gene. The ethics committee approved this consent procedure (registered number 66000116 at ethic committee of TUMA).

Result: The results revealed statistically significant increased expression of miR-34c in moderate oligoasthenoteratozoospermic, nonobstructive azoospermia and an increased expression of p53 in moderate oligoasthenoteratozoospermic, severe oligoasthenoteratozoospermic and nonobstructive azoospermia males. Also, the percentage of DNA fragmentation and oxidative stress was significantly higher in infertile groups (MOAT and SOAT)

Conclusion: These findings provide a novel molecular mechanism of gen regulation during cell-cycle and apoptosis in sperm which give a new regulatory insight into the molecular diagnosis of male infertility.

Keywords: miRNAs, Normozoospermic, Oligoasthenoteratozoospermic, Pathway Studio., Sperm

O27: An opioid-mediated polycystic ovary in Wistar rats

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Background: Polycystic ovary syndrome (PCOS) is a common endocrine disorder that affects 6-10 percent of women in fertility age. The development mechanism of PCOS has been widely studied in laboratory animals. However, the role of the opioid system on ventro-medial hypothalamus is still not clear. The aim of present study was to investigate the effect of morphine in this part on the ovary of Wistar rats.

Methods: Female Wistar rats, weighing 220-250g (in the diestrus phase) were cannulated under anesthetic by a stereotaxic device in the ventromedial hypothalamus (VMH) and spent a period of recovery. Afterwards, they were divided into four groups. The control group only received 1 µL of saline into their VMH. The group which was treated by morphine microinjection only received 0.1 to 0.4 µg of this opioid substance. The two remaining groups were treated by naloxone microinjection, and morphine injection preceded by naloxone pre-injection, respectively, in order to investigate the mediating role of opioid receptors. Three days later, the rats were killed and biopsies of ovaries were prepared for incision and staining. The results were analyzed by ANOVA test. Further analysis of the differences between the groups was conducted by means of Tukey's HSD post-hoc. p

Result: According to the findings, receiving morphine into VMH led to developing PCOS (p

Conclusion: As the competing antagonist of morphine, naloxone prevented the effect of morphine on the axis of HPG. This would make possible an opioid mediation in the occurrence of the symptoms of PCOS.

Keywords: Female rat, Naloxone, Polycystic ovary syndrome, Ventro-medial hypothalamus, Morphine

O28: Proteomic characteristics of human sperm after freezing–thawing treatment

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Background: Despite protective capacity of the seminal fluid during cryopreservation, sperm preparation methods should use to select mature and functional spermatozoa with low rates of apoptosis before cryopreservation. On the other hand, there is an association between dysfunctional spermatozoa due to cryoinjury and protein changes. The application of high-throughput proteomics to study the human sperm cell allows us to identify proteomic changes in human sperm cells throughout the cryopreservation.

Methods: we selected semen samples from normozoospermic men (n=36), after processing sperm with PureSperm gradient, each sample was divided into 2 aliquots: fresh and cryopreserved groups. Sperm quality parameters (motility ,apoptosis status, DNA fragmentation) evaluated after freezing-thawing, then proteins extracted for two different experimental conditions. Extracted proteins from each group were pooled and labeled with tandem mass tags (TMTs) coupled to LC-MS/MS. Bioinformatic analyses were performed using DAVID software. Candidate proteins were further validated by western blot analysis.

Result: We detected 2,912 proteins in human sperm where 238 and 191 proteins were respectively up and down-regulated in cryopreserved sperm compared to fresh sperm .The main down-regulated proteins were involved in metabolic processes and sperm-egg recognition.

Conclusion: Several proteins detected as deregulated could be candidates for diagnostic markers in pathogenic mechanisms involved in cryopreservation and given the unknown impact of some of these proteins on offspring health .This is the first study to compare protein levels in fresh and cryopreserved sperm without seminal plasma using the TMT technology coupled to LC-MS/MS.

Keywords: Sperm, Cryopreservation, Proteomics, Seminal plasma

O29: Detection of DNA fragmentation in infertile men with immotile short tail sperm (ISTS) referred to Royan institute

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