

**Sociedad de
Biología de Cuyo**

**XXXV Reunión
Científica Anual**

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**Villa de Merlo
San Luis**



Libro de Resúmenes

**XXXV Reunión Científica Anual de la
Sociedad de Biología de Cuyo**



**Del 06 y 07 de Diciembre de 2017
Villa de Merlo- San Luis- Argentina**

In memoriam



Dr. Egualdo Oscar Zangheri. (1931-2017)

Poco antes del inicio de la XXXV Reunión Científica Anual de la Sociedad de Biología de Cuyo, falleció en la Ciudad de Mendoza, el Dr. E. Oscar Zangheri, quien fuera miembro de la comisión directiva que refundó la Sociedad de Biología de Cuyo en el año 1973.

Oscar Zangheri fue Profesor Titular de Fisiología en la Facultad de Ciencias Médicas de la Universidad Nacional de Cuyo, realizando además, como investigador del CONICET, importantes e innumerables aportes científicos en el área de la hematología, como la demostración del origen renal de la eritropoyetina, experiencia que cristalizó como autor en varios capítulos del libro “Fisiología Humana” del Premio Nobel Bernardo A. Houssay.

Como docente y colega fue un modelo de maestro y amigo, cuya hombría de bien sembró valores éticos y morales que lo destacaron por su solidaridad ejemplar.

Mendocino por adopción (ya que nació en Córdoba y vivió allí hasta los 12 años), fue un entusiasta colaborador de la Sociedad de Biología de Cuyo. Su disposición y dedicación a su trabajo, así como el compromiso con nuestra sociedad le hacen merecedor de este libro, en su memoria.

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rediae (obtained from digestive gland homogenates), and cercariae (obtained by isolation of host under constant light) showed two morphotypes of parasites. The first morphotype shared morphological characters with species of the Plagiorchida order (xiphidiocercariae armatae opisthioglyphe-type) while the second morphotype showed characters of the Echinostomatidae family (belonging Echinostomida order). A sequence corresponding to the ITS1 (an internal transcribed spacer located between RNA 18S and RNA 5.8S ribosomal genes) was amplified (PCR) using DNA extracted from digestive gland as template. Sequencing and phylogenetic reconstruction by maximum likelihood were made. Two sequences were found: one of them (~900 bp) was akin to the Xiphidiata order, while the other (~700 bp) was related to Echinostomatidae family. The latter taxon has parasitic, symbiotic relationships with prosobranch snails. Although the morphological and molecular findings were congruent, other molecular studies are being conducted for the identification of these parasites at species level.

155 AGING ABOLISHES CIRCADIAN RHYTHMS OF ROR α AND ANTIOXIDANT ENZYMES EXPRESSION IN TEMPORAL CORTEX OF FREE RUNNING RATS

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ROR α is a transcription factor that binds RORE motifs in the promoter of clock Bmal1 and other target genes. Antioxidant enzymes contribute to the cellular redox state which is crucial for the molecular clock function. Previously, we showed antioxidant enzymes activity follow a daily variation in temporal cortex (TC), which was abolished in aged rats. Herein we aimed: 1) to investigate endogenous rhythms of Cat, Gpx and Nrf2 genes expression and ROR α protein levels in rat TC, and 2) to evaluate whether aging could affect those temporal patterns. Three- and 22-month-old male Holtzman rats were maintained under constant darkness for 15 days before the experiment, in order to validate the endogenous nature of circadian rhythms. TC samples were isolated every 4 h during a 24h period. ROR α protein levels were assessed by immunoblotting. Cat, Gpx and Nrf2 mRNA levels were determined by RT-PCR. Specific softwares were used to circadian analysis. We observed circadian endogenous rhythms of ROR α , Cat and Gpx expression in the TC of young free running rats (Chronos fit, $p < 0.05$, $p < 0.001$ and $p < 0.05$, respectively). We found Ebox and RORE sites in the Cat and Gpx genes regulatory regions. ROR α rhythm's acrophase occurs at the beginning of the subjective day, preceding Cat and Gpx mRNA peaks. Consistent with previous results, aging abolishes ROR α , Cat, and Gpx circadian rhythms in TC. Interestingly, Nrf2 gene expression becomes rhythmic in the TC of aged rats. Our observations would contribute to the knowledge of circadian alterations in TC of the aged brain.

156 MORPHOFUNCTIONAL ANALYSIS OF CREB HETEROGENEITY IN THE RAT PINEAL GLAND

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Adaptation to environmental changes is facilitated by the endogenous circadian clock. The pineal gland (PG) via the nocturnal melatonin production is a key effector and regulator of the mammalian circadian timing system. The PG is under sympathetic regulation by local norepinephrine (NE) release from the conary nerves at night. In rat, the NE-dependent phosphorylation of the transcription factor CREB initiates the expression of the aa-nat gene, which encodes for one of the pivotal enzymes in the melatonin synthesis. To challenge the well-accepted concept of pineal homogeneity and to determine if a spatiotemporal dynamism of CREB occurs within the PG, we analyzed and quantified the protein levels at different ZTs (Zeitgeber time; L:D 12:12) in adult naive, ganglionectomized (GCSx) and sham-operated rats. We performed immunohistochemistry (IHC) in PG sections followed by confocal microscopy, and morphometric and statistical analyses. CREB was found in pinealocyte nuclei at ZT6, 10, 14, 18 and 22. Immunoreactive granules of variable size and different nuclear distribution patterns were observed. The fluorescence intensity of CREB varied among the ZTs, with higher values during the night-time (ZT14 and ZT18). Although the nuclear area was significantly higher at ZT14, the relative area occupied by CREB within the pinealocyte nuclei increased at night. The disruption of the circadian circuit by GCSx reduced both the abundance and the area occupied by CREB at ZT14. These findings suggest a NE effect over CREB availability and distribution in the pinealocyte nuclei and therefore over its transcriptional capacity.