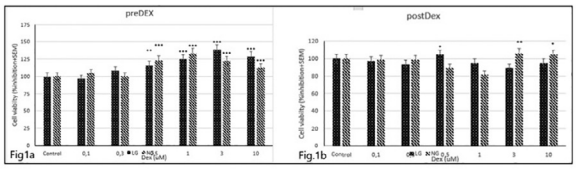

Fig 1. The effect of different concentrations of dexmedetomidine on cell viability (MTT) in Nb2A cells incubated in low- and normal-glucose medium and exposed to hypoxic conditions and 4% sevoflurane.

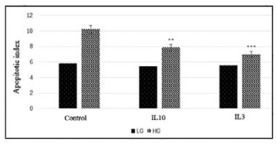

Fig.2. The apoptotic index in the pre-DEX group at 3 and 10 μM concentrations in Nb2A cells exposed to hypoxic conditions and 4% sevoflurane.

Results and conclusions: Results: Dexmedetomidine administered before hypoxic conditions increased cell viability at 0.5, 1, 3, and 10 μM concentrations in both low and normal-glucose medium in cells exposed to OD and 4%sevoflurane ($p<0.01$, Figure 1a). Dexmedetomidine also increased cell viability after hypoxia, but only at 3 and 10 μM concentrations in normal-glucose medium and 0.5 μM concentration in low glucose medium. The apoptotic index and IL1 ß were decreased significantly in the pre-DEX group at 3 and 10 μM concentrations ($p<0.001$), Fig. 2.

Conclusions: Dexmedetomidine increased the cell viability at 0.5, 1, 3, and 10 μM concentrations in both low and normal-glucose medium in cells exposed to OD and 4%sevoflurane ($p<0.01$). Before injury treatment with 3 and 10 μM of DEX decreased apoptosis induced by hypoxia-ischemia in NB2a cells. Dexmedetomidine can reduce the damage caused by OGD and Sevoflurane by utilizing its antiapoptotic properties.

39th EACTAIC Annual Congress
FREIBURG (GERMANY), 23/10/2024 - 25/10/2024
ID PAX: 131 - ID ABS: 87 - ID ABS WEB: 141214
Topic: V. Multidisciplinary teamwork

Sepsis after cardiac surgery: preliminary analysis of cytokines gene expression

Rosa Paola Radice[1,*], Giuseppe Martelli[1], Mauro D'Amora[2], Pierpaolo Dambruoso[3], Domenico Paparella[3], Raffaele Mandarano[4], Giuseppe Olivo[4], Massimo Scolaro[5], Domenico Sarubbi[6], Alessandro Strumia[6], Maria Calabrese[6], Andrea Scarpigliati[6], Francesco Greco[8], Mary Nardi[8], Stefano Beccaria[9], Andrea Costamagna[10], Luca Brazzi[10], Pasquale Raimondo[7], Gianluca Paternoster[2]

[1]*Università degli studi della Basilicata, Potenza, ITALY*
[2]*AOR San Carlo, Potenza, ITALY*
[3]*Ospedale Santa Maria, Bari, ITALY*
[4]*Cardioanestesia Careggi, Firenze, ITALY*
[5]*Ospedale del cuore Gaetano Pasquerucci, Massa, ITALY*
[6]*Policlinico campus Biomedico / Policlinico Gemelli, Roma, ITALY*
[7]*Policlinico di Bari, Bari, ITALY*
[8]*Casa Cura Sofferenza, San Giovanni rotondo, ITALY*
[9]*A.O Ordine Mauriziano, Torino, ITALY*
[10]*Ospedale Molinette, Torino, ITALY*

Objective: According to SSC Sepsis is defined as "life-threatening organ dysfunction caused by a dysregulated host response to infection".Sepsis remains one of the leading causes of morbidity and mortality (17-65 %) worldwide and it remains a challenge to be defined and for which an appropriate cure is desired. Different studies have been conducted on genes coding for inflammatory cytokines that could predispose to the development of sepsis [e.g., IL-10 and PD1]. This multicentric observational prospective study aims to evaluate the genetic expression kinetics of two molecules involved in the inflammatory process, IL10 and PD1, to search for a possible molecular marker predictive of the development of sepsis

Design and method: 162 patients scheduled for planned cardiac surgery were enrolled in the study. For each patient, 4 blood samples have been collected at 4 different time points. Patients were defined as septic according to SSC guidelines. From each blood sample, RNA was extracted and used for a qPCR.

Results and conclusions: Of 162 patients enrolled (100M and 62F), 25 (15%) developed sepsis (15M and 10F). The results show that the CBP time was longer in septic patients (143 Vs. 105 means in minutes) than in Clamping time (89.6 Vs 76.29 mim). The expression of IL10 highlights how 30 minutes after the start of the intervention, septic patients showed much lower levels of IL10 expression ($p<0.05$). This result, however, is reversed upon entry into the ICU. The same results are confirmed by the expression of PD1, which appears to be deactivated in septic patients ($p<0.05$). This expression kinetics demonstrates how patients who developed sepsis show a dysregulation of the immune response, which leads to decompensation of the immune system, which is thus unable to respond adequately. These data suggest how CBP and Clamping time influence more patients genetically predisposed to sepsis.

39th EACTAIC Annual Congress, FREIBURG (GERMANY), 23/10/2024 - 25/10/2024, ID PAX: 194 - ID ABS: 121 - ID ABS WEB: 141515Topic: W. Early Recovery after Surgery

USE OF FAST TRACK, CARBOHYDRATE PRELOAD AND REGIONAL TECHNIQUES IN ADULT ELECTIVE CARDIAC SURGICAL PATIENTS IN THE UNITED KINGDOM

Shin Chia[1,*], George Perrett[2], Vlad Shevchenko[2], Peter Wicks[2]