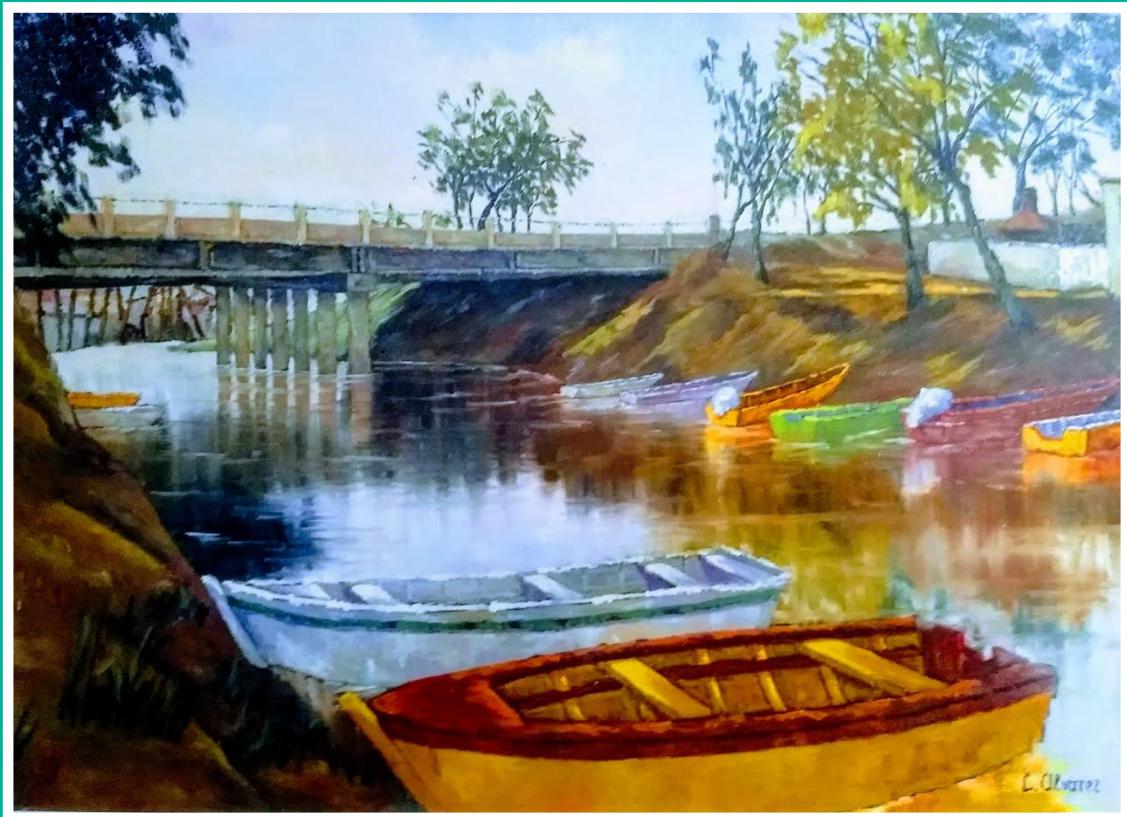


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# **REUNIÓN DE SOCIEDADES DE BIOCIENCIAS 2020**

**LXV REUNIÓN ANUAL DE LA  
SOCIEDAD ARGENTINA DE INVESTIGACIÓN CLÍNICA (SAIC)**

**LXVIII REUNIÓN ANUAL DE LA  
SOCIEDAD ARGENTINA DE INMUNOLOGÍA (SAI)**

**REUNIÓN ANUAL DE LA  
SOCIEDAD ARGENTINA DE FISIOLOGÍA (SAFIS)**

**10-13 de noviembre de 2020**

**EDITORES RESPONSABLES**  
María Cristina Carrillo  
Analía Trevani  
Maria Cecilia Larocca

# **ANNUAL MEETING OF BIOSCIENCE SOCIETIES 2020**

**LXV ANNUAL MEETING OF  
SOCIEDAD ARGENTINA DE INVESTIGACIÓN CLÍNICA (SAIC)**

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**ANNUAL MEETING OF  
SOCIEDAD ARGENTINA DE FISIOLOGÍA (SAFIS)**

**November 10-13, 2020**

**RESPONSIBLE EDITORS**  
María Cristina Carrillo  
Analía Trevani  
Maria Cecilia Larocca

1+CD4+ T cells. The aim of our work is to characterize the phenotype of regulatory PB and the mediators involved in the PB-Tcell interactions. Therefore, B6 mice were infected with *T. cruzi* and splenic, lymph node and bone marrow (BM) lymphocytes were evaluated by FACS at different days post infection (dpi). The 99% of splenic PB expressed high levels of PD-L1 and CD39 until day 23pi and this frequency was significantly reduced from day 28pi ( $p < 0.005$ ). Only the 15% of BM-ASC from mice in the chronic phase of infection (130dpi) expressed high levels of PD-L1 and CD39. Splenic PD-L1<sup>hi</sup>CD39<sup>hi</sup> PB also expressed high levels of CXCR4, MHCII, CD80, CD86 and Ki-67<sup>+</sup> and produced IL-21, IL-6 and IL-10, probably conditioning T-helper response. In addition, we found CXCR5<sup>+</sup> and CXCR5<sup>neg</sup>P-D1+ICOS+Bcl-6+CD4+Tcell populations in spleen of infected mice, which produce TNF, IFNγ, IL-4, IL-6, IL-21, probably sustaining PB response since infected Bcl-6<sup>fl/fl</sup>CD23<sup>Cre</sup> mice did not exhibit this ASC population. The CXCR5<sup>neg</sup>Tfh-like population could be located in the EF-area and could be interacting with PB, either collaborating with ASC or being regulated by them.

Supported by ANPCYT, CONICET, NIAID-RAI116432A

**379. (248) B CELLS ACQUIRE A UNIQUE AND DIFFERENTIAL TRANSCRIPTOMIC PROFILE DURING PREGNANCY IN MICE**

Natalin Valeff<sup>1</sup>, Marcos Dibo<sup>1</sup>, Agustina Dimarzio<sup>1</sup>, Lorena Juriol<sup>1</sup>, Martín Abba<sup>2</sup>, María Silvia Ventimiglia<sup>1</sup>, Federico Jensen<sup>1</sup>

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Pregnancy is an intriguing state of double compromise where maternal immune system must undergo certain adaptations to tolerate the semi-allogeneic fetus and fight pathogens. B cells are key components of the adaptive immunity, responsible for humoral immune response. There is solid evidence that pregnancy induces strong modifications in B cell development and function. Hence, our aim was to characterize the transcriptomic profile of B cells during pregnancy in mice. We performed a genome-wide transcriptome profiling on isolated splenic B cells from pregnant (P) and non-pregnant (NP) mice. We identified 1136 genes with differential expression in B cells from P mice compared to NP animals ( $\approx 1.5$ -2fold changes, Limma eBayes test,  $p < 0.0001$ ,  $n=4$ ). For biological interpretation we performed a functional enrichment analysis with InnateDB source (<http://www.innatedb.com/>). Significantly over-represented (ORA) gene ontology (GO) terms and biological pathways showed up-regulation on DNA replication and cell cycle nodes, while down-regulated genes were grouped into an immune response node (hypergeometric algorithm:  $FC > 1.5$ ; BH multiple test correction:  $p < 0.05$ ,  $FDR < 0.05$ ). Within the immune response node, B cell activation, antigen processing and presentation, B cell differentiation, cytokine and TLR mediated signaling pathways were downregulated in B cells from P compared to NP mice ( $p < 0.05$ ). Diminished mRNA expression levels of key genes implicated on these processes were confirmed by qPCR (Unpaired-t-test, one-tailed,  $p < 0.05$ ,  $n=8$ ). Differential mRNA expression pattern could traduce in a diminished capacity of B cells to differentiate, proliferate, and to produce cytokines and antibodies in response to antigens. Our results strongly suggest that B cells acquire a state of hyporesponsiveness during pregnancy, most probably to tolerate the semi-allogeneic fetus. However, this could also break new paths for understanding why pregnant women are at higher risk for certain infections.

**380. (250) INFLAMMATORY RESPONSES AT THE BOUNDARY BETWEEN THE HOST AND THE WORLD BEYOND: THE DILEMMA OF INFECTION VERSUS COLONIZATION FROM A TONSILLAR PERSPECTIVE**

Sarmiento Varón L<sup>1</sup>, De Rosa J<sup>1</sup>, Fernández PM<sup>1,2</sup>, Arabolaza ME<sup>3</sup>, Paoli BP<sup>3</sup>, Vay C, Barberis CM<sup>4</sup>, Arana EI<sup>1,2</sup>

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Obstructive sleep apnoea (OSAS) is a syndrome suffered by children with hypertrophied tonsils. We have previously demonstrated that these tonsils present a defective Breg compartment. Here, we extend those findings by evidencing the inflammatory cytokine pattern of tonsillar mononuclear cells (TMC) and investigating the grounds of such profile. OSAS TMC were the only cells used for this work. We showed the ability of Bcs to promote the loss of immune homeostatic control by promptly producing TNFa. Using FACS, we determined TNFa production by stimulated TMC in culture. Upon 24 hours, Bcs represented the majority of TNFa<sup>+</sup> cells ( $52.4\% \pm SEM 4.2\%$  CD20<sup>+/down</sup> cells vs  $41.7\% \pm SEM 4.0\%$  CD3<sup>+</sup> cells,  $p < 0.05$ ). Conversely, at the same time point, IL17 was produced primarily by CD4<sup>+</sup> T cells (Th17) which comprised 90% of the IL17<sup>+</sup> population. Also at 24 hs post stimulation, two thirds of the Th17 population ( $59\% \pm SEM 4\%$ ) co-expressed TNFa. Despite the pro-inflammatory profile displayed by TMC in culture, OSAS has long been considered of non-infectious etiology. We cultured the core tonsillar tissue of 31 children and identified 89 bacterial species by MALDI-TOF MS. The species identified had been previously found either causing ENT pathology or as harmless local flora, both situations in competent hosts. Pathogens differ from commensals in being able to penetrate the epithelial barriers. Hence, we performed fluorescence *in situ* hybridization (FISH) with a universal eubacterial (EUB338) probe followed by immune-fluorescence staining, on cryo-sections from excised tonsils. By confocal microscopy, we confirmed bacterial presence within the lymphoid compartment from OSAS biopsies. To conclude, while we cannot ascertain that the microorganisms detected *in situ* as well as through culture are the initiators of the ongoing inflammatory response characteristic of OSAS, the chronification of the process must be related to the evidenced bacterial spreading beyond the normal boundaries.

**381. (282) A NANOSTRUCTURE OF ASCORBYL PALMITATE USED AS VACCINE PLATFORM IMPROVE ANTIGEN-SPECIFIC MEMORY RESPONSE AND RETAINS THE ANTIGEN AT THE INJECTION SITE**

Ruiz Moreno, F<sup>1,2</sup>; Marín, C<sup>1,2</sup>; Dho, N<sup>1,2</sup>; Pascual, M<sup>1,2</sup>; Allemandil, D<sup>3,4</sup>; Palma, S<sup>3,4</sup>; Pistoresi-Palencia, M C<sup>1,2</sup>; Morón, G<sup>1,2</sup>; Maletto, B<sup>1,2</sup>.

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Previously, we demonstrated that the nanoformulation of OVA and CpG-ODN with a nanostructure formed by self-assembly of 6-O-ascorbyl palmitate (Coa-ASC16) elicited immune response superior to those induced by the soluble counterpart. Here, we studied the effects of various formulations of vaccine components on antigen-specific memory response and on antigen persistence at injection site. Mice were subcutaneously immunized with a single-dose of OVA and CpG-ODN nanoformulated with Coa-ASC16 (OCC), with OVA and CpG-ODN in solution (OC) prepared to room temperature (RT), with OVA and CpG-ODN solution heated and then cooled down to RT (OC<sub>0</sub>), with OVA solution heated and then cooled