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LXVI REUNIÓN ANUAL DE LA SOCIEDAD ARGENTINA DE INVESTIGACIÓN CLÍNICA (SAIC)

LXIX REUNIÓN ANUAL DE LA SOCIEDAD ARGENTINA DE INMUNOLOGÍA (SAI)

LIII REUNIÓN ANUAL DE LA ASOCIACIÓN ARGENTINA DE FARMACOLOGÍA EXPERIMENTAL (AAFE)

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17-20 de noviembre de 2021

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PCR) and dnaA gene (real time PCR by Taqman probes). Frequency of Tpp47-positive samples was 47%, while dnaA-positive was 94%. Also, nested PCR for the TP0136, TP0548, TP0705 and 23s genes were performed. The sequences were sequenced by commercial kit (BigDye) in a genetic analyzer (3500 analyzer).Then, edition and alignment were performed compared to the reference sequences of cluster SS14 (CP004011.1), Nichols (CP004010.2) and Escherichia coli 23s rRNA genes at the positions 2058 and 2059 (V00331) for macrolide resistant mutation. As adults in Argentina, the Nichols clade was greater than 10% and macrolide resistant mutation (A2058G mutation in 1 patient) was nearly 10%, although in our pediatric cases the prevalence of Nichols clade was higher (57%) that the reported. Among patients, positive PCR corroborate active lesions while clade and macrolide resistant evaluation shares similarity with studies in adults in Argentina.

158. (349) **CHARACTERIZATION OF SARS-COV-2 INFECTION USING RT-PCR IN SALIVA SAMPLES AND ACE2 GENOTYPING**

Guillermo Alberto Keller[1,2], Elizabeth Ruth García[1], Ivana Colaianni[1], Julian Bartolomé[1], Luciana Madeo[1], Kian Ghorbani[1], Hector Enrique Di Salvo[1], Guillermo Bramuglia[2], Guillermo Di Girolamo[2].

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Introduction: New biological matrices (i.e. self-collected saliva) has been postulated as a strategy to massify testing for SARS-CoV-2. In adittion, it has been shown that SARS-CoV-2 uses the ACE2 protein as a receptor to enter host cells, and although genetic variants are known, their frequency has not been described in the local population.

Methods: Nasopharyngeal swabs (reference control) and saliva samples were processed by RT-PCR for the detection of SARS-CoV-2. An additional blood sample was used to genotype the ACE2 gene variants 2158A> G (N720D, rs41303171) and 631G> A (G211R, rs148771870).

Results: 95 patients were included. The analysis of the characteristics of the studied population showed an average age of 48±22 years. The time between the onset of symptoms and the hospital evaluation was 4±2 days. A high correlation was obtained between nasopharyngeal swab and saliva obtained using the column extraction methodology, with an analytical sensitivity of 92%. The disaggregated analysis based on population characteristics showed greater sensitivity in patients with more severe symptoms (requiring hospitalization and high-flow oxygen) and long lasting symptoms at the time of consultation (> 2 days). Saliva samples showed higher Cycle threshold (Ct) amplification results compared to nasopharyngeal swab samples. By RT-PCR, the amplification cut-off points are between 37-40 cycles. Several Saliva samples, although "detectable" (Ct <37), amplified at higher cycles (around 5 cycles) compared to nasopharyngeal swab samples. Analysis of the variants of the ACE2 gene show the wild-type form for 2158A>G and 631G>A in all the cases analyzed.

Discussion: The detection of SARS-CoV-2 in saliva seems to be an appropriate method for the diagnosis of COVID-19, presenting excellent sensitivity, which increases depending on the severity and duration of the condition. ACE2 genetic variants do not appear to be common in the local population.

159. (392) **IMPLEMENTATION OF AN EPIDEMIOLOGICAL SURVEILLANCE STRATEGY FOR COVID-19 FOCUSED ON GROUPS AT HIGH RISK OF SARS-COV-2 INFECTION**

María del C Esandi1, Joel Marinovich2, Ignacio Bergé1, Nicolás A García3, Olga L German1, Victoria Ayala1, Fermín Sierra2, María G. Serralunga4, María E. Esandi5, Marta Del Valle2 and Cecilia Bouzat1.

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The COVID-19 pandemic has been a challenge to implement strategies to mitigate the transmission of the SARS-CoV-2 virus. Asymptomatic transmission among healthcare workers (HCWs) at the front line of care is particularly concerning due to the potential emergence of outbreaks at healthcare centers. With the final goal of early identification and isolation of asymptomatic infected HCWs, we validated a pooled-sample screening and assessed implementation outcomes and results of an epidemiological surveillance strategy carried out during a 12-month period at public health institutions in Bahía Blanca. To develop and validate a coronavirus detection method, RNA was extracted from nasopharyngeal swabs and identification of the viral *E* gene was done by an "in-house" RT-qPCR using Taqman probes and the human gene *RNAseP* as a control. Validation against a commercial kit demonstrated high sensibility and specificity of our test (95%, IC 95%: [85%-100%]). To increase our testing capacity, we validated sample pooling (n= 5) prior to RNA extraction. The results showed a sensibility of 73% (IC 95%: [46%-99%]) and specificity of 100% against individuals. A tailor-made software called "VIGI-COVID" was designed to properly manage data. A prospective cohort study was conducted since 15/09/20 to 15/09/21. 860 HCWs were included in the epidemiological surveillance and 1765 swabs were performed. The annual cumulative incidence was 2,30% IC95% [1,26% - 3,39%] (20/860), and 43% of the 860 HCWs were swabbed more than once. Our study demonstrated the utility of comprehensive screening of asymptomatic HCWs during the COVID19 pandemic. Early identification and isolation of infected HCWs prevent the onward transmission of SARS-CoV-2, reducing the risk of healthcare-associated outbreaks.

160. (413) **INTRACELLULAR HISTONE H2A IS RECOGNIZED BY CE AND OTHER PARASITOSIS IMMUNE SERA**

Facundo Agüero[1,2], Andrea Maglioco[1,2], María Pía Valacco[3], Alejandra Juárez Valdez[1], Margot Paulino[4], Alicia G Fuchs[1,5].

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Echinococcus granulosus (*Eg*) causes cyst echinococcosis (CE), a worldwide distributed parasitic disease that affects livestock and humans. Our laboratory has developed the EGPE cell line from bovine *Eg* G1 protoscoleces (Echeverria et al, 2010) for studies of antiparasitic drugs and identification of relevant molecules in diagnosis and treatment of CE. This work **aimed** to identify and characterize proteins from *Eg* in the EGPE cells recognized by CE patients' sera. **Materials and methods:** total proteins extract from EGPE cells 20 days grown was passed through a gel filtration column. Protein fractions were concentrated through a 3K cut-off membrane concentrator. Reactive fractions to Western Blot were passed through affinity columns with CE or other parasitosis patient's sera. Then isolated proteins were identified by proteomic in CEQUIBIEM (FCEyN, UBA). Proteins were modeled using Robetta platform (TrRosetta method) and validated by molecular dynamics simulations with software NAMD 2.14. Epitope prediction was performed with IEDB (linear epitope prediction and Discotope 2.0) and ABCpred. **Results:** We identified *Eg*'s Histone H2A (W6U0N3, 195 aa) recognized by sera from CE and others parasitosis patients. W6U0N3 has 81% identity in the first 58 aa with *Fasciola hepatica*'s histone H2A. Generated model was validated showing in 10-50 ns section of the trajectory an averaged potential energy resultant -168208 ± 198 kcal/mol. This model presented two regions with different RMSD values for the trajectory taking the averaged structure as reference: for 1-14 aa region, 3.32 +/- 0.77 Å and for 14-195 aa region, 2.16 +/- 0.61 Å. Linear epitopes were predicted in 123-138, 138-153 and 170-185 aa, meanwhile conformational epitopes were predicted in the 1-14 aa region. **Conclusion:** Intracellular Histone H2A from EGPE