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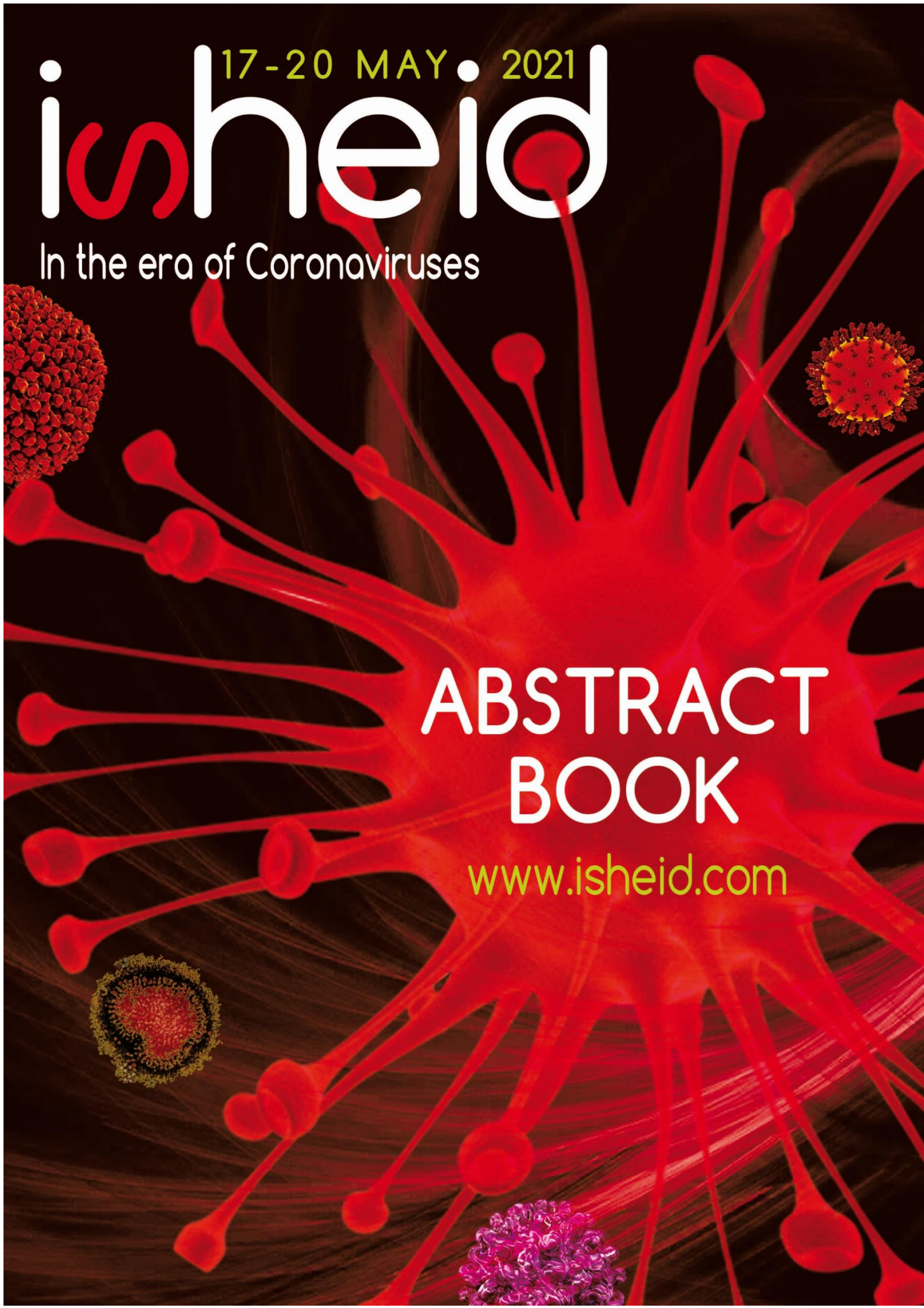
In the era of Coronaviruses



ABSTRACT BOOK

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Oral communications

O1 - Impact of early antiretroviral therapy on tissue resident myeloid cells in the liver and lung of SIV-infected rhesus macaques

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Introduction
Viral dissemination occurs early after infection targeting CD4 T cells and monocytes/macrophages. Monocytes derived from bone marrow and tissue resident macrophages (TRMs) derived from yolk sac, are short-lived and long-lived cells, respectively. Whereas we demonstrated that early antiretroviral therapy (ART) efficiently prevents infection of monocytes in the blood, spleen and intestine of SIV-treated rhesus macaques (RMs) [1], little is known so far about the role of TRMs, and whether these cells may represent VRs in SIV-infected RMs after early ART.

Materials and methods
RMs were infected with SIVmac251 and treated at day 4 with a cocktail of antiretroviral drugs. Cells from liver and lung were mechanically isolated. The phenotype of TRMs was analyzed by flow cytometry using specific antibodies including antibodies against CD14, CD16, CD44, TIM-4, CD117, CD206, MERKT, and LYVE (these markers were previously defined in mice). The levels of viral DNA and RNA were quantified by qPCR for each tissue. In situ hybridization was used to detect vRNA in tissues.

Results
Our results revealed that myeloid cells from liver and lung of SIV-infected RMs expressed mostly CD44, CD117, CD206 and LYVE markers, but represent a small proportion of liver and lung cells. Concomitantly, our data revealed that liver and lung of non-treated SIV-infected RMs both contain viral RNA and DNA that are positively correlated with the viremia. Furthermore, treated-RMs have no viral RNA and DNA both in the liver and lung.

Conclusions
Herein, we characterized the phenotypes of long-lived TRMs that colonize lung and liver of SIV-infected RMs. We also showed that early ART efficiently prevents early viral seeding both in the liver and lung. These results highlight the crucial importance of early treatment by decreasing anatomical VRs.

[1] Rabezanahary, H., et al., Early antiretroviral therapy prevents viral infection of monocytes and inflammation in SIV-infected rhesus macaques. Journal of Virology, 2020: p. JVI.01478-20.

O2 - Sexual satisfaction in women living with HIV. Are they the forgotten ones?

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Introduction
Sexual satisfaction (SS) is an important part of health, and must be considered when addressing the `fourth 90' of UNAIDS/WHO. The aim of this study is to evaluate the sexual satisfaction in women living with HIV (WLWH).

Materials and methods
Cross-sectional study carried in two reference hospital of Spain. All WLWH on regular follow-up were invited to answer an anonymous questionnaire to evaluate their SS, by the New Sexual Satisfaction Scale (NSSS). Pregnant and transgender WLWH were excluded. The influence of immunovirological control, ART exposure, epidemiological data and gynecological and obstetric variables were evaluated. Factors associated with SS were analyzed using paired T-test and correlations by R- Pearson correlation coefficient.

Results
Data of 150 patients were analyzed, the main characteristics are shown in the table. Globally, the SS was good but 3.7% were considered unsatisfied and 22.4%little satisfied, with lower scores on the ego-focused subscale. Age (but not length of HIV infection) was inversely correlated with SS (R= -.27, p<.01). Stable partner and use of contraceptives were significantly associated with higher

SS and menopausia with lower. The presence of symptoms as vaginal dryness (34.0) or decreased libido (24.0) were frequent in non-menopausal women. The acceptance of the questionnaire was good (80.6% marked 4 or 5 points).

Conclusions
It's important to explore SS in regular consultations of WLWH. More than one every 4 WLWH have poor SS and it worsens with age and menopausia. Treatable symptoms as vaginal dryness are frequent y WLWH
Specific programs to improve WLWH sexual health must be developed and validated.

Age (years, mean±SD)	49.8±9.1
Lenght of HIV infection (years, mean±SD)	16±8
Taking ART (n, %)	147 (98.7)
Undetectable viral load (n, %)	126 (84.0)
<200 CD4/mcl (n, %)	11 (7.3)
Tobacco smoker (n, %)	76 (50.7)
Alcohol consumption (n, %)	35 (23.3)
Drugs user (n, %)	24 (16.0)
Unemployment	79 (52.7)
Stable partner (n, %)	87 (58.0)
History of STI (n, %)	57 (38.8)
Pregnancy history (n, %)	126 (84.0)
Menopausal WLWH (n, %)	81 (54.0)
Use of contraceptives (n, %)	68 (45.3)

O3 - Influence of Hepatitis E virus genetic variability on the viral circulation between humans and environment.

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Introduction
Hepatitis E virus (HEV) is the main cause of acute hepatitis worldwide. In France, HEV seroprevalence is evaluated at 25% up to 60 %, with zoonotic and possible waterborne transmission. Our aim was to explore the influence of HEV variability on viral fitness and circulation between humans and environment.

Materials and methods
HEV prevalence was explored on 401 samples (serum, stool) from humans with hepatitis failure and from environmental samples (urban wastewater treatment plant [n = 30], wastewater from pig slaughterhouse [n = 30], pigs [stool, n = 29]). HEV was detected by qRT-PCR and the genome variability studied using ultra-deep sequencing –UDS on ORF2/ORF3 gene (protein capsid and a key phosphoprotein). In silico and in vitro assays investigated the impact of HEV genome mutations on antigenicity and hydrophobicity, involved in host anti-HEV immunity and viral behaviour in the environmental reservoirs.

Results
In patients, 11% of sera and 48 % of stool samples were HEV-positive, such as 20 % of urban wastewaters and 60 % of pig slaughterhouse effluent samples.
A major HEV variant was regularly observed in clinical and environmental samples. But raw wastewaters were contaminated with a mixture of variants, such as was one chronically infected patient. For a second patient, a 67-(D/G)P(H/R)PGSGAK-75 motif (ORF2) typical of rabbit HEV G3ra strains was observed with a specific amino acid antigenicity and increased hydrophobicity. Naked particles from stools were more hydrophobic than the corresponding enveloped particles from blood (p = 0.1) and a higher hydrophobicity was observed for HEV G3ra strain compared to the common HEV G3f (p = 0.1).

Conclusions

HEV can circulate in humans and in the environment including the water potentially contaminated by humans or animals. A high HEV variability has been observed, modulating both antigenic and surface properties. Some mutations associated to a modification of antigenicity and/or hydrophobicity might provide HEV a possible host and environmental adaptation.

O4 - Effect of Metformin in non-diabetic people living with HIV: weight loss, decrease in inflammation and modification of the gut microbiota

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Introduction
People living with HIV (PLWH) on antiretroviral therapy (ART) have increased risks of inflammatory comorbidities associated with changes in gut microbiota and increased weight. The anti-diabetic drug metformin was shown to decrease inflammation by interacting with the gut microbiota in diabetic and non-diabetic people. Herein, we evaluated the effect of metformin on inflammation and gut microbiota composition in non-diabetic PLWH on ART (CIHR/CTN pilot study).

Materials and methods
We recruited 22 non-diabetic (HbA1c <6%) PLWH on ART with a viral load <50 copies/ml for more than 3 years and a CD4/CD8 ratio ≤0.7 to select participants with higher risk of inflammation. Each participant was followed clinically at baseline (V1), after 12 weeks of metformin (V2), and 12 weeks after metformin discontinuation (V3). Blood was collected at each visit and soluble CD14 (sCD14) measured by ELISA. In stool samples, the 16S rRNA gene was sequenced to analyze bacterial composition. Serum butyrate was measured by LC-MS-MS.

Results
No serious adverse events were reported during the study. Interestingly, a median loss of 2.5 kg after metformin treatment was observed at V2. Participant weight returned to baseline value at V3. Levels of inflammatory plasma marker sCD14 levels decreased at V3 compared to V1. In stools, we observed a significant increase of Escherichia/Shigella and Lachnoclostridium abundance at V2 compared to V1. The abundance of butyrate producing Lachnospiraceae was also increased at V3. Concomitantly, serum levels of the anti-inflammatory short-chain fatty acid butyrate were also increased at V3.

Conclusions
A 12-week metformin therapy was safe and decreased weight in non-diabetic ART-treated PLWH. An enrichment of butyrate-producing bacteria in stool after metformin discontinuation was observed concomitantly with a decrease in inflammation marker sCD14. Results from this pilot study suggest that a longer metformin therapy in PLWH may decrease risk of inflammatory co-morbidities

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O5 - Extensive proteomic and transcriptomic changes quench the TCR/CD3 activation signal in latently HIV-1 infected T cells.

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Introduction
The ability of HIV-1 to reside in a latent state in CD4+ T cells constitutes a critical hurdle to the development of a curative therapy. Recent ex vivo studies suggest that TCR/CD3 stimulation only triggers HIV-1 reactivation in a fraction of the latently infected CD4+ T cell reservoir. Therefore, large parts of the CD4+ T cell reservoir must have been rendered inert to TCR/CD3 activation and cannot be depleted by the recognition of cognate antigen.

Materials and methods
We demonstrated the presence of CD3-inert T cells in primary T cell and T cell line models of HIV-1 latency and utilized kinome array and RNA-seq analysis to dissect the molecular biology of this phenomenon.

Results
Protein- and RNA- level analysis comparing CD3-responsive and CD3-inert latently HIV-1 infected T cells, followed by software-based integration of the data into interaction networks suggested two phenomena to govern CD3-inertness: (i) defined changes to specific pathways and (ii) the generation of transcriptomic noise. These findings could be validated by pharmacologic interference studies. Experiments demonstrated that compounds which increased transcriptomic noise would stabilize latent HIV1 infection. Conversely, targeting specific key network nodes, such as STAT3 or c-raf improved the ability of TCR/CD3 activation to trigger HIV-1 reactivation.

Conclusions
The data emphasize that latent HIV-1 infection is largely the result of extensive biomolecular changes to the signaling networks of the infected host T cells that can induce an activation inert phenotype. In extension, the data imply that therapeutic restoration of host cell responsiveness could enable reservoir depletion through cognate antigen recognition, removing the need for therapeutic activators.

O6 - Myocardial abnormalities in HIV: Insights from Cardiac Magnetic Resonance Imaging (MRI)

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Introduction
People living with HIV (PLWH) experience significant rates of cardiovascular disease (CVD) as they age, including acute myocardial infarction (MI), heart failure (HF) and sudden cardiac death (SCD). Cardiac MRI is used for investigating young patients as there is no radiation exposure, good reproducibility of results and accurate comparative data during follow-up testing. It can be used to assess ischaemia, left (LV) and right ventricular function, structural heart disease and fibrosis/scar such as in MI, HF and SCD.

Materials and methods
The study analysed 42 PLWH from cardiology clinic with cardiac MRI (37 men, mean age 55.7±11.07yrs and HIV duration 16.2±9.27yrs) against 39 healthy volunteers (39 men, mean age 46.1±7.8yrs).

Results
Compared to healthy volunteers, PLWH had significantly decreased ejection fraction(59.4±15.6 v 64.7±5.3%; P<0.05) , increased LV mass(80.0±23.8 v 59.7±13.0g; P<0.01), but no significant difference in native T1(1023±57 v 1001±41; P=0.053), a marker of diffuse fibrosis . T2, a more specific marker of myocardial oedema, was elevated in PLWH (48.3±3.7 v 45.9±3.2; P<0.01). Sixteen PLWH (41%) showed late gadolinium enhancement (LGE) (8 ischaemic and 8 non-ischaemic pattern) another 3 had scar. Only 7 (18%) PLWH were classified as having normal test results, 78 pathologies were found with many patients have 2 or more findings on MRI.

Conclusions
In PLWH, the elevated LV mass may be associated with long-standing hypertension, common within this patient population.The high myocardial T2 may be due to chronic low grade cardiac inflammation. Focal areas of non-ischaemic scarring were present and may relate to previous myocarditis and provide a link to the increased SCD seen in PLWH. This study identifies a number of cardiac pathologies which may be associated with chronic HIV infection and prolonged ART. It illustrates the benefit of cardiac MRI in providing additional structural information which may require early medical intervention.

MRI Images

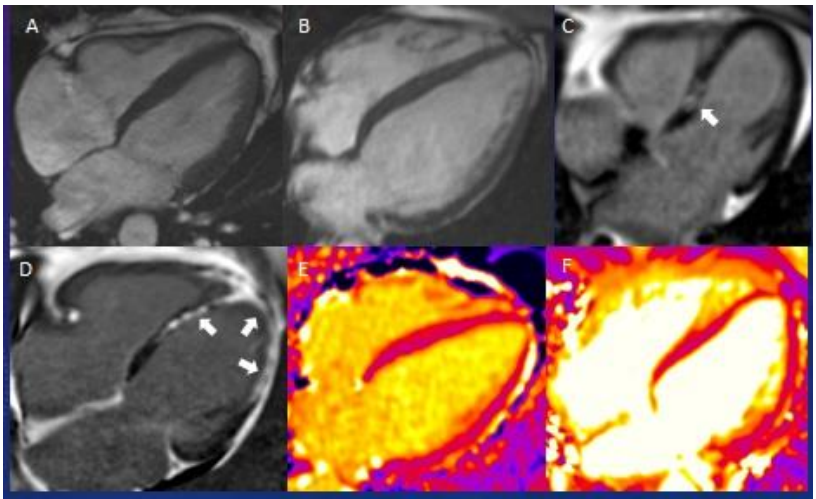

Figure 1. Static Cardiac MRI images demonstrating different pathologies in PLWH: A) Normal Heart B) Dilated Cardiomyopathy with Heart Failure C) Patchy LGE D) Old MI with Scar E) Native T1 Mapping showing increased fibrosis F) T2 Mapping which is normal.

O7 - Cardiomyopathy, pulmonary hypertension and myocarditis not as prevalent in well controlled HIV: H-ART to Heart study

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Introduction
HIV/AIDS previously was associated with heart failure, pulmonary arterial hypertension (PAH) and myocarditis. Studies in asymptomatic PLWH have revealed a high burden of underlying cardiovascular disease (CVD) and subclinical myocardial inflammation as detected by cardiac magnetic ressonance imaging (CMR).The H-ART to Heart study is designed to examine the burden of CVD in asymptomatic PLWH compared to negative controls(-) without traditional CV risk factors.

Materials and methods
We compared PLWH aged 35-55yrs (diagnosed >10 yrs, viral load <60) to negative controls. Caucasian men who have sex with men (MSM) and Black African/Caribbean women (BW) without CV risk factors or hepatitis co-infection were included. Assessments included endothelial function (EndoPAT), echocardiography and CMR.

Results
90 participants were recruited (26 HIV+MSM; 19 HIV-MSM; 21 HIV+BW; 24 HIV-BW) with no significant differences in baseline data apart from higher cLDL in HIV+BW (3.49±1.2 v 2.42±0.7;P<0.01). HIV+BW had more endothelial dysfunction (50% v 10%;P<0.01) and PAH (27.8±4.8 v 22.3±5.9mmHg;P<0.05). Of those who had a LVEF <55%, 3 were HIV+MSM (range 47.5-53.1%), 3 were controls (range 52.6-54.6%). CMR parameters were similar across groups aside from significantly higher T2, a specific marker for myocardial odema, (46.2±1.6 v 44.4±2.5;P<0.05) and Late Gadalinum Enhancement (LGE), a subtle non-specific finding in the HIV+MSM (76.5%) group compared to controls (14.3%;P<0.001). There was no evidence of ischaemia or myocarditis in any groups.

Conclusions
Our study of asymptomatic PLWH with low CVD risk, demonstrated subtle differences compared to controls. This, however, did not translate to evidence of detectable pathology classically associated with HIV; namely cardiomyopathy, pulmonary hypertension and myocarditis.The subtle findings of more endothelial dyfunction, higher PAH, raised T2 and LGE on CMR may be suggestive of underlying processes that may contribute to more CVD in PLWH which requires further investigation.

O8 - Sexual Transmission of HTLV-1 and Expanded Spectrum of Clinical Manifestations

V. Soriano [1], J.M. Ramos [2], H. Pinargote [2], C. De Mendoza [3], A. Spanish H T L V Network [3]

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Introduction
Ten million people are infected with HTLV-1 worldwide. Given migration flows, HTLV circulates in Europe mostly through sexual transmission. Around 10% of carriers will develop typical illnesses, namely adult T-cell leukemia (ATL) or tropical spastic paraparesis (TSP).
A recent meta-analysis (*Schierhout et al. Lancet ID 2020*) reported a 57% increased risk of premature death in HTLV individuals that was independent of ATL and TSP. The authors identified a broader number of illnesses that could contribute to the poorer survival of HTLV carriers.

Materials and methods
In order to explore the clinical burden associated with HTLV, we analyzed diagnoses at discharge in all patients with HTLV-1 hospitalized in Spain during the last two decades (1997-2015). The methodology has been reported elsewhere (*Ramos et al. AIDS 2020*).

Results
From a total of 66,462,136 hospital admissions recorded in Spain during the study period, 115 included HTLV as diagnosis (rate 1.73/million). Median age of HTLV patients 49.3 years-old; 47.5% female; sexual transmission 70%. Although the most frequent illnesses recorded alongside with HTLV diagnosis were TSP (61; 53%) and ATL (29; 25%), other from the Schierhout's list were noticed (**Table 1**).

Conclusions
Beyond ATL and TSP, a broader list of clinical conditions are linked to HTLV. However, most are non fatal, and therefore does not explain the 57% shorter survival of HTLV carriers having neither ATL nor TSP.
In other chronic viral illnesses (HIV, HBV, HCV), prolonged viral replication results in persistent immune activation and chronic inflammation that ultimately cause accelerated aging. We propose that common age-related illnesses (24.3% in our hospitalized patients) may occur earlier in HTLV carriers, being largely responsible for their shortened survival in the absence of ATL or TSP.
HTLV should no longer be considered as a neglected disease. Screening should be added to the list of sexually transmitted agents.

HTLV-1 illnesses other than ATL/TSP linked to HTLV

		Global Meta-analysis (39 studies; OR)	Hospital admissions in HTLV-1 patients in Spain (n=115)
1. Due to shared acquisition routes with HTLV-1 (i.e., other sexually transmitted infections)			
	- Cervical cancer (HPV)	3.6	0
	- Liver cancer (HBV)	1.5	0
2. Due to immune impairment as result of infection of CD4+ T lymphocytes by HTLV-1			
• Infections:	- Strongyloides	120	1
	- Tuberculosis	1.7	0
	- Bronchiectasias	2.9	1
	- Pneumonia	1.4	3
	- Urinary tract infections	1.8	15
	- Dermatophytosis	3.3	1
• Allergic-inflammatory phenomena:	- Asthma	3.4	4
	- Seborrheic dermatitis	3.9	0
	- Arthritis	2.8	0
	- Sicca syndrome	3.2	2
3. Due to persistent immune activation as result of sustained HTLV-1 replication			
• Lymphomas other than ATLL		2.8	0
• Chronic inflammation and accelerating aging (cardiovascular events, osteoporosis, neurodegenerative conditions, metabolic abnormalities, etc.)		-	28 (24.3%)

Discussed posters

DP1 - Tracing the patterns of HIV-1 transmission among individuals with different diagnosis status in Greece

E-G. Kostaki [1], S. Limnaios [1], S. Patrinos [2], D. Chatzidimitriou [3], G. Magiorkinis [1], L. Skoura [3], V. Sypsa [1], A. Hatzakis [1], D. Paraskevis [1]
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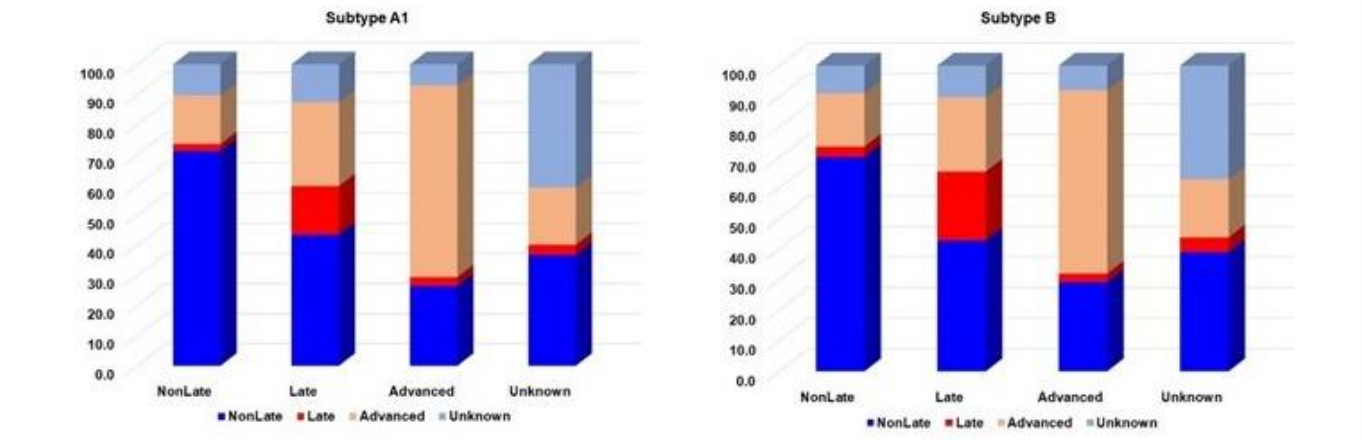
Introduction
Late presentation of HIV infection continues to occur at considerable rates in Europe. Our aim was to investigate the contribution of late and recent diagnosis to subsequent HIV transmission in Greece, using current state of the art molecular epidemiology methods.

Materials and methods
We analyzed 3,095 sequences of subtypes A1 and B, collected from people living with HIV (PLHIV) during 1999-2015 in Greece. Individuals were categorized according to the first CD4 measurement: very late (CD4 < 200 cells/μl or clinical AIDS), late (200 ≤ CD4 ≤ 350 cells/μl) and non-late diagnosis (CD4 > 350 cells/μl). The HIV dispersal patterns between PLHIV with different diagnosis status were estimated by a modified statistical phylogeography method.

Results
Firstly, we estimated the number of putative transmissions within each group. For the non-late diagnosed group, 71.2% and 70.1% of A1 and B transmissions, respectively, originated from individuals of the same group. PLHIV with very late diagnosis were infected at 63.6% and 60.0% from those with the same diagnosis status, for subtypes A1 and B, respectively. Secondly, we estimated the number of putative transmission events between PLHIV with different diagnosis status. For both subtypes, PLHIV with non-late diagnosis did not provide a significant source of HIV transmission to the other groups. The number of transmissions from those with very late diagnosis was significantly higher to all groups for both subtypes ($p < 0.001$).

Conclusions
A large proportion of infections took place among PLHIV with non-late diagnosis, suggesting that for this group most transmissions occur early, and probably close to their HIV acquisition dates. Notably, very late presenters are sources of HIV transmissions to all groups, suggesting that besides the 90-90-90 target to be reached, additional effort is needed to improve diagnosis rates across different groups and to initiate treatment rapidly.

HIV-1 dispersal patterns among different groups



DP2 - Identification of fast-growing HIV-1 transmission clusters in Spain and its potential application in Public Health

H. Gil [1], E. Delgado [1], S. Benito [1], M. Sánchez [1], J. Cañada [1], E. García-Bodas [1], M.M. Thomson [1], S. Spanish Group For The Study Of New Hiv Diagnoses [2]

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Introduction
To reduce HIV-1 infections in the United States by 90% by 2030, a strategic plan based on 4 pillars has been designed: 1) early diagnosis; 2) fast and effective treatment; 3) pre-exposure prophylaxis; and 4) rapid response to HIV-1 outbreaks, based on the identification of fast-growing transmission clusters (FGTC). In this study we analyze FGTCs among newly-diagnosed HIV-1 infections in Spain during 2019 as a step towards the implementation of an HIV-1 molecular epidemiological surveillance system in this country.

Materials and methods
A total of 11,656 HIV-1-infected individuals attending health centers of 14 regions of Spain during 1999-2019 with a partial pol sequence were included in the study. Patient samples were sent to our laboratory for antiretroviral drug resistance testing and molecular epidemiological studies. Sequences were phylogenetically analyzed by approximately-maximum likelihood with FastTree. Transmission clusters (TCs) were defined as those comprising viruses of four or more individuals with a node support ≥0.95. TCs with at least one newly diagnosed patient (ND) in 2019, whose size increased by 5 or more NDs over a year, were considered FGTCs.

Results
A total of 4,008 (34.4%) patients belonged to any of the 382 TCs identified, whose size ranged from 4 to 200 patients. Among them, 18 FGTCs were identified, which increased in size from 5 to 23 NDs in the last year. A 33% (6/18) of FGTCs corresponded to non-B genetic forms and 78% (14/18) were associated with transmission among men who have sex with men.

Conclusions
Molecular epidemiology has shown to be a useful tool in the identification of active HIV-1 FGTCs in Spain. The rapid identification of FGTCs and the implementation of control measures to prevent their expansion could have a direct effect on the reduction of new HIV-1 infections. The implementation of a molecular epidemiological surveillance system should be included among the new strategies for the control of the HIV-1 epidemic in Spain.

DP3 - No Impact of SARS-CoV-2 on the Activation Status of ART+HIV+ Patients

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Introduction
Although some studies have reported insignificant impact of SARS-CoV-2 infection on ART+HIV+ individuals, data on important variables characterizing the low-level immune activation is limited.
Aim. To assess the impact of COVID-19 on the residual immune activation in HIV+ patients with undetectable HIV viral load using CD4/CD8 ratio and number of CD38 molecules (CD38ABS) on CD4 and CD8T cells.

Materials and methods
Consecutive HIV+patients (27 men, 5 women; age 41±11y) who presented for immune monitoring after a positive SARSCoV-2 PCR result were included. All had been on continuous cART for 62±49mo, with standard triple regimens. Time since PCR+ was 37±23days. Absolute counts (AC), percentage of CD4 and CD8T and CD4/CD8 ratio were determined by single-platform flow cytometry. The number of CD38ABS on CD4 and CD8 T cells was calculated in SARS-CoV-2 recovered patients using Quantibrite kit (FACSDiva 6.1.2, BD Biosciences).

Results
All patients presented mild/moderate symptoms of COVID-19. AC and percentage and CD4/CD8 index did not differ significantly as compared to values before SARS-CoV-2 infection (807vs.877; 33vs.40; 0.94vs.0.92, p>0.05 for all). CD8CD38ABS (1502±493) did not differ from reference values, and CD4CD38ABS was increased in only 3 patients (9%). To assess the effect of residual immune activation, patients with baseline CD4/CD8<0.9 (0.6±0.2, n=17) and >0.9 (1.2±0.3, n=15) were compared. No significant differences were seen between post-Covid lymphocyte AC (2834vs.2514), CD4AC (795vs.942) or activation markers: CD4CD38ABS(3273vs.2816) and CD8CD38ABS(1513vs.1498), p>0.05 for all. In addition, SARS-CoV-2 co-infection did not deteriorate neither CD4AC nor CD4/CD8 ratio in group A (p>0.05)

Conclusions
SARS-CoV-2 co-infection does not augment or incite residual immune activation in HIV+ patients on stable cART.
Acknowledgement:Supported by the European Fund for regional development, Grant BG05M2OP001-1.002-0001-C04 Fundamental Translational and Clinical Investigations on Infections and Immunity

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DP4 - Factors Associated with Willingness to Participate in End-of-Life Cure Research: perspectives from People Living with HIV

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Introduction
HIV cure research focuses on HIV persistence within body reservoirs. Canadian HIV Cure Enterprise (CanCURE) members have established a protocol for an HIV biobank to collect tissue biopsies post-mortem. However, End-of-Life (EoL) research poses ethical challenges. Our objective is to evaluate determinants of participation and preferences to ensure acceptability and a positive experience for PLHIV and their close or family circle.

Materials and methods
Following principles of patient-oriented research, we discussed EoL HIV cure research with 2 community members. Participants will be PLHIV aged ≥65 years. We designed a mixed-method research methodology based on surveys filled by all participants (n=50), followed by audio-recorded in-depth semi-structured interviews in a subset of participants (n=16). Surveys were reviewed with members CanCURE's community advisory board (CAB) and modified appropriately.

Results
Participants will decide with recruiters with whom and the context in which they answer surveys and interviews to increase comfort, acceptability, and accessibility. Surveys will elicit: 1) sociodemographic characteristics, 2) quality of life and experience of health, 2) experience of health, 3) willingness to participate in EoL HIV cure research, 4) willingness to donate tissues for HIV biobanking, and 5) willingness to undergo a postmortem research autopsy. Interview schedules examine more thoroughly participants' perspectives, motivation and barriers, perceived risks and benefits, relative to these themes, in association with their understanding of life and mortality, as well as their family's and social circles'. Results will be presented in May 2020.

Conclusions
A better understanding of PLHIV's perspectives, in association to their social context, could then be taken into consideration when designing ethical, respectful, and meaningful patient-centred interventions to approach, include, and interact with participants in the CanCURE HIV Autopsy Biobank and other EoL HIV cure studies.

DP5 - Fibrosis regression in HIV-HCV coinfected patients treated by DAAs

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Introduction

The HCV revolution driven by oral DAAs was associated with a sustained virological response (SVR) > 95% but the hepatic fibrosis regression remained unclear in HIV/HCV coinfected pts, due to limited published cohorts. We report 6-year trends of hepatic fibrosis evolution over time in HIV/HCV coinfected pts treated by DAAs.

Materials and methods
Epidemiological, clinical and virological data from HIV/HCV coinfected pts included in the French DAT'AIDs cohort treated by DAAs were collected for the study since mid-2014.Two scores of hepatic fibrosis, APRI and FIB-4, were assessed before, after and 12 weeks after DAAs and beyond when available up to 5 years. A linear mixed model analyzed APRI's and FIB4's scores to explore the impact of DAAs on the evolution of hepatic fibrosis over time.

Results
58 HIV/HCV coinfected pts (43M, 15F; median age: 48y; main routes of viral transmission (36 IDUs, 17 HSH) received (all but 2) a 12-week sofosbuvir-based combination.
Main HCV genotypes were 1a(32) and 3a(10). Median HCV virus load (VL) was 6.1 log10 UI/mL. Before AAD, 30(52%) pts had a F0-F2 and 28(48%) a F3-F4 Metavir score including 6 pts with a severe liver disease (5 biological hepatic failure,1 history of cured HCC). All treated pts achieved SVR without relapse over time. 2 HCV reinfections occurred 1 year after DAA. No liver event including HCC occurred over time.
There was a statistically significant reduction over time of the proportion of APRI score > 1.5 (from 15 to 0 pts; $p < 0.001$) and FIB-4 score > 3.25 (from 11 to 1 pt; $p<0.001$) in the two groups F3-F4 and F0-F2 treated. Time to obtain a negative HCV VL was longer in F3-F4 pts than in F0-F2 pts ($p<0.001$).

Conclusions
The elimination of HCV was associated with a statistically significant regression of hepatic cirrhosis in F3/F4 pts and with a significant regression of hepatic fibrosis in F0-F2 pts according APRI & Fib-4. It implies an active screening and a test and treat approach for HCV infection in PLWHIV.

DP6 - Differential Serotyping of HEV genotype 1 and 3

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Introduction
Epidemiologic studies of risk exposures to Hepatitis E viral infection are difficult to perform because viremia is short-lived and HEV genotyping is routinely performed by HEV RNA PCR. Consequently, alternative methods of HEV genotyping are needed. Herein, we report the development of a highly specific serotyping assay to differentiate HEV genotype 1 and 3 infections.

Materials and methods
We developed an HEV-specific IgG serological assay of HEV-infected sera targeting selected HEV ORF-2 specific epitopes predicted from HEV genotypes (1 and 3). Genotype specific peptides (15-mer) were selected from the peptides with the highest overall sequence differences between genotypes 1, and 3 and their differential binding capacity to sera from HEV infected patients with genotype 1 and 3 in early screening. Sera from 20-HEV infected genotype 1 and from 10 HEV infected genotype 3 were used in enzyme-linked immunosorbent assay (ELISA) coated with the selected peptides.

Results
Anti-HEV IgG positive sera, with known HEV genotypes, previously determined by HEV RNA sequence analysis were tested. Overall, binding to selected specific HEV ORF2 genotype 1 peptides (10 peptides) is highly selective and specific to genotype 1-infected sera. Using cut off ratio of signal/background (>4), and ORF2 genotype 1 and 3 specific peptides, the ELISA sensitivity was 77% (95% C.I. =46 -95%) and the specificity was 100% (95% C.I. = 54-100%). By further selecting two highly genotype 1 specific peptides, we were able to improve the ELISA sensitivity to 87% (95% C.I. =66 -97%) and specificity 100% (95% C.I. = 80-100%). The positive predictive value was 100 (95% C.I. =83-100%), and negative predictive value was 85% (95% C.I. =62-96%)

Conclusions
Our data suggest that a customized ORF2 specific peptides in ELISA HEV IgG assay could be utilized to identify the HEV genotypes with high specificity and good sensitivity. Confirmation of the sensitivity and the specificity of the developed serotyping assays with blinded samples is underway.

DP7 - Nlrp3 inflammasome activation in peripheral blood leukocytes from HIV-infected patients and its contribution to chronic inflammation

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Introduction
During the chronic HIV-1 infection, a dysregulated NLRP3 activation could be involved in chronic inflammation and immune exhaustion contributing to HIV-associated non-Aids conditions. This activation was previously reported in total peripheral blood mononuclear cells (PBMCs), but whether its activation occurs only in myeloid cells or also in lymphocytes is not yet understood. We hypothesize that NLRP3 inflammasome could be activated in CD4+ T and CD19+ B lymphocytes during chronic HIV infection influencing the chronic inflammation and the profile of immune response.

Materials and methods
NLRP3 inflammasome activation was evaluated in 60 HIV-infected patients (HIV) and 60 healthy donors (HD) in total PBMCs, as well as purified CD14+ monocytes, CD4+ T and CD19+ B lymphocytes by the meaning of caspase-1 cleavage, IL-1β and IL-18 production and NLRP3+ASC+ “specks” formation. We also evaluated the contribution of genetic variants to inflammasome activation state in HIV patients and the effect in clinical parameters and comorbidities development.

Results
Total PBMCs and CD14+ monocytes from HIV patients presented an augmented constitutive NLRP3 activation compared to HDs, as well as lower responsiveness to NLRP3 stimulus. Similarly, in CD19+ B lymphocytes from HIV patients, we also observed a constitutive NLRP3 inflammasome activation, but with a higher responsiveness to NLRP3 stimulation and also a higher IgM production in a NLRP3-dependent way. Lastly HIV CD4+ T cells also presented an augmented inflammasome activation, but with the participation of more than one inflammasome receptor (IFI16, NLRP1). This activation profile in the different cells was also influenced by genetic variants and as a whole affected several clinical parameters.

Conclusions
Inflammasome is constitutively activated in monocytes and lymphocytes from HIV-infected patients in a cell and receptor specific manner, and is strongly influenced by genetic background which could contribute to disease outcome during chronic infection.

DP8 - Viral rebound (VR) 14 years after discontinuation of antiretroviral therapy (ART)

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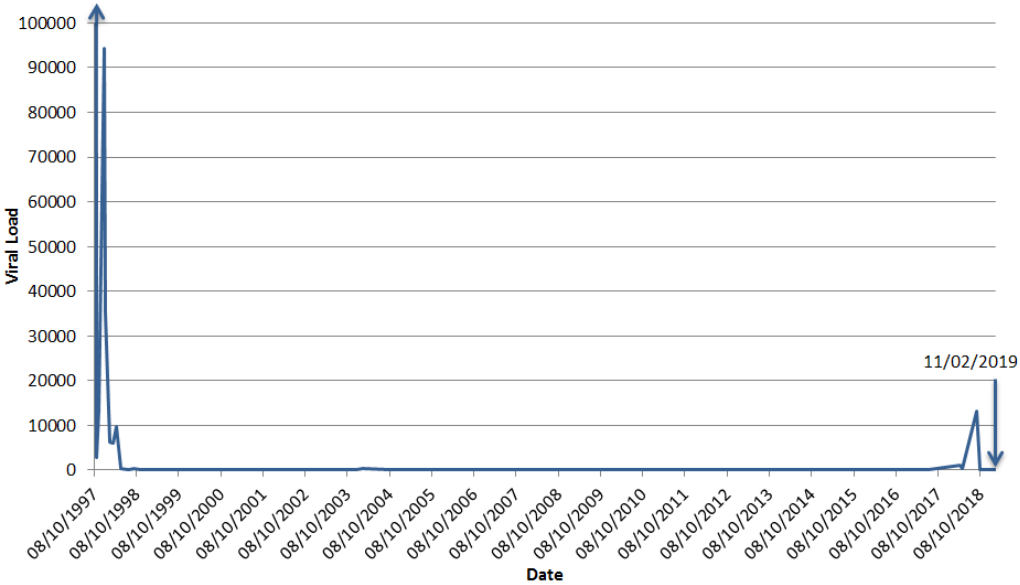
Introduction
Prolonged post-treatment control of HIV-1 viremia (VL) after stopping ART following primary HIV-1 infection (PHI) can occur. Whether virological rebound (VR) is preceded by clinical symptoms remains unclear

Materials and methods
Case note and laboratory review over a 22-year period of a patient presenting with symptomatic PHI in 1997.

Results
A young female initiated ART for symptomatic PHI in October 1997 (CD4 <200 cells/mm3, VL >750,000 HIV-1 copies (c)/mL). She failed to suppress on treatment until April 1999 (07.01.1998: 94,000 c/mL; 15.04.1998: 9,700 c/ml; 18.11.1998: 109 c/mL) when she became undetectable after ART switch. During ART discontinuation from January 2004, she maintained aviremia until 12 July 2017 (all yearly VL <50 HIV-1 c/mL) (Figure 1) with preservation of her CD4 T cell count and CD4/CD8 ratio, detectable HIV-1 DNA and an asymptomatic clinical status.
While still undetectable in 2017 the patient presented in early March 2017 with low-level constitutional symptoms (headache, tiredness, urinary symptoms). All investigations including a CSF (<40 HIV-1 c/mL) and CT chest-abdominal-pelvis remained negative. VR was noted in April 2018 at 1,047 and 308 HIV-1 c/mL, in May at 380 c/mL and in early September at 13,183 HIV-1 c/mL (CD4 of 554 cells/mm^3). ART was restarted with an undetectable VL on 04.10.2018 and 12.2.2019 (Figure 1). Symptoms subsided after ART restart.

Conclusions
Very prolonged aviremia can be sustained in ART-only treated individuals, even after initial virological failure, with late VR. Atypical constitutional symptoms may precede VR and should raise suspicion of potential VR. Close clinical and laboratory monitoring is needed in the long-term in post-treatment controllers for ART re-initiation and prevention of clinical progression and onward transmission.

Figure 1. HIV-1 viral load 1997-2019. ART stopped in January 2004 - restart September 2018.



DP9 - Frailty phenotype is associated with antiretroviral exposure among older persons living with HIV

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Introduction
Aging persons living with HIV (PLWHIV) may develop multiple comorbidities, altered physical and mental health, and frailty phenotype earlier than non-infected people. Determinants of the high prevalence of frailty are not completed understood. We assessed the prevalence of frailty phenotype and its relationship with antiretroviral treatment (ART) in older PLWHIV.

Materials and methods
An 18-month multicenter cross-sectional study was carried out focusing on patients > 50-years old in the South of France. The following data were recorded: health indicators, comorbidities, HIV data, five frailty markers (nutrition, energy, mobility, physical activity, strength), socioeconomic, behavioral and age-related variables. PLWHIV with 3 or more frailty markers were defined as frail and pre-frail if they had 1 or 2. The history of ART was documented in medical records.

Results
A total of 484 patients completed the frailty evaluation and history on ART. Mean age was 58.5 ± 7.0 years and 72.9% were male. These patients received 6.01 ART regimens on average. Univariate analysis found that number of different ART regimens, duration on all ART regimens, protease inhibitors and reverse transcriptase inhibitors, number of comorbidities, dyslipidemia, cancer, lipodystrophy, depression, falls, ADL disability, and chronic pain were independent predictors for frailty and pre-frailty phenotype. On logistic regression multivariable analysis with factors selected at a threshold of $p<0.10$ by univariate analysis and with sex, we found that the independent predictors for frailty and pre-frailty phenotype were a higher number of different ART regimens, cancer and chronic pain (OR=1.09; 2.00 & 1.11).

Conclusions
Our study confirms a significant association between presence of frailty markers and a high number of different ART regimens among older PLWHIV. As frailty phenotype could be reversible, a better understanding of the underlying determinant is warranted. The burden of cancer and pain shows the importance of comprehensive care.

DP10 - HIV-2 in Spain - steadily increasing and new challenges

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Introduction
HIV-2 infection is a neglected disease despite estimates of 1-2 million carriers worldwide. HIV-2 is less efficiently transmitted than HIV-1 by sex and from mother-to-child. In the absence of treatment, AIDS develops in most HIV-2 carriers, although it takes longer than in HIV-1 patients. There is no global pandemic caused by HIV-2, remaining the virus largely confined to West Africa. Due to historical ties, HIV-2 is prevalent in Portugal and its former colonies in Brazil, India, Mozambique and Angola. In Europe, HIV-2 is present in France, Belgium and Spain.

Materials and methods
A nationwide registry of HIV-2 cases exists in Spain since 1989. Information from each patient is recorded within a case report form. A plasma specimen is shipped to the coordinating center in Madrid.

Results
A total of 393 cases of HIV-2 infection had been reported at the Spanish HIV-2 registry until December 2019, of whom 63% were male. Overall 76% were Sub-Saharan Africans whereas 14% were native Spaniards. Dual HIV-1 and HIV-2 coinfection was found in 10%. **Heterosexual contact** was the route of HIV-2 acquisition in >90%. Roughly one third presented with CD4 counts <200 cells/mL and/or AIDS clinical events. Plasma HIV-2 RNA was undetectable at baseline in 40%. To date, one third of HIV-2 carriers have received antiretrovirals, using integrase inhibitors 48 individuals. New diagnoses of HIV-2 in Spain have remained stable since 2010 with an average of 20 cases yearly. Illegal immigration from Northwestern African borders accounts for over 75% of new HIV-2 diagnoses.

Conclusions
Given the relatively large community of West Africans living in Spain and the continuous flux of immigration from endemic regions, HIV-2 either alone or as coinfection with HIV-1 should be excluded once in all HIV-seroreactive persons, especially when showing atypical HIV serological profiles, immunovirological disconnect (CD4 count loss despite undetectable HIV-1 viremia) and/or high epidemiological risks (birth in or sex partners from endemic regions).

Posters

01. Basic and translational science

P1 - Deciphering the link between HIV seropositivity and religious minority in India

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Introduction
This paper aims to look at the overall prevalence of HIV in India and more specifically among the religious minorities with a gender lens.

Materials and methods
HIV file and household file of DHS India2015-2016 (NFHS-4) was merged and used for analysis.

Results
Initial results indicates that in India HIV prevalence was higher among Christians, Neo-buddhists, urban residents, those having less or no education and those who were ever married, belonging to the richer/richest wealth quintile and living in a nuclear family. HIV prevalence among the formerly married Christian males was 1.7% as compared to 0.4% among the formerly married Hindus and 0.2% never married Hindu men. Also, 0.7% male respondents who were never married but belonged to Christian religion also had HIV. Gender segmented analysis suggests that religious minority specifically Christians women had high prevalence of HIV . As high as 2.6% formerly married females and belonging to Christian religion were HIV positive as compared to 1.5% Hindus. Again this percentage among the currently married Christian females was also very high (1.0%). Among the HIV positive Christian females who were formerly married, 61% belonged to urban areas, a quarter of them was less than 30 years and half of them belonged to 35-39 years age group. Type of family played a pivotal role in explaining seropositivity among religious minorities since 89% of those HIV positive Christian females were from nuclear families.

Conclusions
Results portrays that HIV prevalence is high among the respondents belonging to religious minorities particularly among Christians and Neo Buddhists. It is well known that Christian religious discourse often also results in misguided epidemiological understandings about HIV/ AIDS, so the study results holds importance in the arena of public health.The results were more apprehensive and concerningfor females indicating that women are also vulnerable among Christian minority who are historically considered demographically advanced and informed.

P2 - Association between HIV transmission patterns and k-cores of social networks among people who inject drugs in Greece

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Introduction
HIV transmission requires risk behaviors among people in social contexts. One measure of sociometric risk context is the k-core, where all members of a k-core are risk-linked with at least k other members of that core. This study investigates associations between sociometric risk network characteristics (k-cores) and HIV transmission patterns using risk network data and molecular data from the Transmission Reduction Intervention Project (TRIP) Athens site.

Materials and methods
Phylogenetic trees were inferred from HIV-1 sequences of TRIP participants in protease and partial reverse transcriptase (RT) by maximum likelihood with bootstrapping, using the GTR+G as nucleotide substitution model. Analyses included only non-recombinant sequences clustered within subtypes A1, B, CRF14_B, and CRF35_AD. The number of transmission events between individuals with different k-core was estimated by a modified statistical phylogeographic method.

Results
The analysis involved 96 HIV-positive TRIP participants (males 74%, median age 34 years). CRF14_B (N=53), and CRF35_AD (N=18) were the predominant subtypes. There was no significant clustering of viruses infecting individuals with similar core characteristics. Statistical phylogeographic analysis revealed that the number of transmissions was significantly higher from larger to smaller cores. Specifically, the number of infections was higher from HIV-infected participants in 3-core to those in 2-core or in 1-core and from those in 2-core to HIV-infected participants in 1-core.

Conclusions
This is one of the few studies that combines sociometric risk network data and molecular analyses. We found that HIV infections occur between individuals in different cores. The directionality of transmissions was from those in a higher to those in a lower k-core. Approaches of this kind can help better understand and prevent HIV spread.

P3 - Atypical serology in an HIV-infected patient treated at Fiebig stage 1: evaluation of different diagnostic kits

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Introduction
It is now recommended to initiate antiviral therapy as soon as possible after the diagnosis. If serological tests can be defective at the time of primary infection, a very early treatment can also modify the kinetic of seroconversion.
The objective of this work was to compare different 4th generation tests for HIV screening, on sequential sera sampled in the months following a primary HIV infection treated at the Fiebig stage one.

Materials and methods
Blood samples were obtained from a HIV-1 infected patient. The primary HIV infection was diagnosed in the course of a blood donation through viral load quantification (4.85 log10-Aptima Panther Hologic) and treatment with tenofovir/emtricitabine/darunavir/ritonavir was immediately initiated.
Samples from D0 to D358 post-treatment were analyzed for the isolated detection of p24 antigen (Vidas® HIV P24 II, Biomérieux), and the combined search for antibodies and antigens using Architect® HIV Ag / Ab Combo (Abbott), Vidas® HIV Duo Quick, Vidas® HIV Duo Ultra (bioMerieux) and Liaison® XL HIV Ab / Ag (Diasorin).

Results
Detection of P24 Antigen was negative at D0, D8, D26, D38 and D92 post-treatment using the Vidas® HIV P24 and the VIDAS® HIV Duo Ultra that differentiates the antigen and antibody signals.
The combined tests were all negative at D0 and D28, and positive at D8. The Architect® HIV Ag / Ab Combo test was negative on samples from D36 to D358 while the Vidas® HIV Duo Quick was positive from D36 to D358. The Liaison® XL HIV Ab / Ag test was positive on the samples tested (from D92 to D358).

Conclusions
In early treatment of HIV primary infection, anti-HIV antibodies may not appear or decrease rapidly. The absence of detection of p24 Ag can be due to an undetected transient peak or a shorted infection. The differences observed between the different kits can be linked to the panels of antigens used for the preparation of the reagents.

P4 - Immunological characterization of non-responders to Direct Acting Antiviral Therapy in Egyptian Patients with Chronic Hepatitis C

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Introduction
Directly acting antivirals (DAA) have revolutionized Hepatitis C (HCV) therapy. Although sustained virologic response (SVR) rates have been high, few patients failed to response to DAA therapy (NR). The immunological influences in response to DAA therapy are poorly understood. In this study, the circulating T-lymphocytes, regulatory T cells (Treg), regulatory B-cells (Breg), and the serum cytokine profiles of HCV infected patients who were NR to Sofosbuvir/Daclatasvir (SOF/DCV) DAA were evaluated

Materials and methods
1000 HCV infected patients (Genotype 4) under DAA therapy at the Center for Management of Viral Hepatitis and Assiut University hospitals, Assiut, Egypt were enrolled in the study. Flow cytometric analysis was used to analyze circulating T-lymphocytes, Treg and Breg among 50 NR to (SOF+DCV) and 50 SVR (randomly selected from 950 SVR patients). Multiplex Luminex assay was used to measure sera levels of 10 cytokines; TNFα, IL1β, IL2, IL4, IL6, IL12, 1L17, IL10, IP10 (CXCL10) and IFN -g.

Results
No significant change was observed in the total number of T cells between NR and SVR groups. However, the frequency of Treg and Breg cells were significantly increased in NR group compared to SVR group (p=0.0002 and p =0.005, respectively). Additionally, the frequency of Treg cells and Breg cells were positively correlated (r=0.61, p=0.002, and r=0.55, p=0.02 respectively) with viral load.

Moreover, there were significant differences in the levels of TNFα, IL1β, IL6, IL17, IL10 and IP10 (CXCL10) between NR and SVR groups (p=0.0001, p=0.0001, p=0.0001, p=0.005, p=0.001 and p= 0.003 respectively)

Conclusions
NR to DAAs displayed a significant increase in the frequency of Treg, and Breg which associated with different cytokine profiles compared to SVR indicating that immunological responses are important in response to DAA therapy in HCV infection, and may be used as surrogate markers for response to DAA therapy

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P5 - Characterization of HIV epidemics in general population in Kyrgyzstan

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Introduction
HIV prevalence in Kyrgyzstan is relatively low, but the virus spreading rate is one of the highest in Central Asia. We investigated the HIV diversity and drug resistance, and reconstructed the history of HIV-1 subtypes A6 and CRF02_AG in general population in Kyrgyzstan.

Materials and methods
We analyzed 555 HIV *pol* sequences collected in four Kyrgyz provinces in 2016-2019. Three automated subtyping tools and phylogenetic analysis were used to identify HIV subtypes. HIV drug resistance was assessed using Stanford HIVdb. Phylogenetic relationships using IQTree and phylodynamics using BEAST were investigated for major circulating HIV subtypes.

Results
The most common HIV subtype was CRF02_AG (60.5%) followed by A6 (33%). The minor subtypes such as CRF63_02A, G, B, and URFs were also detected. Major drug resistance mutations (DRMs) were detected in 151/555 (27%) samples; DRMs to multiple ART drug classes were detected in 100 of them. Most if the individuals acquired HIV infection through the heterosexual (38.6%) contact, followed by nosocomial (20.7%) and parenteral (19.4%) transmission routes. Phylogenetic analysis was performed for subtypes CRF02_AG/63_02A and A6. CRF02_AG/63_02A tree showed explicit geographic clustering of study samples in 4 well-defined groups suggesting several main introduction events of the virus in Kyrgyz population. The A6 subtype tree showed no well-defined group of study samples; Kyrgyz sequences scattered across other sequences suggesting multiple introductions of A6 subtype. The origin date for A6 were estimated as 1995, 1997 for subtype CRF02_AG, and 2004 for CRF63_02A.

Conclusions
This study demonstrates the high HIV-1 genetic diversity and high prevalence of ARV resistance in Kyrgyz population; phylodynamic analysis suggests the relatively young HIV-1 epidemics with A6 and CRF02_AG subtypes entering in mid-1990s. These data provide an important insight into HIV-1 epidemics in Central Asia and may be used for future public health priorities and interventions in the region.

P6 - Propagation of an HIV-1 CRF72_BF-like cluster of Brazilian ancestry in Spain

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Introduction
High HIV-1 genetic diversity and rapid evolution has led to the emergence of 10 subtypes, around 100 circulating recombinant forms (CRFs) and numerous unique recombinant forms. 19 CRFs derived from subtypes B and F have been reported, 17 originated in South

America. Here we report a new BF recombinant cluster closely related to CRF72_BF, of Brazilian ancestry, currently propagating in Spain.

Materials and methods
Samples were collected from HIV-1-infected patients diagnosed in Spain. Protease-reverse transcriptase (PR-RT) sequences were obtained through RT-PCR from plasma RNA. Phylogenetic analyses were performed with Fasttree and IQ-Tree. Near full-length genome (NFLG) sequences were obtained by RT-PCR in 4 overlapping fragments. Recombination was analyzed by bootscanning. Time and location of the most recent common ancestor (MRCA) were estimated with a Bayesian coalescent method.

Results
Newly diagnosed HIV-1 infections frequently grouped in clusters. One of them was of subsubtype F1 (F1_2), comprising 14 individuals, diagnosed in 2007-2019, 13 from Galicia, Northwest Spain. Transmission was predominantly heterosexual (7 of 13 with available data). Most individuals were Spanish, but 1 was Brazilian and 1 Ukrainian. A phylogenetic tree with F1 sequences from databases showed that 3 additional viruses, from Portugal, Brazil and Germany, grouped in F1_2, and that viruses from Brazil were most closely related to F1_2. NFLG of 4 viruses exhibited 12 breakpoints, 11 of which coincided with CRF72_BF. In phylogenetic trees of NFLG sequences, F1_2 grouped with CRF72_BF, but they branched apart in partial pol sequences. The MRCA of F1_2 was estimated around 1989, most probably in Brazil.

Conclusions
A BF recombinant cluster of Brazilian ancestry is propagating in Northwest Spain, associated with a predominantly heterosexual transmission, which contrasts with other clusters of South American origin reported in Western Europe, mostly associated with transmission among MSM.

P7 - Vulnerabilities and HIV: a co-constructed health pathway between the concerned people and healthcare stakeholders

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Introduction
Our research-action consists in co-constructing and implementing the health pathway of people living with HIV (PLWHIV) in vulnerable situations in the city of Marseille.The first phase objective is to model a health pathway adapted to this key population and based on the shared diagnosis between PLWHIV, healthcare, and social welfare professionals.

Materials and methods
A comprehensive literature review explored the latest recommendations on holistic care for PLWHIV. Concurrently, participatory action research was used to conduct a shared diagnosis between PLWHIV (n=40) which participated in eighteen focus group interviews, hospital professionals (n=26) and association professionals (n=12) in order to cooperatively define vulnerability, develop means of identification, incorporate the health path, and co-construct the intervention modalities of the different actors.

Results
Based on the elements of discourse collected, analysed and condensed, a health path was modelled in accordance with the latest recommendations for PLWHIV. It takes into account (a) the time required to assess the person's overall situation, (b) temporal needs for coordination between the professionals, (c) the identification of key roles required for the management of social determinants of health (resource person, social and medical referent in the personalised health plan), and (d) the methods of intervention. Four stages were defined: (1) identification of vulnerability, (2) overall assessment of the individual’s situation, (3) co-construction of a personalised health plan, and (4) monitoring and re-evaluation of the plan.

Conclusions
The proposed health pathway will be implemented for fifteen PLWHIV at the outset of 2020. The first analyses can be presented on the occasion of this communication. Two further phases of inclusion will then be carried out with an additional group of participants of equal size to ensure the aforementioned professional practices, care methods, and coordination are sustainable and fit for purpose.

P8 - Health-related Quality of Life among Adults Living with HIV: A Cross-Sectional Survey in Armenia

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Introduction
Few studies have examined health-related quality of life (HRQoL) among people living with HIV (PLWHIV) in Eastern Europe and Central Asia. Patient-level HRQoL is essential for monitoring health interventions and designing support programs.

Materials and methods
We conducted a cross-sectional survey of 180 PLWHIV aged 18 years+ in Armenia who were on cART and used the 36-Item Short-Form Health Survey to assess HRQoL. We enrolled a convenience sample of beneficiaries of the "Positive People Armenian Network" (PPAN) HIV program in March-May 2017. The following domains of HRQoL were assessed: physical functioning, physical role-functioning, emotional role-functioning, energy/fatigue, emotional well-being, social functioning, general health, and pain.

Results
The highest HRQoL domain score was 85.3 (SD 24.7) for physical functioning, followed by 82.1 (SD 25.0) for pain, 77.9 (SD 24.2) for social functioning, 76.4 (SD 39.6) for emotional role-functioning, 71.1 (SD 39.7) for physical role-functioning, and 64.0 (SD 20.3) for energy/fatigue, 63.7 (SD 22.7) for emotional well-being and 63.4 for general health 63.4 (SD 21.2). In the physical domain, chronic comorbidities and low emotional support were associated with worse physical functioning, physical role-functioning, general health and pain scores ($p<0.05$). Unemployment and hepatitis C coinfection were associated with worse physical role functioning and pain scores ($p<0.01$). As for mental HRQoL, we found that unemployment, chronic comorbidities, and lower emotional support were associated with poorer emotional well-being, energy, and emotional role-functioning scores ($p<0.05$).

Conclusions
These findings suggest that improved social support, employment opportunities, mental health services and integrated care for noncommunicable comorbidities may improve HRQoL in Armenia and similar settings.

P9 - Emerging pathogen and changing sensitivity pattern of pyogenic meningitis in a teaching institute from India

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Introduction
Bacterial meningitis is a medical emergency associated with high mortality rates. Cerebrospinal fluid (CSF) culture is the "gold standard" for diagnosis of meningitis and it is important to establish the susceptibility of the causative microorganism to rationalize treatment.

Materials and methods
All cerebrospinal fluid samples were examined macroscopically/ microscopically Culture was done by conventional methods. Organisms were identified by various bio chemical and serological tests. Atibiotics susceptibility tests was done as per standard protocol.

Results
A total of 4500 samples of CSF were collected in microbiology department in a 2 years study period (June2017-June2019). 22% (950) of samples showed bacterial growth. The ratio of adult:pediatrics population was =5:1. Maximum number of cases (534) were seen during September-December. In pediatrics population the commonest organism was Acinetobacter (35%) followed by Staphylococcus aureus (30%), α Streptococcus (20%), Pneumococcus, Eschirichia coli Klebsiella pneumoniae and Haemophilus influenza (10%). Staphylococcus aureus was the commonest organism in the adult population. Among gram negative isolates, maximum were sensitive to cefoperazone+salbactum (91%) followed by imipinem (85%), piperacillin tazobactum (78%), meropenem (71%) and netilmicillin, amikacin and ceftazidime (50%). In gram positive organisms all were sensitive to vancomicin, chloramphenicol followed by clindamicin (70%), erythromycin (64%), gentamicin (55%) and ciprofloxacin and penicillin showed least sensitivity (41%) only.

Conclusions

Acinetobacter was found to be the most common and a new emerging pathogen in the pediatric population whereas Staphylococcus aureus was the commonest organism in the adult population The resistance of the common isolates to penicillin was high.Due to emerging drug resistance to common antibiotics, Cefoperazone salbactum combination, Carbapenems (e.g., meropenem) and piperacillin-tazobactam should be considered for treating severely ill patients.

02. Clinical research

P1 - Impact of IL-10 (C-592A) polymorphism on cytokine plasma levels in HIV-infected Ukrainians

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[2]*Sumy State University - Sumy (Ukraine)*

Introduction
IL-10 regulates the immune response and remains intrinsically related to HIV/AIDS pathogenesis. Several lines of evidence suggest important roles for IL-10 gene single nucleotide polymorphisms in variations of HIV infection. The aim of this study was to identify IL-10 plasma levels depending on genotype carrier state. We hypothesized that minor genetic variant may influence cytokine concentration in HIV-infected Ukrainians.

Materials and methods
Cross-sectional comparison of IL-10 plasma level using multiplex immunoassay between 78 HIV-infected persons and 100 healthy controls in Sumy region (Ukraine). IL-10 (C-592A) polymorphism was determined by PCR-RFLP. Statistical analysis was performed using SPSS software.

Results
Concentrations of IL-10 in healthy controls with minor allele were less than those with CC genotype ($p<0.01$). We found the same pattern in patients with HIV: cytokine levels in HIV-infected with homozygous CC variant prevailed over heterozygotes CA ($p<0.05$) and minor AA variant carriers ($p<0.001$). Plasma concentration of IL-10 in patients with HIV exceeded healthy controls with relevant genotypes ($p<0.01$). We registered higher values of cytokine in HIV-infected with CD4 T-cell count ≤200 cells/μL (genotype CC - (22.76±6.82 pg/ml), CA - (17.46±3.76) pg/ml), that exceeds AA genotype ($p<0.01$) and demonstrates increased production of IL-10 in the terminal stage of illness, regardless of the genotype variant.

Conclusions
Allelic variants of IL-10 gene determine cytokine plasma levels in Ukrainians - minor genotype is associated with low concentration of IL-10. High levels of IL-10 in HIV-infected minor allele carriers may suggest severe immunodeficiency and can be considered as an unfavorable factor.

03. HIV, hepatitis and ageing comorbidities

P1 - Late Presenters Among Newly Diagnosed Individuals with HIV/TB co-infection

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Introduction
Early initiation of antiretroviral therapy (ART) significantly reduces the morbidity and mortality in HIV-infected people. Nerveless, about 45% of persons with HIV worldwide present for care at late stages of HIV-infection. Starting ART at an advanced stage of disease significantly reduces the risk of successful therapy, especially in people with TB co-infection. The goal of the study was to analyze the factors associated with late presenting (LP) for care among persons with HIV/TB comorbidity.

Materials and methods
A retrospective data collection and analysis was performed among cohort of patients admitted at the Tuberculosis Clinic from 2018-2020 years. Individuals with CD4 ≤350 cells/μL were defined as late presenters (LPs).

Results
Out of 704 HIV/TB patients enrolled in the study 55.3 % (95% CI: 51.4-59.2) were newly diagnosed (ND) with HIV. Out of ND patients, LPs accounted for 78.9%: 11.6% (95% CI: 8.4-14.8) patients with CD4 ≤350 cells/μL and 67.4% (95% CI: 64.1-70.7) with CD4 ≤200 cells/μL. There was a decrease of LPs among ND in 2019 63.9% vs 83.2% in 2018. However, in 2020 the number of LPs amounted up to 92.5%, (p< 0.001). About 21.8% (95% CI: 17.9-25.7) of the LPs had a persistently low CD4 count, below 200 cells/ml despite ART. There was no difference in age median between LPs and non-LPs: 39.4 years (IQR 21÷62) and 38.9 years (IQR 22÷75), respectively. The age median for men was 39.5 and for women 38,3 years. LPs age group 34-39 years was dominant vs non-LPs: OR 1.62 (CI: 0.92-2.93). The majority of LPs were male: 80.8%, OR 1.49 (CI: 0.95-2.24). Heterosexual route of HIV transmission and IDU among LPs vs non -LPs were: 49.8% vs 43.9% and 50.5% vs 56.1%, respectively. MSM accounted for 7.8% in non-LPs.

Conclusions
Significant risk factor for LP was being male and of younger age group 34-39 years. Rather high number of LPs with advanced HIV disease (70.8%) among HIV/TB patients' cohort indicates the need for targeted interventions with special focus on this group of individuals.

04. Clinical management of PLHIV

P1 - Prevalence of renal disorders in people living with HIV/AIDS on ARVs treatment at the foumban district hospital, Cameroon

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[2]Université Des Montagnes - Bangangté (Cameroon)

Introduction
HIV remains a major public health threat and the uses of ARVs have proven to be only effective weapon in limiting the occurrence and prolonging life expectancy and livelihood of PLWHIV. The objective of our study was to assess impaired renal function in people living with HIV/AIDS on ARVs at Foumban District hospital.

Materials and methods
An analytical and descriptive study was conducted and blood samples were collected from PLWHIV on ARVs followed at Foumban District hospital. The assay of serum creatinine and urea using to evaluate the kidney function of all our participants.

Results
Of 106 patients recruited 87 were on ARVs and 19 were naïve on ARVs,34 had high creatinine serum and 32 had a high urea serum. There was a significant difference of renal disorders to Tenofovir and a significant difference in the distribution or renal insufficiency according to the duration of treatment.

Conclusions
The prevalence of renal disorders was significantly is 29.88% based on use of ARVs in PLWHIV. This study showed that Tenofovir antiretroviral therapy was a significant risk factor of renal disorders in PLWHIV in Foumban Cameroon.

P2 - Examining the efficacy in clinical practice of the dual antiretroviral therapy regimen of boosted protease inhibitors with maraviroc

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Introduction
A focus on reducing long-term drug exposure while maintaining viral suppression has led to new strategies for treatment-experienced patients involving dual therapy. Maraviroc (MVC), a chemokine receptor 5 co-receptor antagonist, is licensed for use in treatment experienced HIV-1 positive patients. Boosted protease inhibitor (bPI) with MVC is not a recommended combination in guidelines. In

the past, this option was chosen for selected patients with some declining to switch despite evidence. We set out to assess the outcomes of patients who have or are currently receiving this combination in our clinic

Materials and methods
All patients prescribed a bPI with MVC until December 2018 were identified through our HIV database. Age, sex, and time on ART before/after switch were collected. A review of medical records determined reasons for switch off bPI/MVC where relevant

Results
In total 114 patients (mean age 53 years (range 33-76), 80% male) had been prescribed a bPI/MVC. The median time on ART prior to bPI/MVC switch was 13 years. Patients stayed a median of 4 years on bPI/MVC; 63 (55%) patients were on MVC 300mg dosing while 51(45%) were dosed at MVC 150mg. At censure 69 (61%) remained on bPI/MVC, 30 (26%) had switched ART, 7 (6%) died, 7 transferred their care, and 1 was lost to follow up. Reasons for switching included hyperlipidaemia (n=6), lipodystrophy (n=2), rationalisation (n=6), drug interactions (n=5), potential toxicity (n=5), side effects (n=1), no documentation (n=1) and viral failure (n=5). Four of the five patients who failed therapy reported issues around adherence. Of patients who remained on bPI/MVC 97% (67/69) were virally suppressed (median duration 4.5 years)

Conclusions
We continue to proactively review patients on bPI/MVC and suggest contemporary alternatives but our data suggest that, if adherence is good, established patients may be reassured about the safety and efficacy of this approach

05. Prevention

P1 - Effective Communication for Disease Prevention in Remote Areas of Sub-Saharan Africa (Community Tablet Pilot Project)

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[2]*Community Tablet Southern Africa - Maputo (Mozambique)*

Introduction
Communities in the remote areas of Sub Saharan Africa are marginalized in what concerns to health care services and basic information that affect their well-being. During the Coronavirus pandemic we have implemented a pilot project for dissemination of effective information for the prevention of the spread of the disease using digital tools such as quizzes, videos, virtual interaction with health practitioners. The purpose of the study was to assess how digital tools can increase the level of understanding of such messages in the disadvantaged communities.

Materials and methods
The Community Tablet is a trailer that comprises a 110 inch screen with loud speakers, 4 touch screens that allow quizzes, educational gaming, questionnaires. A video was showed with the basic explanation about the coronavirus pandemic, how it is spread and the prevention measures recommended by the Health Institutions. After the video an online Q&A session with a health practitioner was carried out and attendees had the opportunity to clarify their concerns, including regarding the vaccination process. The gaming, quizzes and questionnaires were used to assess the level of understanding of the message conveyed. Direct interviews were also carried out in order to identify possible shortcomings of the used tools. All materials were translated into local dialect, sign language and text to voice and vice versa as the majority of the attendees couldn't read or write.

Results
98% of the attendees understood the basic message on the prevention of the spread of the disease and were satisfied with the campaign. 32% were skeptical regarding the effectiveness of the use of masks.

Conclusions
80% of the attendees had never heard of the coronavirus nor new about the seriousness of the pandemic. Digital tools makes communication easier when compared with traditional campaigns. More campaigns on the matter are necessary particularly when skepticism regarding vaccination is taken into consideration.

Community Tablet for Effective Communication

P2 - No more no less. My health is priceless. An intervention based on Human Rights and gender equality, to promote access for sex workers to sexual health services and prevention of HIV an

J. Ramírez Urbina, E. Ramírez Balderas
Colectivo Seres, A.c. - Fraccionamiento Arboledas (Mexico)

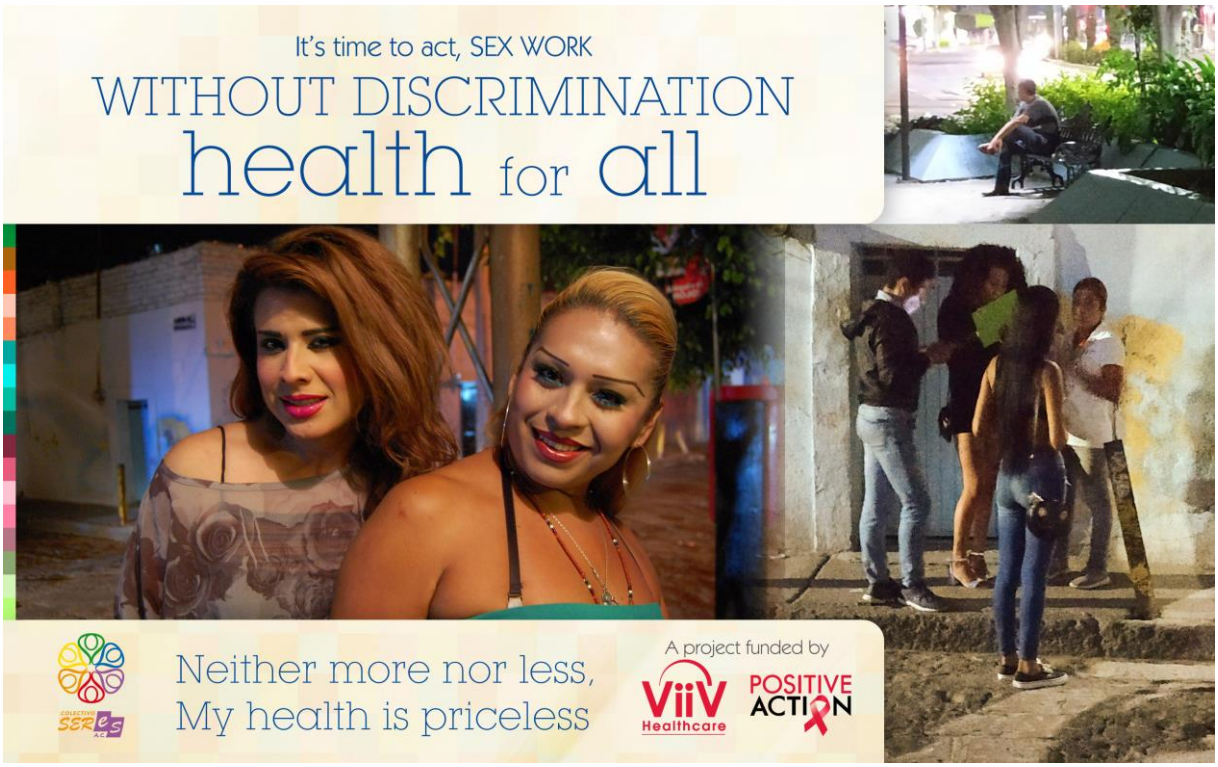
Introduction
As a consequence of the internal stigma in people who practice sex work, originated and accentuated by the social stigma associated with HIV, these are factors that represent barriers to achieving the exercise of the Right to Health, to impact prevention, care, diagnosis and timely and quality treatment of people.Eliminating structural and social barriers, to guarantee social inclusion to the Right to Health, constitute priority actions to advance in the Sustainable Development Goal 3.

Materials and methods
The general method of the intervention is based on the components of Combined Prevention, introductions Bio-Psycho-Social strategies for the development of people, promoting self-care through reflection, self-criticism and empowerment. Implementation of a space for communication and care in Bio-Psycho-Sexual Health for sex workers, which favors the elimination of internal stigma, self-esteem and trust. A strategy to generate key intersectoral alliances to promote a social environment free of violence and discrimination, and recognition as subjects of Human Rights.

Results
The project reached 160 people who practice sex work in three municipalities of the state, favoring the increase in effective access to the Right to Health. At the end of the intervention, 33%, 52.8 people declared having attended a sexual health service, promoting the habit of self-care. The participation of public institutions favored the provision of inclusive health services. Sex workers got into the habit of getting tested for HIV on a regular basis.

Conclusions
Knowledge of the socio-cultural context is necessary to identify risk practices and implement strategies in the prevention, care, diagnosis and treatment of HIV. Services should be based on people's priorities, this allows people to be actively included in HIV prevention and social transformation in relation to stigma and discrimination.

Project image



06. Emerging infectious diseases

P1 - Bidirectional transmission of viral pathogen.

J. Nandi [1], S.S. Rathore [2], B.R.J. Mathur [3]
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[2]Rajasthan Zoo, - Jodhpur (India), [3]Govt. Veterinary Dept. - Jodhpur (India)

Introduction
Unlike the African scenario, consumption of 'bushmeat' is not common in India. But because of the religious status of monkeys, there has been a close man-monkey interaction here. The presentation reveals for the first time natural lentiviral infection of wild Indian rhesus monkeys (*Macaca mulatta*) and langurs (*Semnopithecus entellus*) by SIVs that are phylogenetically diverse from all known SIVs, including "SIVmac", which infects captive rhesus monkeys. The novel SIVs are intriguingly homologous to HIV-1, based on serology and partial lentiviral genomic sequence analyses.

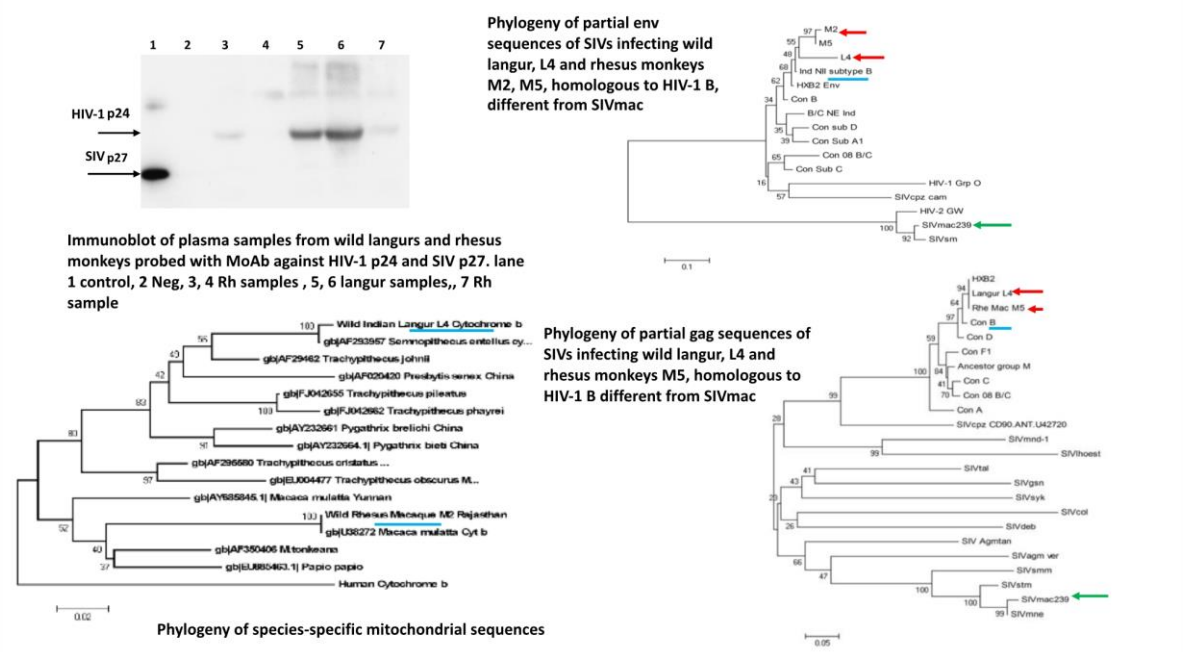
Materials and methods
Blood samples from 36 feral rhesus monkeys from Jaipur and 9 langurs from Jodhpur were collected in 2010 and 2016 by temporary trapping of the feral simians in collapsible cages, with official permission to investigate natural lentiviral infection. Preliminary screening of the samples was performed using HIV-1 WB test, and immunoblot test using monoclonal antibody against gag antigens of HIV-1 (p24) and SIV (p27). Positive RT-PCRamplicons were directly sequenced Viral sequences were determined by standard bioinformatics tools and molecular phylogeny.

Results
Fifteen rhesus macaques out of 35 samples analyzed (45%), and 6 of 9 (66.6%) langur samples were found to be seropositive by HIV-1WB assay. Amplification of partial lentiviral genome and sequencing of the amplicons revealed unexpected, striking homology with HIV-1 subtype B sequences.

Conclusions
A counter-intuitive reverse transmission of HIV-1 from infected humans to simians through aggressive monkey bites in India is proposed From the present report, it cannot be stated if the reverse transmission events represent more than one transmission from

man-to-monkey or if this was a single transmission event that led to subsequent transmission between langurs and macaques living in close proximity in the natural habitat. Only further detailed epidemiological and virological studies will address these questions.

Bidirectional transmission of pathogens



P2 - A novel antiviral micro-RNA targeting the NS1 protein of the H1N1 pandemic human Influenza virus and a corresponding viral escape mutation

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Introduction

The NS1 protein is one of the major regulators of IAV pathogenicity, able to suppress innate immune response and host protein synthesis and it is exclusively produced in infected cells. A number of aminoacidic substitutions in the NS1 gene have been reported to have accumulated during pandemic and post-pandemic circulation of A(H1N1)pdm09 viral strains and strong evidence support a role for positive selection at different amino acid positions important for antigen recognition and immune escape.

Materials and methods

The sequences of the NS1 protein from 200 Italian strains of the A(H1N1)pdm09 IAV in the 2009-10 (n = 89) and 2010-11 (n = 111) were stratified according to the severity of symptoms. The C112A polymorphism showed strong association ($p < 0.02$) to the most severe symptoms group. Bionformatic analysis identified the human micro RNA hsa-miR-1307-3p as affected by this mutation. Stable hsa-miR-1307-3p overexpressing cell lines were used for infections with wild tye and C112A clinical isolates and NS1 levels as well viral replication was assessed. Transcriptomic analysis was perfomed on the same cell lines to identify genes regulated by hsa-miR-1307-3p.

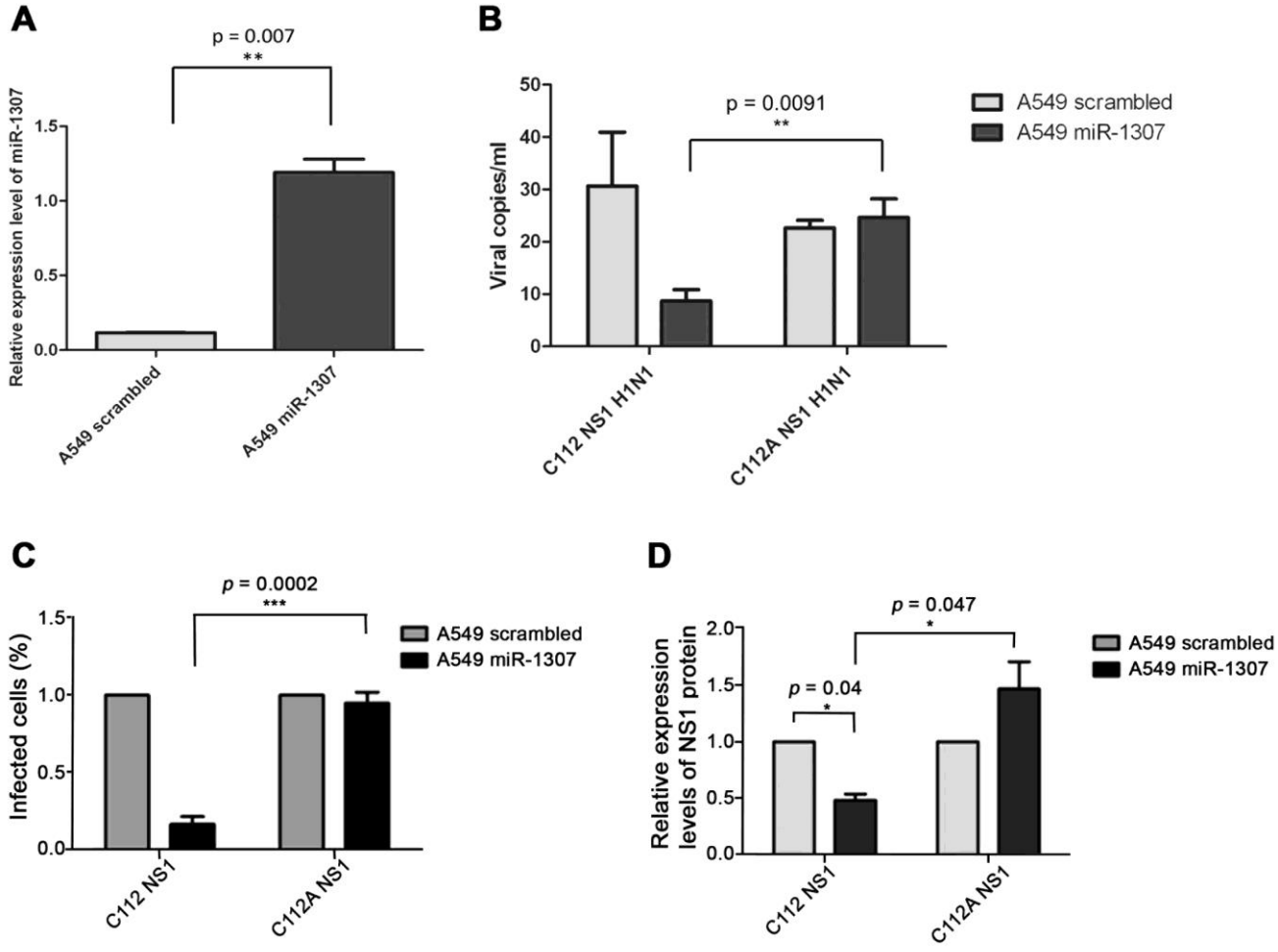
Results

In the present study, we identified a natural polymorphism causing nucleotide substitution C112A at codon 38 of the NS1 protein, which is within the target site of the human micro RNA hsa-miR-1307-3p. We found that overexpression of hsa-miR-1307-3p in A549 cells reduced wild type NS1 expression and replication of A(H1N1)pdm09 viruses carrying the wild type gene, but it did not affect viruses bearing the NS1 C112A mutation. Our microarray analysis indicated a role of hsa-miR-1307-3p in promoting cell proliferation and inhibiting apoptosis.

Conclusions

To the best of our knowledge, this is the first validation of suppression of IAV H1N1 NS1 by a human micro RNA and the first example of an escape mutation from micro RNA-mediated antiviral response for the A(H1N1)pdm09 virus.

C112A confers resistance to miRNA inhibition



07. Coronaviruses

P1 - Calpeptin blocks SARS-CoV-2 entry

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Introduction
The severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) responsible of the Coronavirus disease 2019 (COVID-19), is an ongoing threat to humankind. Vaccines against SARS-CoV-2 have proven highly effective, but highly transmissible virus strains with mutations on the viral entry Spike (S) protein may limit vaccine effectiveness overtime, highlighting the need for additional therapeutics against this virus, namely small molecule inhibitors of virus entry into target cells.

Materials and methods
We performed a robust high throughput of SARS-CoV-2 entry screening assay of 15,000 small molecules, using a pseudotyped virus luciferase reporter expressing the SARS-CoV-2 S protein (SARS2-S). The activity of the best molecule was validated in a suite of mechanism-directed assays and against viruses pseudotyped with SARS-CoV-1 S (SARS1-S) and SARS-CoV-2 S from novel circulating variants. Molecular docking of the best molecule was performed.

Results

Calpeptin, an inhibitor of Calpain I/II and Cathepsin L/K, was identified as a potent cell entry inhibitor of SARS2-S, blocking both the endosomal and cell membrane fusion entry pathways. Calpeptin specifically inhibited the infection of susceptible SARS-CoV cells with SARS1-S or SARS2-S with S protein from newly highly transmissible strains. As expected, Calpeptin did not affect the main SARS-CoV-2 proteases activity. Importantly, Calpeptin blocked SARS-CoV-2 infection of Vero E6 cells rich in the SARS-CoV-2 receptor, the ACE2 receptor, better than the FDA approved Remdesivir. Molecular docking shows direct binding of Calpeptin to the residues involved in the interaction S protein – ACE2.

Conclusions
Calpeptin was identified as a specific anti-SARS-CoV-2 entry inhibitor. Calpeptin has been previously shown to safely block aberrant calpain activation that induces pulmonary, heart and neurologic diseases in mice. Similar conditions overlap with coronavirus infection. Together, these results suggest that Calpeptin should be explored for the treatment of COVID-19.

P2 - Evaluating Awareness of Preventive Measures for COVID-19 and Their Presence in Behaviour of HIV-Infected Individuals during Epidemic

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Introduction
To study the dynamics of understanding of the preventive measures for coronavirus, and scenarios of preventive behaviour of HIV-infected individuals during the spread of coronavirus with the aim of correction of preventive actions.

Materials and methods
A survey was conducted with the HIV-infected individuals. Group 1 consisted of 79 HIV-infected individuals who participated in the survey in the period from 21st May to 15th June 2020; Group 2 consisted of 81 HIV-infected individuals who participated in the survey in the period from 16th October to 27th November 2020.The awareness of preventive measures for coronavirus was evaluated based on the responses to an open-ended indicator question “Which preventive measures for coronaviral infection do you know?”.The behavioural strategies aimed at prevention of coronavirus were analysed based on the responses of the respondents to an indicator question “Which methods of protection against coronavirus do you use?”. The survey was also aimed at the analysis of the needs of the patients related to getting help with coronavirus.

Results
Most of the respondents mentioned personal protective equipment (PPE) as the preventive measure for coronavirus: 75 and 77% in Groups 1 and 2, accordingly. Most frequently the respondents use PPE to prevent coronaviral infection: 86 and 94% in Groups 1 and 2, accordingly. The most pronounced demand in both groups related to getting medical care (26 and 28%); 4 respondents in Group 2 mentioned immunization, while in Group 1 no such demand was registered.

Conclusions
When providing counselling for people with HIV from the perspective of coronaviral infection, including that related to immunization, it should be taken into account that the target group has low awareness of the preventive measures for COVID-19;however, these people tend to use PPE.Self-isolation is the least supported restrictive measure among the respondents. The biggest demand is for getting medical care.

P3 - In-depth longitudinal comparison of clinical specimens to detect SARS-CoV-2

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Introduction

Testing and isolation of COVID-19 patients are indispensable tools to control the ongoing COVID-19 pandemic. PCR tests are considered the “gold standard” of COVID-19 testing and mostly involve testing of nasopharyngeal swab specimens. Our study aimed at comparing the sensitivity of various samples specimens, including nasopharyngeal, oropharyngeal, saliva, throat washing and rectal specimens.

Materials and methods

75 COVID-19-confirmed participants were included in the study. Nasopharyngeal swabs, oropharyngeal swabs, saliva, throat washing and rectal specimens were collected as well as pooled swabs. Participants were asked to fill a questionnaire in order to correlate specific clinical symptoms and symptom duration with sensitivity of various sample specimens. Sampling was repeated overtime to perform a longitudinal analysis of sample specimens’ sensitivity.

Results

At the first time point, the highest percentages of SARS-CoV-2 positive samples were observed for nasopharyngeal samples (84.3%) while 74%, 68.2% and 58.8% were tested positive for throat washing, saliva and oropharyngeal samples respectively. Interestingly, 64% of samples tested negative via nasopharyngeal samples were positive using throat washing specimens collection method. Sensitivity of all sampling methods but throat washing samples decreased rapidly at later time points compared to the 1st collection date. Indeed, throat washing method performed better than the gold standard nasopharyngeal swab at the second and third time points after the 1st positive testing date.

Conclusions

Nasopharyngeal swabs were the most sensitive specimens early after symptoms onset. Throat washing is an easy-to-perform, cheap and sensitive alternative method. SARS-CoV-2 persists longer in the throat and the saliva than in the nasopharynx.

Figures 1. Sensitivity of sample specimens

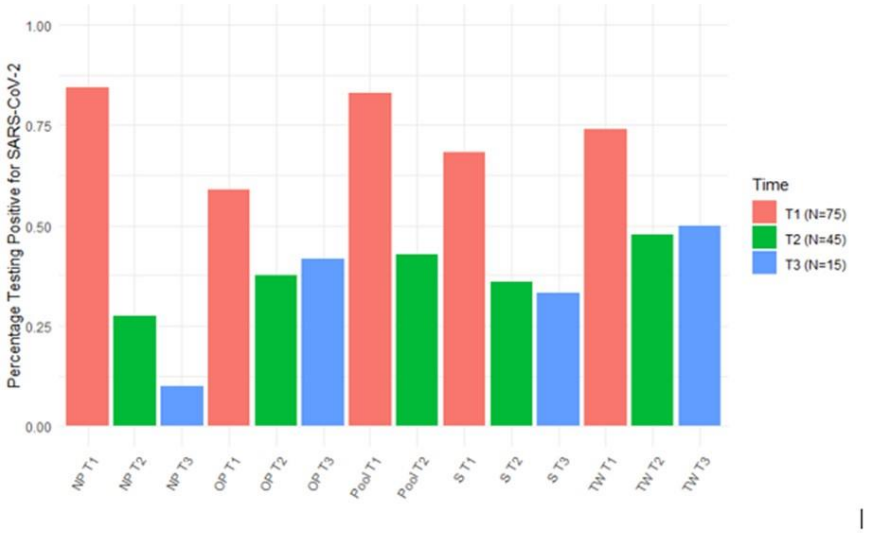

Figure 1. Percentage of positive tests per samples type at T1 (N=75), T2 (N=45) and T3 (N=15). Percentage of pool sample at T3 is not indicated, as only one sample was available.