Diagnotics, Indianapolis, IN, USA). The correlations with HIV viral loads and CD4+ T-cell counts were further analyzed.
Results: Totally 291 HIV-infected cases were enrolled. Their mean ages were 35.9 (standard deviation; 9.4) years, male : female ratio ; 254 (87.3%) : 37(12.7%). Among them, 98.8% (168/170) showed CMV IgG positivity. Ninety-five patients (32.6%) had CD4+T cell count >=500 cells/uL; 156 patients (53.6%), >=200 - <500cells/uL; and 40 patients (13.7%), <200cells/uL. In addition, 23 (7.9%) patients had HIV viral load >=100,000 copies/ml; 98 patients (33.7%), >=400 - <100,000; 50 patients (17.1%), >=20 - <400; and 120 patients (41.2%), < 20 copies/ml. Among them, 268 cases (92.1%) had negative CMV DNA detection, 16 cases (5.5%) had detectable CMV DNA (<150 copies/mL), and 7 cases (2.4%) had CMV DNA>150 copies/ml. Patients who had CD4+ T cell counts<200 cells/uL have 5 times of odds ratio to develop CMV viremia, compared to subjects who have CD4+ T cell counts > 500 cells/uL. Patients who had HIV viral load >100,000 copies/ml have 129 times of odds ratio to develop CMV viremia, compared to subjects who have HIV viral load <20 copies/ml.
Conclusion: Early initiation of highly active antiretroviral therapy would prompt the recovery of immune deficiency, and certainly alleviate the burden of CMV viremia.

PS 2-338

CLINICAL EXPERIENCES IN INTERPRETATION OF HIV-1 WESTERN BLOT INDETERMINATE RESULTS

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Purpose: According to the guidelines published by Taiwan Centers for Disease Control, status of HIV infection has to be confirmed by a positive Western blot (WB) results after the HIV-1/2 antibody screening assay. However, the interpretation of WB results might vary according to the package inserts of the commercial manufacturers, which might cause disagreement between different clinical laboratories.
Methods: The clinical outcomes of 1712 patients whose specimens were sent for HIV WB tests between May 2006 and April 2012 were analyzed. The BIO-RAD NEW LAV BLOT I, II was used by the Virology laboratory of the National Taiwan University Hospital.
Results: Between the study period, a total of 1712 HIV WB-I tests were performed, which include 1015 positive, 285 indeterminate, and 412 negative results. For those who are determined as HIV WB-I positive, they are sero-positive for GP160 (N=1,014), GP110/120 (N=995), P68/66 (N=973), P55 (N=885), P52/51 (N=941), GP41 (N=945), P40 (N=602), P34/31 (N=902), P24/25 (N=937), and P18/17 (N=679). For the indeterminate HIV WB-I, four patterns are most common and they are P24/25 (N=46), P18/17 (N=26), GP160 + P55 + P24/25 (N=22), and P55 (N=22). Among the 22 patients reactive with GP160 + P55 + P24/25, 20(91%) are confirmed with HIV infection status and two were lost of follow-up.
For HIV WB-II, among the 228 tests, none was positive. 98 are indeterminate and 130 are negative. Most of the indeterminate HIV WB-II are sero-positive with P26(N=57). None of them are confirmed with HIV-2 infection at the end of the study period.
Conclusions: Based on the study results, for those who have indeterminate WB results, two or more interpretation criteria are suggested to help interpretation, such WHO CRITERIA: 2ENV ± GAG ± POL and US CENTER FOR DISEASE CONTROL CRITERIA: ENV + P24 / 25.

PS 2-339

HIV-1 CRF08_BC MUTANTS RESISTANT TO REVERSE TRANSCRIPTASE INHIBITORS

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Purpose: Human immunodeficiency virus type (HIV)-1 circulating recombinant form 08_BC (CRF08_BC), carrying recombinant reverse transcriptase (RT) gene from subtype B and C, has recently become highly prevalent in Southern China. As the number of patients infected by CRF08_BC increases, it is important to characterize the drug resistance mutations of CRF08_BC, especially against widely used antiretrovirals.
Methods: In this study, clinically isolated virus was propagated in human peripheral blood mononuclear cells (PBMCs) with increasing concentrations of nevirapine (NVP), efavirenz (EFV) or lamivudine (3TC).
Results: Three different resistance patterns led by initial mutations of Y181C, E138G and Y188C were detected after *in vitro* selection with NVP. Virus variants with initial mutations, in combination with three other previously reported substitutions (K20R, D67N, V90I, K101R/E, V106I/A, V108I, F116L, E138R, A139V, V189I, G190A, D218E, E203K, H221Y, F227L, N348I and T369I) or novel mutations (V8I, S134N, C162Y, L228I, Y232H, E396G and D404N) developed during NVP selection. EFV-associated variations contained two initial mutations (L100I and Y188C) and three other mutations (V106L, F116Y and T139V). Phenotypic analyses showed that E138R, Y181C and G190A contributed high level resistance to NVP, while L100I and V106L significantly reduce virus susceptibility to EFV. Y188C resulted in a 20-fold reduction of susceptibility to both NVP and EFV. M184V was selected by 3TC as expected. This mutation, alone or with V90I or D67N, decreased 3TC susceptibility by over 1000 folds.
Conclusion: These results have brought new insight into the development of drug-related mutations in patients and provided useful information for the optimization of antiretroviral regimens.

PS 2-340

PEGYLATED INTERFERON/RIBAVIRIN TREATMENT HIGHLY EFFECTIVE IN HIV/HCV-COINFECTED MEN WHO HAVE SEX WITH MEN IN TAIWAN: SINGLE MEDICAL CENTER EXPERIENCE

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Purpose: A recent outbreak of HCV infection has been identified among HIV-infected men who have sex with men (MSM) worldwide, including Taiwan since 2006. Pegylated interferon (PEG-IFN) with ribavirin (RBV) remains standard of treatment in most Asian countries. However, very few studies have evaluated the treatment efficacy in such particular population.
Methods: We conducted a single-centered, retrospective cohort study of HIV-1 infected patients in Northern Taiwan from 2006 to 2014. Persistent HCV infection was diagnosed with positive anti-HCV serology and a detectable HCV viral load. Clinical characteristics, HIV-1 infection status, use of antiretroviral therapy (ART), HCV genotypes, and IL-28B genotypes were collected at baseline, during PEG-IFN plus RBV treatment, and at follow-up.
Results: Fifty-four patients had persistent HCV infection, of whom 43 were MSM. They were significantly younger and received ART with an undetectable HIV-1 viremia more often than the other cohort (Table). Thirty-four MSM were eligible for treatment and had a very high sustained virological response (SVR) rate regardless of HCV genotypes (80.0% [4/5] for GT 1, 100.0% [7/7] for non-GT 1, $p = .417$). Skin manifestations (local injection reaction and alopecia), anemia, and depression were the most frequent adverse effects.

Table Demographic Features and Treatment Outcome

Characteristics	MSM (N=43)	IDU and others (N=11)	P value
Age (years)			
Median [IQR]	34 (30–40)	43 (41–51)	.011
Ongoing ART			
Any	41 (95.3%)	5 (45.5%)	< .001
Last HIV-1 RNA (copies/mL)			
<40	32/40 (80.0%)	4/11 (36.4%)	.009
HCV Genotype			
GT1	11/31 (35.5%)	7/10 (70.0%)	.075
GT2	18/31 (58.1%)	2/10 (20.0%)	.067
GT6	0/31 (0.0%)	1/10 (10.0%)	.244
Treatment Outcome			
RVR	17/26 (65.4%)	3/6 (50.0%)	.647
EVR	21/21 (100.0%)	5/5 (100.0%)	NA
SVR	18/19 (94.7%)	0/1 (0.0%)	.100

Conclusions: Given a highly effective and relative safe profile in HIV/HCV coinfected MSM in Taiwan, more aggressive treatment with PEG-IFN plus RBV should be considered.

PS 2-341

HIGH RATE OF HIV-1 DRUG RESISTANCE IN TREATMENT-EXPERIENCED PATIENTS IN SOUTHERN TAIWAN, 2009-2014.

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Purpose: Genotype testing for HIV-1 drug resistance is useful for selecting antiretroviral drug regimens for patients experiencing therapeutic failure. The aim of the present study is to monitor the resistance trend in treatment-experienced patients to guide the antiretroviral therapy in southern Taiwan.
Methods: A retrospective cohort study on HIV-1 drug resistance was conducted in antiretroviral therapy -experienced HIV-1 −infected individuals at Kaohsiung Veterans General Hospital from 2009 to 2014. Genotypic drug resistance was determined by ViroSeq™ system. Risk factor for drug resistance was analyzed by Chi-square or Fisher's exact tests, and non-categorical variables were compared using the Mann-Whitney *U* test
Results: From 2009 to 2014, a total of 65 patients had tested for resistance, of whom 87% were infected by MSM, and 13% were infected by heterosexual. The prevalence rate for syphilis infection was 45%, hepatitis A 18%, hepatitis B 8% and hepatitis C 3%. Subtype B HIV-1strains were found in 86% of the individuals, subtype CRF01_AE in 11% and subtype C in 3%. The resistance rates to any three classes of antiretroviral therapy (NRTI, NNRTI and PI) were 94%. The prevalence rate for NRTI, NNRTI and PI resistance was 72%, 77% and 9%, respectively. The most common NRTI resistance associated mutation was M184V (65%) and L74V (17%).The most common NNRTI resistance associated mutation was K103N (29%), Y181C (29%) and V179D (20%). The most PI resistance associated mutation was A71T (17%), A71V (12%) and L10I (8%). The presence of drug resistance was associated with longer duration of current failing anti-retroviral therapy (p=0.036).

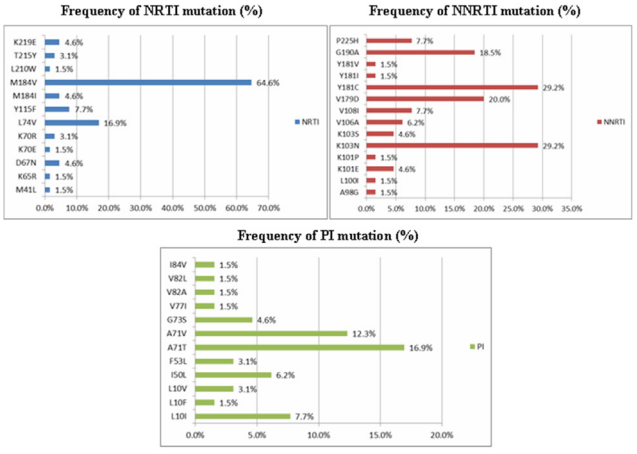

Figure. Frequency of NRTI, NNRTI and PI-associated mutation (%).

Conclusions: Our findings showed a high rate of antiretroviral drug resistance in patient failure to the first line anti-retroviral therapy in southern Taiwan. This result could better guide us in the development of efficacious and effective management plans and strategies for treatment failure patients.

PS 2-342

INVESTIGATION OF YMDD MOTIF ANALYSIS FOR SIMULTANEOUS DETECTION OF HBV GENOTYPE AND LAMIVUDINE RESISTANCE

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Purpose: The aim of this study is to investigate the YMDD motif amplification and sequencing for detection of HBV genotype and Lamivudine resistance simultaneously.
Methods: The YMDD motif was amplified by polymerase chain reaction (PCR) with specific primers and the products were sequenced. The sequence of YMDD motif was analyzed by "The genotype" software of the NCBI (http://www.ncbi.nlm.nih.gov/projects/genotyping/formpage.cgi) for HBV genotyping and detection of 3TC resistance (YMDD motif analysis). RFLP of the S gene was also performed for HBV genotyping and comparison with the results of YMDD motif analysis. HBV viral load was measured by the COBAS TaqMan 48 Real-Time PCR System.
Results: A total of 90 HBsAg positive specimens with vial load >1000 IU/ml were included for study. By YMDD motif analysis, 60 genotype (GT-) B (66.7%), 29 GT-C (33.2%), and 1 GT-D (1.1%) were identified and these results were 100% in accordance with the results obtained by RFLP (**Figure**). Eighty-seven (96.7%) were YMDD wild-type, 2 (2.2%) were YVDD mutant, and 1 (1.1%) was YIDD mutant.
Conclusions: YMDD motif analysis is a simple and accurate method for simultaneous detection of HBV genotype and Lamivudine resistance.