

Viral and Host Factors are Related to the Progression of HIV Diseases in Mimika, Papua

Mirna Widiyanti^{1*}, Moch Irfan Hadi²

¹Balai Penelitian dan Pengembangan Kesehatan Papua, Indonesia, ²Universitas Islam Negeri Sunan Ampel, Surabaya, Indonesia

Abstract

Citation: Widiyanti M, Hadi MI. Viral and Host Factors are Related to the Progression of HIV Diseases in Mimika, Papua. Open Access Maced J Med Sci. 2019 Oct 30; 7(20):3429-3432.

https://doi.org/10.3889/oamjms.2019.437

Keywords: HIV-1 genotype; HIV/AIDS progression; Mimika

*Correspondence: Mirna Widiyanti. Balai Penelitian dan Pengembangan Kesehatan Papua, Indonesia. E-mail: ninawidhy@gmail.com

Received: 14-Aug-2019; Revised: 15-Sep-2019; Accepted: 16-Sep-2019; Online first: 14-Oct-2019

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Funding: This research did not receive any financial support

Competing Interests: The authors have declared that no competing interests exist

BACKGROUND: Papua has a high cumulative number of HIV, which has expanded epidemic status with the most risk factors are heterosexuals.

AIM: This study aims to determine factors associated with HIV disease progression include host and viral factors.

METHODS: Eighty-four subjects recruited in Rumah Sakit Mitra Masyarakat (RSMM) VCT's laboratory, interviewed with questionnaires and also did laboratory examinations. HIV-1 subtypes were identified using RT-PCR, nested PCR and sequencing. Then, CD4+ data is checked using PIMA Analyzer. Demographic and clinical data obtained from the patient's medical record. After collected, data were analysed using Fisher's exact test.

RESULTS: The results showed two factors that influence the progression of HIV disease were HIV subtypes (p = 0.002) and Body Mass Index (p = 0.033). The HIV-1 subtype also correlated with CD4+ levels with a value of p = 0.04.

Introduction

The report that provides by UNAIDS that the number of people living with HIV in the world reached 34 million people with 17 million (50%) are women, and 2.1 million are children less than 15 years [1]. In June 2018, Papua recorded with the cases of HIV were 14.315 inhabitants and 2.114 people are dead because of AIDS. Heterosexuals are the highest risk factors of HIV transmission in Papua with 13.888 cases, followed by mother to infant transmission by 208 cases [2].

Generally, it needs eight to ten years for HIV to develop into AIDS. Several factors were found to contribute to the progression of HIV infection is a factor immunological, virological, environmental and genetic factors hosts [3], [4], [5], [6]. Factors that may affect the host is the Human Leukocyte Antigen (HLA), CYP polymorphisms, gender, age, ethnicity,

psychosocial and body mass index (BMI). Environmental factors that affect the progression of diseases such as transmission modes and socioeconomic status [7]. Viral factors, including viral subtypes or mutations that destroy the virus [8].

A study in Thailand found that the subtypes of HIV-related manner and speed of transmission, where subtype B associated with the transmission of homosexuals and intravenous drug users (IDUs), while subtypes A, CRF01_AE, and C related to heterosexual transmission [9]. Studies conducted in Tanzania and Uganda found that subtype D correlated faster with a decrease in CD4⁺ T cells and increased disease progression than other subtypes and recombinant forms [10], [11]. However, a retrospective cohort study conducted during 1996 and 2007 reveals that Africans infected with subtype B has the progression of HIV/AIDS faster than those infected with non-B subtypes [12].

Many studies in other countries have reported

Open Access Maced J Med Sci. 2019 Oct 30; 7(20):3429-3432.

correlations between various factors with the progression of HIV disease, but in Indonesia, the data is still limited or limited.

The purpose of this study is to determine what factors associated with the progression of HIV disease, including host factors, environmental and viral factors.

Material and Methods

Study and subject

The study was conducted for ten months, from January to October 2015. Blood sampling was taken at the VCT Laboratory of Rumah Sakit Mitra Masyarakat (RSMM) Mimika. Samples are HIV/AIDS patients were selected for continuous sampling and has received antiretroviral therapy who have met the inclusion criteria. Calculation of sample size for crosssectional design uses the Lemeshow formula from the calculation results obtained eighty-four respondents. The results from interviews of demographic and clinical data with questionnaire collected for further processing. CD4⁺ examination uses the PIMA and haematology Analyzer examination using Sysmex.

Subtyping HIV

The extraction process uses a standard kit from Qiagen with catalogue # 52906. Firstly RT-PCR (Reverse Transcriptase-Polymerase Chain Reaction) amplification using a specific primer. The primers used are obtained from the HXB2 reference journal access code Geneva K03455 (http://hiv.web.lanl.gov/NUM-HXB2.MAIN.html).

Second is electrophoresis, and this stage aims to see the results of amplification in the previous step. The PCR results were detected by electrophoresis of 5 ul PCR products plus 1 ul loading buffer on 2% agarose gel and 100 v voltage for 40 minutes. The PCR product was visualised by placing the gel on the docgel. DNA isolates which showed a band of 460 bp were affirmed to contain the target gene. The next stage is sequencing; Sequencing is done to find out the nucleotide sequence in several PCR gene envelope products. Sequencing using ABIPrism 3500 Genetic Analyzer (Applied Biosystem, USA). This sequencing process is carried out in 2 stages, namely, cycle sequencing reaction and purification of PCR products and sequencing. Sequencing results were analysed using Bioedit software. The last is BLAST (Basic Local Alignment Search Tool) process, the purpose of which is to get the HIV genotype and subtype. BLAST was conducted using the internet to two gene bank sites to confirm; the two sites are BLAST from NCBI (National Center for Biotechnology

Information) at www.ncbi.nlm.nih.gov and the HIV sequence database at www.hiv.lanl.gov.

Statistical Analysis

Statistical analysis was performed using Fisher's exact test for categorical variables. Briefly, a 2×2 contingency table on the selected Data was constructed, and the two-tailed p-value. P values less than or equal to 0,05 were considered to be significant.

Results

Demographic Characteristics of Subjects

Demographic characteristics showed that HIV/AIDS patients in Rumah Sakit Mitra Masyarakat (RSMM) Mimika dominated by women as many as 61 people (72.6%), Papuans 60 people (71.4%), educated (81%), Working (83.3%), body mass index 18.5-25 kg/m2 69 people (82.1%), married 47 people (56%), heterosexual transmission routes 80 people (95.2%), CD4⁺ levels as much as > 350 cells/mm³ 77 people (91.7%), and opportunistic infections of tuberculosis 69 people (82.1%).

The factors associated with the progression of HIV

A significant relationship between demographic variables clinical and clinical stage of HIV/AIDS is a subtype variable, BMI and Route transmission. The results of the analysis are shown in Table 1.

Table 1: Demogra	phic Characteristic	of stud	y Subject
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Characteristic	Clinical Stage (WHO)		Σ	р
	I, II, III	IV		
Sex				
Male	17	6	23	0.356
Female	51	10	61	
Ethnic				
Papua	50	10	60	0.375
Non-papua	18	6	24	
Subtype				
CRF01_AE	30	8	38	0.002*
Non-CRF01_AE	20	26	46	
Opportunistic Infection				
ТВ	56	13	69	1.000
Non-TB	12	3	15	
Body Mass Index				
Other	9	6	15	0.033*
Normally	59	10	69	
CD4 ⁺				
< 350 cell/mm3	6	1	7	1.000
> 350 cell/mm3	62	15	77	
Hemoglobin				
< 12 g/dl	22	14	36	0.826
12-15 g/dl	28	20	48	
Trombosit				
< 150.000 ul	5	6	11	0.340
150 – 400.000 ul	45	28	73	
CD4 Failure, < 50				
cell/mm3/year				
Yes	37	7	44	0.580
No	31	9	40	

Table 2 shows the analysis of the relationship between the subtypes and clinical characteristics of the levels of CD4⁺ HIV patients in Mimika. Results indicated exhibited significantly between subtypes of HIV-1 and CD4⁺ cells of patients with p = 0.04 ($\alpha < 0.05$). The results of the analysis are shown in table 2.

Table 2: The correlation between HIV-1 subtypes and the level of CD4 $\,$

Characteristic	Cluster Differentiation-4		Σ	р
	< 350	> 350		
Sex				
Male	2	21	23	0.62
Female	5	26	61	
Ethnic				
Papua	6	54	60	0.66
Non-papua	1	23	24	
Subtype				
CRF01 AE	6	33	39	0.04*
Non-CRF01 AE	1	44	45	
Opportunistic Infection				
ТВ	7	62	69	0.34
Non-TB	0	15	15	
Transmission Mode				0.70
Heterosexual	7	73	80	
Others	0	4	4	
Body Mass Index				
Other	3	12	15	0.10
Normally	4	65	69	
Hemoglobin				
< 12 a/dl	4	32	36	0.45
12-15 g/dl	3	45	48	0.10

Discussion

Many factors affect the disease progression of HIV/AIDS, including host factors, environmental and viral factors [13]. Two factors that affect the progression in this study is a host factor is the body mass index and factor virus itself is a subtype of HIV-1. One element that has a relationship with the clinical stage is the body mass index (BMI). BMI is one of the WHO's clinical assessment parameters that weight loss in people with HIV/AIDS. However, the association of BMI with CD4⁺ levels did not show significant results. In this study, the patients' BMI is normal for clinical stage I, II and III. A study in France showed that mortality was higher in patients with BMI between 16-18.4 kg/m² with HR 2.2 (CI: 1.6-3.0) and a BMI < 16 is 4.4 (CI: 3.1-6.3) and standard BMI 18.5 [14], [7]. These results are similar to studies in Surabaya which is one of the factors that affect the progression of HIV disease is the body mass index [7].

In addition to body mass index, HIV-1 subtype also has a significant relationship with clinical stage and CD4⁺. Correlation between HIV-1 subtypes and the development of the disease is controversial. Several studies have reported a correlation between subtypes of HIV-1 and the progression of HIV/AIDS by relating the time needed by HIV to develop AIDS, the rate of change low CD4⁺ counts, viral load high, and mortality associated with HIV/AIDS. CRF01_AE commonly identified in HIV/AIDS patients in Papua. This indicates that the recombinant form of the virus worldwide associated with faster disease progression, such as in Cuba and Brazil [15], [13].

This study shows that CRF01_AE associated with faster HIV/AIDS progression. Similarly, studies in China (Li, 2014; Ng, 2011). It found that CRF01_AE-infected seroconversion experienced a faster rate of decline in CD4⁺ T cells, requiring earlier initiation of ART compared to non CRF01_AE patients [16].

The study held by Chu et al. reported that the level of low CD4⁺ changes was related to the CRF01_AE subtype [3]. Research in Indonesia in 2013 reported that CRF01_AE subtype also has a higher prevalence than other subtypes and associated with the level of CD4⁺ cell changes in patients who had received HAART [17]. Subtype connection with deaths related to HIV/AIDS is still contradictory. Subtype CRF01_AE estimated time of the death of people with an average of 7.8 (7.0 to 9.1) years [18].

It remains unclear why CRF01_AE associated with CD4⁺ decline very quickly. However, several studies have shown that the high proportion of tropism X4 in the CRF01_AE subtype and also that X4 tropism is associated with an increased rate of CD4⁺ decline and progression for advanced immunosuppression [19], [20], [21]. Also, a decrease in the immune system on the host after infection with HIV-1 can allow the virus to grow and replicate independently. It can explain the increase in the rate of disease progression in HIV-infected patients with subtype CRF01 AE [22].

Some literature suggests that the virus subtype may affect the pathogenesis and progression of the disease during HIV infection. Hu, has reported that in PWID (people with an injected drug) patients with subtype CRF01 AE have higher plasma viral load compared to patients with subtype B, but there was no difference in the number of CD4⁺ T cells [23]. Recent research in Singapore reported a decline in CD4⁺ T cells faster for a shorter time in patients with subtype CRF01_AE than other subtypes [16]. Besides, in Shanghai, it was also reported that HIV homosexual patients with the CRF01 AE subtype found that more patients had lower initial CD4⁺ T cells. This subtype of HIV disease progression was faster to AIDS and CXCR4 tropism frequency greater than with other subtypes [24].

Direct comparison of HIV subtypes often complicated by uncertainty factors for instance: the way of transmission and timing of infection, host genetic diversity, effects of comorbid conditions, small sample size, identification methods that cannot distinguish between subtypes and recombinant strains. This analysis is limited to a relatively homogeneous population of incidences of cases with a clear infection time and a known mode of transmission (sexual exposure).

It should be noted that despite the historical existence of subepidemics separated by genotypes

and risk factors, CRF01_AE now appears to be dominant in all risk groups throughout Asia [25]. It remains to be determined whether this can be accounted for by genetic DRIFT, or if there are inherent differences between strains such as plasma viral load, transmission or other biological or epidemiological factors that might underlie this shift.

In conclusion, HIV-1 subtype CRF01 AE primarily associated with HIV disease progression, in this case, is a clinical-stage and CD4⁺. Routine surveillance of the subtypes of HIV-1 and CD4⁺ will be useful in monitoring the progression of HIV/AIDS and improving the management and clinical counselling. The further study combines subjects with different ethnic backgrounds, and functional evaluation can be used to examine the relationship between subtypes of HIV-1 and the progression of HIV/AIDS. The research may use more samples, and the factors involved include the use of viral load markers to monitor disease progression. Finally, the sequencing of the HIV genome as a whole is the ideal method for concluding the relationship of the subtype by conducting a co-receptor analysis.

References

1. Dirjen Bina KIA. Pedoman Manajemen Program Pencegahan penularan HIV dan Sifilis dari Ibu ke Anak. Jakarta, 2015.

2. Dinas Kesehatan Papua, 2018. Jumlah kasus HIV/AIDS per 31 Juni 2018.

3. Chu M. CRF01-AE strain is associated with faster HIV/AIDS progression in Jiangsu Province. China Sci Rep Springer US. 2017; 7:1-8. <u>https://doi.org/10.1038/s41598-017-01858-2</u> PMid:28484257 PMCid:PMC5431509

4. Nascimento-Brito S. HIV-1 tropism determines different mutation profiles in proviral DNA. PLoS ONE. 2015; 10:1-22. https://doi.org/10.1371/journal.pone.0139037 PMid:26413773 PMCid:PMC4587555

5. Pananghat AN, Aggarwal H, Prakash SS, Makhdoomi MA, Singh R, Lodha R, Ali S, Srinivas M, Das BK, Pandey RM, Kabra SK. IL-8 alterations in HIV-1 infected children with disease progression. Medicine. 2016; 95(21). <u>https://doi.org/10.1097/MD.00000000003734</u> PMid:27227934 PMCid:PMC4902358

6. Riverra Y. Impact of depression and inflamation on the progression of HIV Disease. J Clin Cell Immunol. 2016; 7:1-8. https://doi.org/10.4172/2155-9899.1000423 PMid:27478681 PMCid:PMC4966661

7. Yunifiar MQ. Correlation between HIV-1 genotype and clinical progression, in: HIV/AIDS Patients in Surabaya, Indonesia, in: Earth and Environmental Science. IOP Conference Series, 2018:012002. https://doi.org/10.1088/1755-1315/125/1/012002

8. McCutchan F. Effect of Human Immunodeficiency Virus Type. J Infect Dis. 2008; 197:707-713. <u>https://doi.org/10.1086/527416</u> PMid:18266607

9. Foy HM, Kunanusont C, Kreiss JK, Phanuphak P, Raktham S, Pau CP, Young NL, Rerks-Ngarm S. HIV-1 subtypes and male-to-female transmission in Thailand. The Lancet. 1995; 345(8957):1078-83. https://doi.org/10.1016/S0140-6736(95)90818-8

10. Kiwanuka N. NIH Public Access. Differences. 2010; 54:180-184.

11. Vasan A, Renjifo B, Hertzmark E, Chaplin B, Msamanga G, Essex M, Fawzi W, Hunter D. Different rates of disease progression of HIV type 1 infection in Tanzania based on infecting subtype. Clinical

Infectious Diseases. 2006; 42(6):843-52. https://doi.org/10.1086/499952 PMid:16477563

12. Keller M, Lu Y, Lalonde RG, Klein MB. Impact of HIV-1 viral subtype on CD4+ T-cell decline and clinical outcomes in antiretroviral naive patients receiving universal healthcare. Aids. 2009; 23(6):731-7. https://doi.org/10.1097/QAD.0b013e328326f77f PMid:19279446

13. Tarosso LF, Sanabani SS, Ribeiro SP, Sauer MM, Tomiyama HI, Sucupira MC, Diaz RS, Sabino EC, Kalil J, Kallas EG. HIV type 1 subtype BF leads to faster CD4+ T cell loss compared to subtype B. AIDS research and human retroviruses. 2014; 30(2):190-4. https://doi.org/10.1089/aid.2012.0243 PMid:23906381

14. Rodolphe T, Denis M, Catherine M, François D. Anthropometric Indices As Predictors Of Survival in AIDS Adults. Aquitaine Cohort, France, 1985-1997. Eur J Epidemiol. 2000; 16:633-639. https://doi.org/10.1023/A:1007696530440 PMid:11078120

15. Kouri V, Khouri R, Alemán Y, Abrahantes Y, Vercauteren J, Pineda-Peña AC, Theys K, Megens S, Moutschen M, Pfeifer N, Van Weyenbergh J. CRF19_cpx is an evolutionary fit HIV-1 variant strongly associated with rapid progression to AIDS in Cuba. EBioMedicine. 2015; 2(3):244-54. <u>https://doi.org/10.1016/j.ebiom.2015.01.015</u> PMid:26137563 PMCid:PMC4484819

16. Ng OT, Lin L, Laeyendecker O, Quinn TC, Sun YJ, Lee CC, Leo YS. Increased rate of CD4+ T-cell decline and faster time to antiretroviral therapy in HIV-1 subtype CRF01_AE infected seroconverters in Singapore. PloS one. 2011; 6(1):e15738. https://doi.org/10.1371/journal.pone.0015738 PMid:21298051 PMCid:PMC3029292

17. Kameoka M. High Prevalence of HIV-1 CRF01_AE Viruses among Female Commercial Sex Workers Residing in Surabaya, Indonesia. PLoS ONE. 2013; 8:82645.

https://doi.org/10.1371/journal.pone.0082645 PMid:24367533 PMCid:PMC3867361

18. Costello C, Nelson KE, Suriyanon V, Sennun S, Tovanabutra S, Heilig CM, Shiboski S, Jamieson DJ, Robison V, Rungruenthanakit K, Duerr A. HIV-1 subtype E progression among northern Thai couples: traditional and non-traditional predictors of survival. International journal of epidemiology. 2005; 34(3):577-84. <u>https://doi.org/10.1093/ije/dyi023</u> PMid:15737969

19. Hamlyn E, Hickling S, Porter K, Frater J, Phillips R, Robinson M, Mackie NE, Kaye S, McClure M, Fidler S, SPARTAC Investigators. Increased levels of CD4 T-cell activation in individuals with CXCR4 using viruses in primary HIV-1 infection. Aids. 2012; 26(7):887-90. https://doi.org/10.1097/QAD.0b013e328351e721 PMid:22313951

20. Waters L, Mandalia S, Randell P, Wildfire A, Gazzard B, Moyle G. The impact of HIV tropism on decreases in CD4 cell count, clinical progression, and subsequent response to a first antiretroviral therapy regimen. Clin Infect Dis. 2008; 46(10):1617-23. https://doi.org/10.1086/587660 PMid:18419499

21. Weiser B, Philpott S, Klimkait T, Burger H, Kitchen C, Bürgisser P, Gorgievski M, Perrin L, Piffaretti JC, Ledergerber B, Swiss HIV Cohort Study. HIV-1 coreceptor usage and CXCR4-specific viral load predict clinical disease progression during combination antiretroviral therapy. Aids. 2008; 22(4):469-79.

https://doi.org/10.1097/QAD.0b013e3282f4196c PMid:18301059

22. Philpott SM. HIV-1 coreceptor usage, transmission, and disease progression. Curr HIV Res. 2003; 1(2):217-27. https://doi.org/10.2174/1570162033485357 PMid:15043204

23. Hu DJ, Vanichseni S, Mastro TD, Raktham S, Young NL, Mock PA, Subbarao S, Parekh BS, Srisuwanvilai LO, Sutthent R, Wasi C. Viral load differences in early infection with two HIV-1 subtypes. Aids. 2001; 15(6):683-91. <u>https://doi.org/10.1097/00002030-200104130-00003</u> PMid:11371682

24. Shen X. Evidence That HIV-1 CRF01_AE Is Associated with Low CD4+T Cell Count and CXCR4 Co-Receptor Usage in Recently Infected Young Men Who Have Sex with Men (MSM), 2014:89462. https://doi.org/10.1371/journal.pone.0089462 PMid:24586795 PMCid:PMC3931781

25. Leelawiwat W, Rutvisuttinunt W, Arroyo M, Mueanpai F, Kongpechsatit O, Chonwattana W, Chaikummao S, De Souza M, Vangriensven F, McNicholl JM, Curlin ME. Increasing HIV-1 molecular complexity among men who have sex with men in Bangkok. AIDS Res Hum Retroviruses. 2015; 31(4):393-400. https://doi.org/10.1089/aid.2014.0139 PMid:25366819