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MEETING ABSTRACTS Open Access

The approach to individualized prediction of human papillomavirus (HPV) infection persistence/clearance in HIV-1-positive adolescent girls based on dynamics of CD4+ counts, viral load, and HAART

Julia Kravchenko[1*], Staci Sudenga[2], Igor Akushevich[3], Craig M Wilson[2], Sadeep Shrestha[2]

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Background

Several studies suggest that $CD4^+$ T-cell count (CD4) is important in pathogenesis of human papillomavirus (HPV) infection in HIV-positive patients including HPV clearance. CD4 dynamics as well as other co-factors such as highly active antiretroviral therapy (HAART), HIV-1 RNA viral load (VL), demographics, behavioral risks and, clinical diagnosis allows for predicting the absolute probabilities of HPV clearance/persistence. The modeling approach allows for the utilization of complete datasets and does not require any additional essential assumptions about missing information and possible violations in study design.

Materials and methods

We analyzed 266 HIV-1 positive adolescent girls from the Reaching for Excellence in Adolescent Care and

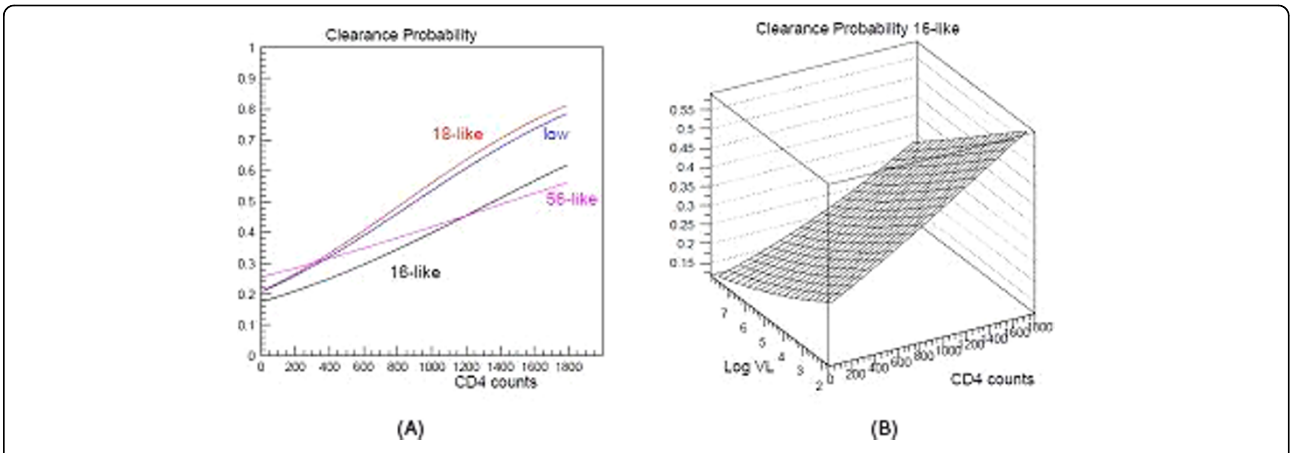

Figure 1 HPV infection clearance probability vs. (1A) CD4 counts and (1B) combination of CD4 and logarithm of HIV viral load (log(VL)).

*Correspondence: yk27@duke.edu
[1]Duke Comprehensive Cancer Center, Duke University, Durham, NC, USA
Full list of author information is available at the end of the article

Health (REACH) cohort. At enrollment and every 6 months thereafter, cervical lavage samples were tested for HPV using MY09/MY11/HMB01-based PCR and 30 HPV type-specific probes. HIV-related clinical data and risk factors were recorded every 3 months. For analytic purposes, HPV types were categorized according to phylogenetic patterns into (1) 16/16-like, (2) 18/18-like, (3) other high risk (56/56-like), and (4) low risk. HPV clearance was defined by the absence of type-specific infection for two subsequent visits after infection. Maximum likelihood estimates based on the logistic-type model were developed for 3-month reconstructed probabilities of HPV clearance/persistent with CD4, VL, and HAART as the main predictors at the moment of examination.

Results

Figure 1A presents the clearance probability for HIV-positive patients depending on CD4 for HPV16/16-like, HPV18/18-like, HPV56/56-like, and low-risk HPV. HPV16/16-like infection has the lowest chance to be cleared by host at low CD4 levels. The probability of 3-month clearance was less than 20% for patients with CD4 <200, but increased gradually with CD4 increase but overall was slower than for HPV18/18-like, other high-risk, and low-risk HPV. Additionally, the 3-D plot in Figure 1B describes CD4 and log (VL) as predictors of probability of HPV16/16-like clearance: the lowest CD4 levels together with the highest VL were significant predictors for HPV persistence. The multiplicative effect of HAART showed tendency to decrease on HPV16/16-like clearance probability with increasing CD4 levels.

Conclusion

This approach could extend opportunities to understand the associations between CD4, VL, and HAART to develop the comprehensive approach to individualized prediction of HPV infection persistence/clearance in HIV-positive patients.

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Author details
[1]Duke Comprehensive Cancer Center, Duke University, Durham, NC, USA. [2]Department of Epidemiology, University of Alabama at Birmingham, Birmingham, AL, USA. [3]Center for Population Health and Aging, Duke University, Durham, NC, USA.

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