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Identifying Recent HIV Infections: An Individualised Assessment of Risk

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INTRODUCTION

The accurate identification of recent HIV infection remains an important area of research to inform population-based HIV prevention and treatment intervention policies.

Methods that use cross-sectional testing and biomarker information might be an alternative to longitudinal testing, as combinations of serological and molecular methods can potentially provide a means to identify recent HIV infections.

HIV surveillance requires monitoring of new HIV diagnoses and differentiation of incident and older infections.

AIMS

The aim of this study was to develop a predictive scoring system which was based on combining the results of Schupbach's Line assay algorithm 15.1 with the viral load (VL) at diagnosis to predict the risk of having recently acquired HIV infection.

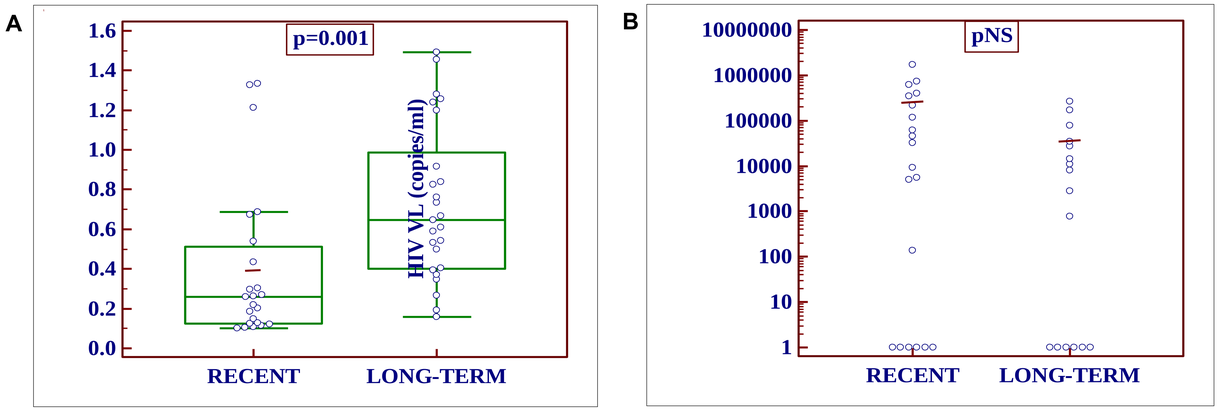
METHODS

Patients: New HIV diagnoses in Ireland from January to April 2016 (n=151) were extracted from the NVRL HIV Database. For each new HIV diagnosis, HIV INNO-LIA assay (LIA) results and risk factor data, where available, were obtained from the NVRL laboratory information management system (LIMS).
Recent HIV infections were identified using the following criteria: evidence of an HIV negative test in the previous 12 months; detection of p24 antigen at first diagnosis and application of the LIA HIV confirmatory assay banding pattern.
Patients on antiretroviral treatment or previously diagnosed (>12 months) were excluded from the analysis (n=43).
HIV Avidity testing: All samples were tested on the Sedia limiting antigen avidity assay (LAg). The normalised cut-off in the LAg assay is 1.5.
Inno-Lia HIV assay: Schupbach's (2015) Algorithm 15.1 was applied to the Line assay results. This algorithm is derived from antibody reaction scores to the 7 HIV antigen bands on the LIA strip(sgp120, gp41, p31, p24, p17, sgp105 and gp36).
Statistical Analysis: The Speigelhalter-Knill-Jones method was used to develop a predictive scoring system which is based on the LAg assay as a gold standard as this assay demonstrated 100% accuracy in identifying recency based on samples tested from the CEPHIA repository. Viral loads above the median of the cohort were used as an indicator of recency.

RESULTS

- Patient demographics showed that the recent cohort was predominantly male (87.1%) and MSM/bisexual (78.9%).
- The LAg assay and LIA Algorithm 15.1 identified 32 cases (21.2%) and 19 cases (12.6%) respectively as recently acquired HIV.
- Figure 1A shows patients who were classified as recent by the LAg assay (Odn<1.5) and further analysed using LIA Algorithm 15.1. The patients classified as recent infections by both assays had significantly lower mean LAg results compared to those patients who were long-term infections according to LIA Algorithm 15.1 (ODn: 0.398 vs 0.729, p=0.001).
- Figure 1B shows that there were no differences in HIV VL between the groups. The median viral load of the cohort was 16,428 copies/ml (log4.2): 50% of patients in the recent group and a third of patients in the long-term cohort had VL above the median VL.
- Although there were similar mean age between the groups (33.9 vs 35.3 years), χ^2 analysis revealed that a significant number of patients in the recent group were ≤35 years of age (p<0.03) (Figure 1C).

FIGURE 1. Comparison of patients identified as recent or long-term according to Schupbach's Algorithm 15.1 with reference to (A) Avidity, (B) HIV VL and (C) Age.



- The predictive scoring system was based on analysis of 50 HIV patient samples (15 recent and 35 long-term) from the CEPHIA repository. Analysis based on the LAg assay and LIA showed a sensitivity of 66.7%, specificity of 94.3%, PPV of 83.3% and NPV of 86.8%.
- The results of the regression model including both the LIA and the HIV VL to predict recency in the patient cohort are shown in Table 1.
- The regression model using only Schupbach's Algorithm 15.1 LIA results demonstrated an observed and predicted risk of being recent of nearly 80% in our patient cohort.
- VL> median was not a good predictor of recency.
- Algorithm 15.1 and VL combined demonstrated that the observed risk of being recent is 100%.

RESULTS

Table 1. Regression Model including both the LIA and the Median HIV Viral Load to predict recency.

	Observed Risk of being recent	Risk Predicted in new scoring system
LIA alone - recent	78.9%	78.8%
VL alone - recent	25.5%	24.2%
Both tests suggest recency	100%	81.3%
Both tests suggest non recency	11.9%	10.8%
LIA suggests recency but VL does not	60%	75.3%
VL suggests recency but LIA does not	10.3%	14.9%

CONCLUSIONS

- We have developed a predictive scoring system which is based on combining LIA Algorithm 15.1 and the VL.
- This proof of concept analysis has demonstrated that data such as LIA and VL can be used to develop a multiassay algorithm to accurately predict an individual's risk of recently acquired HIV infection.
- Using standard laboratory assays, this predictive scoring system allows an individualised assessment of risk for prediction of recency.

ACKNOWLEDGEMENTS

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REFERENCE

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