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A model prediction of pre-treatment HIV RNA: application for the use of abacavir and rilpivirine as the first-line regimen for HIV-infected patients in resource-limited settings

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Background: Abacavir (ABC) and rilpivirine (RPV) are alternative antiretroviral drugs for treatment-naïve HIV-infected patients. However, both drugs are only recommended for patients who have pre-treatment HIV RNA <100,000 copies/mL. In resource-limited settings, pre-treatment HIV RNA is not routinely performed and not widely available. The aims of this study were to determine factors associated with pre-treatment HIV RNA <100,000 copies/mL and to construct a model to predict this outcome.

Material/methods: HIV-infected adults enrolled in the TREAT Asia HIV Observational Database (TAHOD) were eligible if they had an HIV RNA measurement documented at the time of ART initiation. The dataset was randomly split into a derivation data set (75% of patients) and a validation data set (25%). Factors associated with pre-treatment HIV RNA <100,000 copies/mL were evaluated by logistic regression adjusted for study site. A prediction model and prediction scores were created.

Results: A total of 2,592 patients were included in the analysis. Median [interquartile range (IQR)] age was 35.8 (29.9-42.5) years; CD4 count at ART initiation was 147 (50-248) cells/mm³; and pre-treatment HIV RNA was 100,000 (34,045-301,075) copies/mL. Factors associated with pre-treatment HIV RNA <100,000 copies/mL were younger age (p for trend <0.01), hemoglobin \geq 13 g/dL for men or \geq 12g/dL for women (p <0.01), positive HBsAg (p=0.01), higher CD4 count (p for trend <0.01), higher total lymphocyte count (p for trend <0.01), and no prior AIDS-defining illness (p <0.01). Receiver-operator characteristic (ROC) analysis yielded area under the curve of 0.70 [95% confidence interval (CI) 0.67-0.72] among derivation patients and 0.69 (95% CI 0.65-0.74). A cut off score >25 yielded a sensitivity of 48.2%, specificity of 79.0%, positive predictive value of 68.2%, and negative predictive value of 61.9% for prediction of pre-treatment HIV RNA <100,000 copies/mL among derivation patients.

Conclusions: A model prediction for pre-treatment HIV RNA <100,000 copies/mL produced an area under the ROC curve of 0.70. A larger sample size for prediction model development as well as for model validation is warranted.