

Corrections

EVOLUTION

Correction for “Host adaptation to viruses relies on few genes with different cross-resistance properties,” by Nelson E. Martins, Vítor G. Faria, Viola Nolte, Christian Schlötterer, Luis Teixeira, Élio Sucena, and Sara Magalhães, which appeared in issue 16,

April 22, 2014, of *Proc Natl Acad Sci USA* (111:5938–5943; first published April 7, 2014; 10.1073/pnas.1400378111).

The authors note that Fig. 4 appeared incorrectly. The corrected figure and its legend appear below.

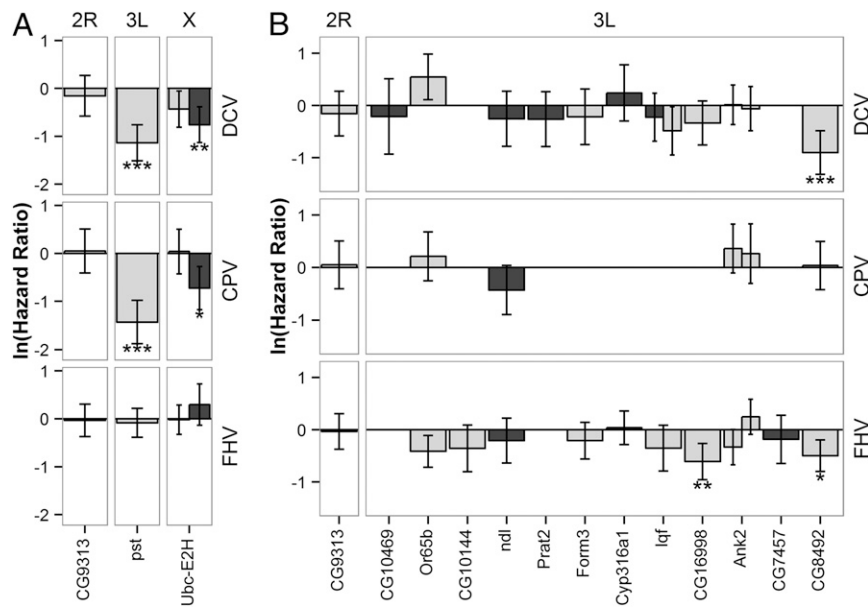


Fig. 4. RNAi knockdown of candidate genes. Natural logarithm of hazard ratios between survival of flies with knocked-down candidate genes and their controls upon infection with DCV (*Top*), CrPV (*Middle*), and FHV (*Bottom*), using as genetic background KK (gray bars), GD (black bars) or both, whenever a construct was available in both backgrounds. (*A*) RNA interference against the candidate genes identified by the peaks in Fig. 3, *pst* and *Ubc-E2H*. (*B*) Tests to other genes in the large 3L peak. Vertical bars correspond to the 95% confidence intervals of the estimated hazard ratios. **P* < 0.05; ***P* < 0.01; ****P* < 0.001.

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MEDICAL SCIENCES, APPLIED MATHEMATICS

Correction for “Predicting the outcomes of treatment to eradicate the latent reservoir for HIV-1,” by Alison L. Hill, Daniel I. S. Rosenbloom, Feng Fu, Martin A. Nowak, and Robert F. Siliciano, which appeared in issue 37, September 16, 2014, of *Proc Natl Acad Sci USA* (111:13475–13480; first published August 5, 2014; 10.1073/pnas.1406663111).

The authors note that, due to a printer’s error, Table 1 appeared incorrectly. The corrected table appears below. The online version has been corrected.

Table 1. Estimated values for the key parameters of the stochastic viral dynamics model

Parameter	Symbol	Estimation method	Ref(s).	Best estimate	Distribution*
LR decay rate	δ	Long-term ART, $\delta = \ln(2)/\tau_{1/2}$	(3, 4)	$5.2 \times 10^{-4} \text{ d}^{-1}$	$\delta \sim \mathcal{N}(5.2, 1.6) \times 10^{-4} \text{ d}^{-1}$
LR exit rate	A	Viral rebound after ART interruption	(5, 58)	57 cells d^{-1}	$\log_{10}(A) \sim \mathcal{N}(1.76, 1.0)$
Growth rate	r			0.4 d^{-1}	$\log_{10}(r) \sim \mathcal{N}(-0.40, 0.19)$
Establishment probability	P_{Est}	Population genetic modeling	(59, 60)	0.069	Composite distribution (Materials and Methods)

*Notation $X \sim \mathcal{N}(\mu, \sigma)$ means that X is a random variable drawn from a normal distribution with mean μ and SD σ .

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