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ERRATUM

Genome analysis of a severe and a mild isolate of *Papaya ringspot virus*-type W found in Brazil

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The Publisher regrets that Figure 2 in article 10.1007/s11262-006-0032-5, Volume 35, issue 1 did not print in color. Below is the figure, as it should have appeared in the issue.

The online version of the original article can be found under doi: 10.1007/s11262-006-0032-5.

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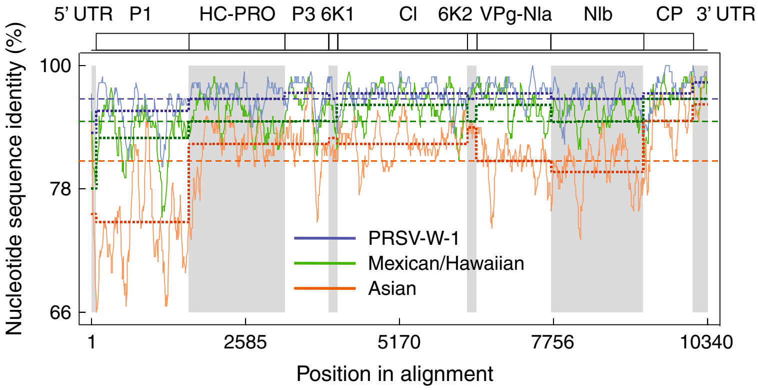

Fig. 2 Mean nucleotide sequence identities shared between PRSV-W-C and PRSV-W-1 (*blue plots*), Mexican and Hawaiianisolates (*green plots*), and Asian isolates (*orange plots*). Solidlines represent averaged "identity scans" between viruses in thedifferent groups calculated by (a) moving a 101 nt slidingwindow one nucleotide at a time along the length of the alignedfull genome sequences, (b) at each window position calculatingpercentage identity matrices by averaging the pair-wise identities of groups of isolates to PRSV-W-C, and (c) plotting these valueson the central nucleotide position of the window. In order toavoid loss of data at the edges of the alignment, the sequence wastreated as though it was circular. *Dotted lines* indicate theaverage identity between isolates across particular genes oruntranslated regions, whereas the *broken lines* indicate meanidentities across the entire genome. A to scale genome map isprovided above the plots