

Continuity in Clinical Education

TO THE EDITOR: I was glad to learn of the pilot project in longitudinally integrated clinical education for third-year medical students at Harvard Medical School and the Cambridge Health Alliance, as reported by Hirsh et al. (Feb. 22 issue).¹ It will be interesting to see whether outcome data from this and other efforts to reform undergraduate medical education by increasing continuity of care, curriculum, and supervision confirm the reasonable expectation of the authors that “enhanced learning, greater patient satisfaction, and more efficient and effective medical care” will result.

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1. Hirsh DA, Ogor B, Thibault GE, Cox M. “Continuity” as an organizing principle for clinical education reform. *N Engl J Med* 2007;356:858-66.

TO THE EDITOR: We studied the effect of an “e-learning” tutorial, on reading electrocardiograms (ECGs); the tutorial, held in October 2006, was for third-year medical students at Imperial Col-

lege London. One group of 83 students was told that the tutorial was compulsory, whereas a second group of 263 students was simply encouraged to use it. Participation rates were 97.5% in the first group and 64.6% in the second. A quiz about ECGs was administered 3 months later; the mean score in the first group was 75.1%, as compared with 60.1% in group 2.

E-learning encourages a deeper approach to learning,¹ and it can be used by students in distant clinical placements to supplement knowledge obtained on the wards. High-quality interactive e-learning will help lessen the discrepancy in knowledge due to different learning opportunities at different sites.²

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1. Masiello I, Ramberg R, Lonka K. Learning in a Web-based system in medical education. *Med Teach* 2005;27:561-3.
2. Cook DA. Web-based learning: pros, cons and controversies. *Clin Med* 2007;7:37-42.

Chikungunya Outbreaks

TO THE EDITOR: In their Perspective article on outbreaks of chikungunya fever, Charrel et al. (Feb. 22 issue)¹ suggest that the recent outbreak in India² could have been caused by the same viral strain that caused the Indian Ocean outbreak.³ Recent data do not support this speculation.^{4,5} We previously described sequence microheterogeneity in the viruses causing the Indian Ocean outbreak.⁴ We have compared E1 sequences from viruses involved in the Indian and Indian Ocean outbreaks (Fig. 1).^{4,5} The strains differed only in a single nucleotide change (T321C), which was found in all Indian Ocean isolates. Isolates from India retained the ancestral T321 nucleotide present in all other African and Asian strains, making it unlikely that the outbreak in India was caused by a strain originating from the Indian Ocean outbreak. Nevertheless, in contrast to se-

quences from all other available chikungunya viruses, the Indian and Indian Ocean isolates shared two nucleotide changes: A306G and C384T. These shared derived characters indicate common ancestry. The strain isolated from Yawat, India, in 2000⁵ retained the ancestral nucleotide at both positions but had a distinctive T468C change, arguing against a direct link between this strain and the strain implicated in the 2005–2006 Indian outbreak.

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