

Letter to the editor: Application of Bayesian methods to the inference of phylogeny for enterovirus surveillance

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To the editor:

We read with interest the article by Niesters et al. describing a pilot study to share enterovirus sequence data within the Netherlands for epidemiological investigation [1]. As the authors note, nucleotide sequence data can extend the identification of virus serotype to the tracing of disease transmission patterns through phylogenetic analysis. The article referred to use of a web-based typing tool for enteroviruses and noroviruses based on BLAST analysis followed by a neighbor-joining phylogeny. We believe such analyses can be further enhanced through the inclusion of temporal and geographical discrete variables for the inference of phylogeny (phylogeography). In particular, the application of Bayesian inference to phylogeography offers several advantages, such as the capacity to explicitly account for parameter uncertainty, reducing potential model bias, especially where data are scarce. This approach was referred to in the same issue of *Eurosurveillance* by Carriço et al. for bacterial molecular epidemiology [2] and has been successfully applied to virological studies for avian influenza A(H5N1) and rabies [3]. Carriço et al. make reference to the computational demands of such methods [2] and indeed, this is an important consideration. From our experience, the use of commodity graphics processing units combined with appropriate parallel threading software extensions can overcome some of the limitations imposed by high computational demand at low cost [4].

Australia established an Enterovirus Reference Laboratory Network – primarily for poliovirus surveillance but also to detect other enteroviruses of public health significance, such as enterovirus 71 (EV71) – through the sharing of enterovirus sequence data. EV71 infection often manifests benignly as hand, foot and mouth disease in infants but has been associated with fatal neurological disease, particularly in the Asia-Pacific region [5]. The correlation of specific EV71 subgenogroups with increased neurological presentation,

such as C4 infection recently in Cambodia, China and Vietnam, highlights the benefit of a phylodynamic analysis that accounts for temporal and geographical parameters. We feel that the application of Bayesian methods to the inference of phylogeny will play an important role in the elucidation of global chains of enterovirus transmission.

Conflict of interest

None declared.

Authors' contributions

Jason A Roberts conceived the idea to respond to the recent articles on molecular epidemiology in *Eurosurveillance* and drafted the letter. The text was revised and edited by Andrew Hung and Bruce R Thorley, and all authors approved the final version of the letter.

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