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The development and deployment of a national web-based system for communicable disease control in England

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Background: After five years of development and formal evaluation, the Health Protection Agency in England deployed a national web-based system for communicable disease control in January 2010. HPZone is now used in all 26 local health protection units covering 9 regions and the national centre for infections. Various challenges were encountered during the rollout and included standards, governance, workflows, integration with other software suites and IT infrastructure. Crucial to the deployment was winning the hearts and minds of users.

Methods: HPZone was developed bottom-up with the users in mind from the start and began with the development of a structured risk assessment. The implementation included the collection of national contextual data sets, procedures for improved security of access, direct import of laboratory data and implementation of recent notification legislation, together with systems for enhanced software flexibility, server resilience and reliability. Nominated disease boards were tasked to populate workflow templates consisting of conditioned actions for cases (possible, probable, confirmed), enquiries and outbreaks.

Results: HPZone was successfully deployed across 26 HPUs from December 2009 to March 2010. Laboratory data from across the country has been linked directly to HPZone. From January 2010 to mid-February 2012, 136,487 confirmed cases have been recorded (including Food poisoning: 102,031, Mumps: 20,166, Measles: 8,358), 13,112 outbreaks and 108,970 enquiries. 4,409 schools and 3,531 care homes have been affected. Lessons have been learned in respect of clinical and surveillance issues, integration with laboratory data and notifications, case and outbreak management, and enhanced IT infrastructure resilience and scalability. Coincidence and threshold alerts were implemented and facilities for automated notifications developed realising the enter-once-use-many paradigm.

Conclusion: HPZone has enabled decision support without replacing professional judgment and provided improved detection, surveillance and control. It has facilitated transparency underpinning national resource allocation. HPZone has enabled targeted support and training, and provided opportunities to capture and share best practice. With a national award received in November 2011, HPZone has been recognised as an innovative web-based decision support system for harnessing infectious disease data, information and knowledge management and for improving service quality and public health outcomes.

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Genome sequencing of *Vibrio cholerae* isolates from an outbreak in the Philippines: unique genome structure and mobile elements

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Background: Cholera is a leading cause of severe diarrhoeal disease. Investigation by the Department of Health of the Philippines of an outbreak of diarrhoeal disease in Palawan in 2011 identified *Vibrio cholerae* as a putative causative agent.

Methods: Three microbial isolates, one environmental and two clinical samples, were characterized biochemically by The Research Institute for Tropical Medicine (RITM) and sent to St. Luke's Medical Center (SLMC) for whole genome sequencing. Extracted genomic DNA was sequenced using a Roche GSJr following standard Roche protocols. Sequencing reads were assembled into contigs using Roche Assembler and compared to Genbank entries using BLAST. Annotation was performed by both RAST and the annotation engine of the Institute for Genome Sciences in Maryland.

Results: Analysis of the shotgun genome data of all three isolates revealed that the Philippines strains are members of the 7th pandemic clade of O1 cholerae and are a hybrid of El Tor and Classical biotypes. The environmental strain was very closely related to one clinical isolate, indicating a possible source of the infection. However, the other clinical isolate differed significantly from the other two isolates. A novel 15kB genomic element containing a predicted type II restriction-modification system was identified in all three isolates. PCR was done to determine toxin gene and prophage genome structure.

Conclusion: The Philippines cholerae strains contain a unique configuration of elements, previously seen only in O1 El Tor MG-116926, isolated in Bangladesh in 1991. In addition, the Philippines strains contain elements and structure similar to the MO10 strain, a type O139 strain, from Africa. These data are the first *Vibrio* genome sequences generated from Philippines isolates and demonstrate the divergent and unique nature of the microbial diversity in the Philippines.

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