Detection of Shigella Outbreaks in Argentina using WHONET and SaTScan

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OBJECTIVE
This paper describes the application of the WHONET software integrated with SaTScan to the detection of Shigella outbreaks in a national database using a space-time cluster detection algorithm in simulated real-time and comparison of findings to outbreaks reported to the Ministry of Health (MOH).

BACKGROUND
Electronic laboratory-based surveillance can significantly improve the diagnostic specificity and response time of traditional infectious disease surveillance. Under the project “Models of Infectious Disease Agent Study” (MIDAS), we wished to evaluate the application of space-time outbreak detection algorithms utilizing SaTScan [1] to a national database of routinely collected microbiology laboratory data.

The Collaborative Group WHONET-Argentina, established in 1986, comprises 70 microbiology laboratories nationwide [2], all of which enter their data into the widely used WHONET 5.4, a free software developed by our group and distributed through the World Health Organization to over 90 countries.

METHODS
We applied Kulldorff’s space-time permutation scan method to WHONET-Argentina data to look for clusters of Shigella spp. from July 2006 through June 2007, simulating prospective surveillance. We searched for clusters on the basis of genus, species, and antimicrobial resistance phenotype in separate analyses, using one year of historical data and a 30-day scanning window. Data analysis was performed using an adapted version of the WHONET 5.4 software into which SaTScan features were integrated. WHONET executes SaTScan in batch mode, and then integrates findings into the WHONET display, as in Figure 1.

RESULTS
There were 2,041 isolates of Shigella spp. analyzed in the twelve-month period during which six outbreaks were reported to the MOH. We identified 19 statistical “events”, depicted in Figure 2, of which 3 overlapped in space and time with known outbreaks and 2 additional ones may have corresponded with known outbreaks, relationships supported by available serotyping and PFGE results. Of the 14 remaining events, several may have represented true outbreaks not reported to the MOH. The most discriminating analyses were those involving resistance phenotypes.

CONCLUSIONS
The prospects for integrating advanced statistical methods with existing national laboratory-based surveillance strategies for outbreak detection seem excellent. The integration of WHONET and SaTScan permits the expansion worldwide of advanced statistical techniques for the detection of outbreaks.

REFERENCES

Further Information:
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