The Utility of Space-Time Surveillance for Tuberculosis

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OBJECTIVE

This paper describes the utility of prospective space-time surveillance to detect genetic clusters of tuberculosis (TB) due to person-to-person spread.

BACKGROUND

TB has reemerged as a global health epidemic in recent years [1]. Although several researchers have examined the use of space-time surveillance to detect TB clusters, they have not used genetic information to verify that detected clusters are due to person-to-person transmission [1,2]. Using genetic fingerprinting data for TB cases, we sought to determine whether detected clusters were due to recent transmission.

METHODS

Records of reported cases of TB were obtained from the records at Montreal Public Health during the period of 1996-2003 (inclusive). We used the first 3 digits of the postal code to geocode active TB cases reported on the Island of Montreal. We identified genetic clusters through restriction fragment length polymorphism (RFLP) typing of *Mycobacterium tuberculosis* [3]. A prospective, space-time SaTScan detection algorithm using a monthly Poisson model was applied to case reports. We determined the accuracy of SaTScan in detecting the genetic clusters by comparing it to random cluster detection [4]. In order to determine the accuracy of surveillance under 'ideal' conditions (genetic clusters that are tightly spatially clustered), we reassigned all cases in each genetic cluster to a single region, and reanalyzed the data.

RESULTS

We extracted 846 cases that had complete postal code of the home address, date of treatment, and genetic information. 111 cases (13%) were part of a genetic cluster while the remaining cases were due to reactivation of a previous infection. These cases formed 38 genetic clusters, with an average of 2.4 cases per cluster. SaTScan detected 18 significant clusters ($p<0.05$). Four of these clusters overlapped spatially and temporally with at least one case in a genetic cluster. In comparision, 32% of 9,999 randomly generated clusters overlapped with at least four genetic clusters, and 8% overlapped with more than four genetic clusters, suggesting that SaTScan was not significantly better than random in detecting genetic clusters.

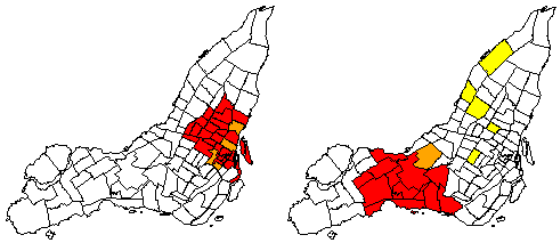

Figure 1 – Two genetic clusters and their intersection with detected clusters. The dark areas represent the clusters detected by SaTScan, the light colours are the real genetic clusters, and the middle is the intersection between the two. Montreal island is 499 km^2.

After collapsing each genetic cluster into a single region, the SaTScan analysis detected 19 significant clusters. Three of these clusters overlapped with a genetic cluster. In comparison, 10% of 9,999 randomly generated clusters overlapped with three genetic clusters.

CONCLUSIONS

Space-time surveillance for TB in an urban area may not be better than random at detecting genetic clusters due to person-to-person spread. Collapsing spatial extent into a single region only improved detection marginally, suggesting that if genetic clusters were also clustered in space, they would not be much easier to detect. In an urban area with a low rate of person-to-person spread, genetic clusters of TB are not likely to be detected through prospective space-time surveillance using the home address of the case.

REFERENCES

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