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Background: The special geographic location of Guangzhou, as well as certain practices of poultry breeding and marketing, and the habits of food handling in Guangdong, have made this region a hot spot of influenza infection. Therefore, since 1997, disease surveillance has been conducted in Guangzhou.

Methods: Surveillance was conducted in Guangzhou from 1997 among a group of workers involved in the breeding, selling and slaughtering of poultry and other animals which may potentially carry avian influenza viruses. Serum samples were collected from this high risk population to detect specific antibodies via the microhemagglutination inhibition test. An epidemiological survey was conducted on people practicing scattering home-breeding of poultry and marketing, and the habits of food handling in Guangzhou, as well as certain practices of poultry selling and slaughtering before the onset of the disease. A poultry slaughtering working in one of these live poultry food markets had no history of direct contact with poultry. The H9 infection rate among people working in poultry was 4.56% (0.51%–10.00%), There was no significant difference among different age groups and different gender, but the rate is higher than that in the urban group that practiced scattered home-breeding of poultry. One characterized human case of avian influenza A (H5N1) in Guangzhou in 2006 was reported to have visited many live poultry food markets, where the H9 infection rate among the occupational group that handled poultry in Guangzhou was 4.56% (0.51%–10.00%), There was no significant difference among different age groups and different gender, but the rate is higher than that in the urban group that practiced scattered home-breeding of poultry. One characterized human case of avian influenza A (H5N1) in Guangzhou in 2006 was reported to have visited many live poultry food markets before the onset of the disease. A poultry slaughtering working in one of these live poultry food markets had a positive anti-H5N1 antibody response, while a person with anti-H5N1 antibody and a patient with anti-H9N2 antibody had no history of direct contact with poultry.

Conclusion: H5N1 and H9N2 may cause an asymptomatic or low symptomatic infection in humans. In addition to people working in poultry farms, those involved in avian breeding, selling and slaughtering of poultry are also at high risk for avian influenza viral infection.

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Rapid analysis of known and unknown pathogens using a pan-microbial detection microarray

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Background: Rapid analysis of known, emerging and unknown viral and bacterial infections is critical for public health. Assays that can only identify a small handful of pathogens are not sufficient to deal with complex microbial infections. In this study, we report our development of a high-throughput microarray designed to detect known and discover unknown pathogens.

Methods: We designed a pan-Microbial Detection Array (MDA) to detect all viruses, bacteria, and plasmids with 2195 viral species and 924 bacterial species represented. We took an approach balancing the goals of conservation and uniqueness for probe design, aiming for uniqueness relative to other families and kingdoms, and for conservation, to the extent possible, within a family. Long probes were selected to tolerate some sequence variation to enable detection of novel, divergent species with homology to sequenced organisms. We have used our arrays to identify pathogen infections from various clinical samples. We developed a novel statistical analysis method, maximum likelihood analysis method that enabled quantifiable predictions of likelihood for the presence of multiple organisms in a complex sample.

Results: The MDA correctly identified multiple viral and bacterial infections in unknown fecal, sputum and nasopharyngeal samples that were later confirmed through independent high-throughput sequencing or PCR assays. Up to strain level identification can be achieved for fully sequenced pathogens in as little as a few hours. Family level identification was achieved for highly divergent viruses. The array is highly sensitive and able to achieve low-copy viral and bacterial detection of spiked samples when coupled with whole genome random amplification.

Conclusion: Our Microbial Detection Array is a fast, efficient and cost-effective tool to rapidly characterize known, emerging and unknown pathogens from clinical and environmental samples. The MDA has higher probe density and larger phylogenetic representation of viral and bacterial sequenced genomes than other available array designs. It can be applied to problems in viral and bacterial detection from pure or complex environmental or clinical samples. It will enable informed responses to novel biological threats and infectious agents and provide a complement to high-throughput sequencing data.

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