

hours, cloud coverage, evaporation rate and air pressure in the past ten years was investigated by using the non-parametric Spearman's correlation test.

Results: Lower average temperature, lower absolute maximum temperature, lower absolute minimum temperature and lower average maximum temperature all showed a strong correlation with the incidence of dengue fever ($r = -0.228$, $p = 0.01$; $r = -0.225$, $p = 0.01$; $r = -0.235$, $p = 0.01$ and $r = -0.268$, $p = 0.003$ respectively). A less strong, but significant correlation with rain (positive correlation) and evaporation rate (negative correlation) could be observed ($r = 0.192$, $p = 0.04$ and $r = -0.192$, $p = 0.04$ respectively).

Conclusion: In 2008, an unexpected and dramatic peak in incidence of dengue fever in Curaçao was observed. In the same year, average- as well as absolute minimum and maximum temperature were significantly lower than in the previous years and were strongly correlated with dengue incidence. As expected from earlier studies, rainfall and evaporation rate were also significantly correlated to dengue incidence.

However, temperature changes showed a stronger correlation with the incidence of dengue fever than rainfall and evaporation rate, suggesting that lower temperatures are an important factor in the development of higher dengue incidence in Curaçao and not merely an epiphenomenon, concurring with the rain period. This is in contrast with results from earlier studies conducted in Mexico and Trinidad.

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Cross-reactive neutralizing antibody response to enterovirus 71 infection in Taiwanese young children

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Background: Enterovirus 71 (EV71) is causing life-threatening hand-foot-mouth disease (HFMD) involving neurological and cardiopulmonary complications in Asian children. Phylogenetically, EV71 viruses can be classified into 3 genogroups (A, B and C) and 11 genotypes (A, B1~B5 and C1~C5). In Taiwan, nationwide EV71 epidemics with different predominant genotypes occurred in 1998 (C2), 2000–2001 (B4), 2004–2005 (C4) and 2008 (B5) but the mechanism is not clear. In early 2007, genotype C5 viruses were isolated sporadically and EV71 epidemic did not begin until genotype B5 viruses were detected in late 2007. This study was conducted to measure cross-reactive neutralizing antibody response to EV 71 Infection in Taiwanese young children to explore the mechanism of the genotype replacement in Taiwan, which is critical to the selection of vaccine strains.

Methods: We prospectively conducted cohort study to follow up healthy neonates starting from June 2006 and sera were collected from participating children for measuring

participating children developing herpangina or HFMD for virus isolation. Isolated EV71 viruses were genotyped using VP1 gene sequences.

Results: In 2008–09, 24 children developed EV71 neutralizing antibody seroconversion, including 11 symptomatic and 13 asymptomatic infections. Five EV71 viruses were isolated from the symptomatic cases and all belongs to genotype B5. These B5 viruses are phylogenetically related to B5 viruses circulating in the South-Eastern Asia recently. Thirty-one post-infection sera collected from the 24 seroconverted children were measured neutralizing antibody titers against genotype A, B4, B5, C2, and C4 viruses. Geometric mean (95% confidence intervals) of neutralizing antibody titers against these viruses were 52 (38–72), 150 (109–205), 234 (176–311), 114 (82–158), and 105 (76–144), respectively. Serological tests show that children infected with B5 viruses have lower neutralizing antibody titers against A, C2 and C4 viruses than B5 virus ($p < 0.05$, t -test).

Conclusion: Antigenic differences could be detected between enterovirus 71 viruses in different genogroups but not in the same genogroup using children post-infection sera. Significant antigenic differences between B5 and C4 viruses may explain the genogroup replacement occurring in the 2008 epidemic.

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'One World One Health' in practice: Integrating public health and veterinary curricula on emerging infectious diseases in Africa

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Background: Research indicates that up to 65% of emerging infectious diseases are zoonotic. This has contributed to the "One World One Health™" paradigm which highlights interactions between humans, domestic and wild animals in a shrinking environment. Though the OWOH theme has gained support within the scientific community, formal training integrating medical, veterinary and public health practices addressing emerging zoonotic disease is rare.

The USAID-funded Stamping Out Pandemic and Avian Influenza (STOP AI) global project is designed to prepare those responsible for the planning, surveillance, response to and prevention of highly pathogenic avian influenza (HPAI). Since inception, STOP AI has drawn upon veterinary and human medicine disciplines, public health, and the social sciences to design its training programs. Through practical field experience, STOP AI determined that effective training required the integration of veterinary, medical and public health aspects.

Methods: STOP AI training modules on HPAI epidemiology, risk assessment, surveillance, outbreak response, bio-safety and bio-security were subsequently integrated by teams of