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**Development of predictive dengue risk map using Random Forest**

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**Background:** Dengue fever, a diseases caused by Dengue virus (DENV) and transmitted to humans by *Aedes aegypti* and *Aedes albopictus* mosquitoes, has been hyper-endemic in Singapore for several decades. In the absence of an effective vaccine or specific treatment to mitigate the infections, control of *Aedes* mosquitoes plays a critical role in controlling the disease. In recent years, Singapore's vector control operations have been overwhelmed by geographical expansion of dengue transmission as well as increasing magnitude of epidemics. At the same time, they have been hampered by the lack of tools to assess the impending risk of dengue fever outbreaks spatially and manpower insufficiency.

**Methods & Materials:** To help operation department allocate limited resources, we developed a predictive risk map for dengue transmission using the Random Forest algorithm, incorporating various risk factors and accounting for temporal and spatial lag effects of the factors. A wide range of factors representing the characteristics of past dengue situation (total number of cases in previous year and number of non-resident cases in previous year), human population (estimated population density), vector population (estimated ratio of *Aedes aegypti* mosquitoes out of all *Aedes* mosquitoes—breeding percentage) and environment (vegetation index, connectivity index and ratio of residential area) were examined and incorporated in the model.

**Results:** Validation using most recent data showed that the observed and the predicted risk ranks had a Pearson correlation of 0.87 ( $P < 0.001$ ) and a weighted Kappa agreement of 0.814 ( $P < 0.001$ ) when categorised to risk groups. In addition, the model was able to estimate the partial effects and relative importance of individual risk factors, which can strengthen our understanding of the risk factors of dengue transmission.

**Conclusion:** Our risk map has strong predictive capability, hence may be an important tool in guiding targeted vector control interventions for dengue.

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**Hand hygiene program: “Go for 100\*”. Whole impact (hospital cost, MRSA attack, nosocomial infections and device related infections)**

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**Background:** Nosocomial infections (NI) are significant cause of mortality and hospital costs.. Annual costs have approximately estimated of US\$6.8 billion in the USA. Hand hygiene is the most important measure to prevent NI reducing them a 30% on average and to reduce MRSA attack rate. There is spare information about this in middle income countries. The aim was to explore the impact of the program in hospital costs, nosocomial infections and MRSA attack rate and clonality.

**Methods & Materials: Program “Vamos por el CIEN-Go for 100”** (CIEN Spanish acronym of infection control by integration and innovative strategies”): based on the WHO hand hygiene multimodal strategy but focalizing education and awareness for every hospital sector and adding periodically innovative strategies. Here we analyze 2013–2015. **Direct** costs of this program were evaluated monthly.

Active nosocomial infections surveillance was done. A collection of 43 *S. aureus* clinical isolates from pediatric patients (one isolate per patient) was collected from January 2012 to May 2015.

**Molecular genotyping assays.** Pulsed-field gel electrophoresis (PFGE) in the *S. aureus* clinical isolates was performed. The DNA fragment patterns generated by PFGE were analyzed using NTSys program 2.0 with the Sorencen-Dice coefficient and the unweighted pair group method with an arithmetic mean (UPGMA) clustering system.

**Results:** Over 1,000 sessions took place from 2013–2015, impacting more than 15,000 people, the consumption of BPA increased from 125L/month to 400L/month, 2400 posters were allocated, the cost of the program per year was \$217,618 dills. Hand hygiene compliance increased from 48% to 74%, NI decreased from 7.68 to 6.47/100 discharges (15.7%), and the MRSA attack from 8.3 to 2.13/100 discharges. High clonality among nosocomial isolates MRSA was found, suggesting the presence of clones scattered in hospital environment that can interfere with program strategies.

**Conclusion:** Probably due to a better distribution of resources the program costs were lower than the year before the program (\$3743031.7dills). We also demonstrate that in a middle income country a hand hygiene program can decrease in NI especially in

*S. aureus*. Phylogenetic analysis showed that hand hygiene has a direct impact on the clonality of MRSA hospital origin.

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#### Morbidity, mortality, and seasonality of influenza hospitalizations in Egypt, november 2007 - november 2014

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**Background:** Influenza typically comprises a substantial portion of acute respiratory infections, a leading cause of mortality worldwide. However, influenza epidemiology data are lacking in Egypt. We describe seven years of Egypt's influenza hospitalizations from a multi-site influenza surveillance system.

**Methods & Materials:** Syndromic case definitions identified individuals with severe acute respiratory infection (SARI) admitted to eight hospitals in Egypt. Standardized demographic and clinical data were collected. Nasopharyngeal and oropharyngeal swabs were tested for influenza using real-time reverse transcription polymerase chain reaction and typed as influenza A or B, and influenza A specimens subtyped.

**Results:** From November 2007–November 2014, 2,936/17,441 (17%) SARI cases were influenza-positive. Influenza-positive patients were more likely to be older, female, pregnant, and have chronic condition(s) (all  $p < 0.05$ ). Among them, 53 (2%) died, and death was associated with older age, five or more days from symptom onset to hospitalization, chronic condition(s), and influenza A (all  $p < 0.05$ ). An annual seasonal influenza pattern occurred from July–June. Each season, the proportion of the season's influenza-positive cases peaked during November–May (19–41%).

**Conclusion:** In Egypt, influenza hospitalizations cause considerable morbidity and mortality and its seasonality mirrors Northern Hemisphere patterns. Additional assessment of influenza epidemiology in Egypt may better guide disease control activities and vaccine policy.

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#### Fecal microbiome therapy in relapsing Clostridium difficile infection – long-term results



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**Background:** Fecal microbiome therapy (FMT) has become an accepted rescue treatment for relapsing or recurring Clostridium difficile infection (CDI). While short-term effectiveness of this treatment approach is high, no data on the long-term efficacy are available.

**Methods & Materials:** From 17 patients (median age 84, range 55–93 years) who underwent 18 FMT procedures for relapsing or recurring CDI long-term outcomes were analysed.

FMT was done via endoscopically placed jejunal tube using 500 ml (0.1 g/ml) of sterile prepared donor stool suspension from healthy first-degree relatives ( $n = 15$ ) or spouses ( $n = 3$ ).

**Results:** All patients had a Charlson comorbidity score  $> 10$  indicating multiple comorbidities. Median number of treatment courses for CDI before FMT was four (range 3–7). Postprocedure efficacy for FMT was 17/18 (94.4%). At day 30 14/18 (77.8%) were without clinical symptoms or signs of relapse, by day 180 7/10 (70%) were free from CDI, and after one year 6/9 (66.7%).

Leukocyte counts, albumin, clinical response measured by the use of the Bristol Stool Chart (BSC) or stool lactoferrin at baseline were not predictive for long-term response whereas a  $> 75\%$  decrease after FMT in stool lactoferrin concentrations by day 7 compared to day 0 was indicative.

**Conclusion:** Even in elderly patients with severe or multiple comorbidities and high risk of recurring CDI the use of FMT protects a substantial number of patients over more than one year.

The decrease in stool lactoferrin concentrations within one week after FMT remained the only predictive biomarker for long-term response in these patients.

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