20.071

Performance of community volunteers in human and animal diseases surveillance by using mobile application

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Purpose: PODD disease surveillance system was developed for monitoring animal diseases, human diseases and environmental issues by using mobile application called "PODD". It was developed and implemented since early 2015 in 74 communities in Chiang Mai, Thailand. Total of 296 community volunteers, 4 people per community, were recruited into the system to be volunteer reporter for their communities. They were trained every 3 months about animal and human diseases and how to report those abnormal events through PODD mobile application. This study aimed to determine the performance of those community volunteers in reporting animal diseases, human diseases and environmental issues by using mobile application in PODD disease surveillance system.

Methods & Materials: The regularity of reporting, participation in training, leadership, enthusiasm and possibility of being role model for other volunteer were evaluation criteria to determine their disease reporting performance. According the criteria, community volunteers were divided into four groups: A was reporter who reported more than 75% of request, attended the training more than 50% and showed excellent performance, B was reporter who reported between 50-75% of request, attended the training 30-50% and showed excellent performance, C was reporter who reported between 25-50% of request, attended trainings less than 30%, but did not show good performance and D was reporter who reported less than 25% of request, attended the training only 1 time and need to be improved their performance.

Results: The results indicated that 20.42% of volunteer reporters showed great performance with Group A. Most of them were grouped in Group B and C (34.60% and 37.72%, respectively). These groups attended PODD training and activities and showed the regularly report. The system needed to maintain these performances and motivate them to proactive for moving to Group A. Group D (7.27%) was focused to improve their performance. This group could be the characters of undesirable people, who would be recruited to be disease surveillance volunteer.

Conclusion: In conclusion, disease surveillance system with digital technology, that needed the participation from volunteers, could evaluate performance of the volunteer and empower them to make better surveillance system in the future.

20.072

Characterization of a Culex theileri flavivirus variant in field-collected mosquitoes from Turkey

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Purpose: The Flaviviridae family includes several strains that only replicate in mosquitoes or mosquito-derived cell lines, generally called as insect-specific flaviviruses, along with the well-known mosquito-borne important human pathogens. Recent evidence indicates wider-than-expected prevalence and dispersion insect-specific flaviviruses in mosquito populations. Here, we describe the near-complete genomic characterization of flaviviruses isolated during a field surveillance campaign in Turkey.

Methods & Materials: Four virus strains, isolated using C6/36 cells from mosquito pool extracts with positive results in screening via generic flavivirus PCR were evaluated. The pools originated from collection sites in Aegean and Thrace regions, and comprised individuals previously identified as *Culex theileri* via morphology and DNA barcoding. Culture supernatants of the 3rd passage were subjected to nucleic acid purification, cDNA synthesis, library preparation and sequencing via Illumina HiSeq 1500 sequencing platform. Assembly of the contigs, alignment with the complete or-near-complete insect flavivirus genomes deposited in public databases and further analyses were performed with relevant software.

Results: Near-complete genomes of 10299-10420 nucleotides, that cover the complete coding region of the flavivirus polyprotein were assembled. Neighbor-joining analyses placed all isolates within a distinct group, which further forms a cluster with two culex theileri flavivirus isolates from Portugal. No association of nucleotide/aminoacid variations with collection sites was observed. The putative polyprotein comprised 3357 amino acids and followed the universal flavivirus polyprotein organization of structural proteins C, preM and E, and nonstructural proteins NS1, NS2a, NS2b, NS3, NS4a, NS4b and NS5. The putative protease cleavage sites were noted as identical to the Culex theileri flaviviruses. Pairwise amino acids comparions demonstrated 0.99-1.33% diversity rates among intramural and phylogenetically-related strains.

Conclusion: The findings indicate the circulation of a novel culex theileri flavivirus variant, tentatively called as the "Culex Theileri Flavivirus Turkey (CTFT)", in various regions of Turkey. This report constitutes the first detailed characterization of insect-specific flaviviruses in Asia Minor.