

countries. In human, *T. solium* larvae (metacestodes) migrates to brain resulting in neurocysticercosis (NCC), the main cause of epilepsy whose social consequences apart from economic lame, includes stigmatization and discrimination. In pigs, infection by metacestodes leads into condemnation of pork resulting to meat protein and economic loss. This study determined the epidemiology, public health and socioeconomic impacts of *T. solium* cysticercosis in human being (human cysticercosis - HCC) in Mbulu district, Tanzania.

Methods & Materials: Sero-screening and cerebral computed tomography scanning (cCT scan) were employed in assessing HCC / NCC prevalence. Questionnaire, interviews, live radio sessions' dialogues, observations and documentary reviews were used to obtain information on public health costs and the combined socio-economic impacts of HCC and porcine cysticercosis (PCC). About 3 mLs of cephalic venous blood were drawn from assorted age groups and serum was extracted. Cysticercus IgG Western Blot Assay was used to determine HCC circulating antibodies (Abs). cCT scan was used to diagnose NCC. The Disability Adjusted Life Year (DALYs) was used to estimate the health burden of HCC.

Results: The mean age of respondents was 34.61 ± 18.4 with a range of 93. The sero-prevalence of HCC was 16.3%. About 76% of HCC sero-positives had single to multiple NCC suggestive lesions and about 73.7% of the people with NCC lesions had epileptic seizures. About 4.9% and 4.7% of the population were those with neurological disorders and epileptic symptoms, respectively. The estimated total annual cost (as a result of direct and indirect losses) due to HCC and PCC was US \$ 3.96 million of which 56.8% was due to HCC. The monetary burden per case of HCC amounted to US \$ 209 per year. The average number of DALYs imposed due to HCC was 2.73 per 1000 population per year.

Conclusion: The prevalence and impact of HCC in Mbulu district is worrying and calls for an immediate deployment of intervention measures.

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Risk factors for death among hospitalized influenza A (H1N1) patients, Punjab, India - 2013

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Background: Since 2009, influenza A (H1N1) has caused significant morbidity and mortality in Punjab state, India. Risk factors for mortality in this context are unknown. We sought to determine risk factors for mortality due to H1N1 among hospitalized patients in Punjab.

Methods & Materials: We defined confirmed case as Patient with acute febrile respiratory illness with laboratory-confirmed (RT-PCR) H1N1 influenza A, who was hospitalized from January-

April 2013. We described hospitalized cases & conducted a case control study; cases were defined as Death among hospitalized patients of confirmed influenza A (H1N1) infection and control as surviving H1N1 cases from same hospitals from 01.01.2013 to 15.04.2013 in Punjab. Socio-demographic and clinical data were collected using an existing WHO questionnaire through hospital record reviews and via telephonic interviews with controls and next-of-kin of cases. Multivariate logistic regression analysis was performed to identify independent risk factors for deaths among hospitalized cases, controlling for severity of disease at presentation.

Results: From January-April 2013, a total of 183 lab-confirmed H1N1 cases (99 males, 84 females) were hospitalized from 21 hospitals in Punjab; 42 (23%) patients died. All districts (22) reported H1N1 cases with median age of those who died and survived were same 47 years (IQR: 40-55). About half of the cases and deaths were from four districts. We compared 42 cases with 80 controls. Those who died were significantly more likely to be younger than 50 years (AOR=10.6, 95%CI=1.8-21.1), be obese (AOR=16.7, 95%CI=1.6-170.7) and visit more than two healthcare facilities before laboratory confirmation (AOR=25.8, 95%CI=5.4-121.6). Gender, residence, educational level, religion and HIV infection were not significantly associated with deaths among these patients. To control for disease severity, ventilator support (AOR=19.1, 95%CI=7.3-363.1) was retained in the model and found to be independently associated with mortality.

Conclusion: Mortality among hospitalized influenza A (H1N1) patients was high in Punjab. Young overweight patients who had a delayed diagnosis were at high risk of an adverse outcome. The community should be sensitized about influenza symptoms, risk factors and to seek medical advice early in the course of illness in order to reduce the risk of death due to H1N1 in the State.

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Evaluation of antimalarial and antimicrobial activities of extract and fractions from *Areca catechu*

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Background: Infectious diseases are clinically evident diseases that results from the presence of pathogenic microbial agent in the body system. These include malaria, amoebiasis and other microbial ailments. *Areca catechu* (AC), commonly called betel nut is chewed regularly by at least 10% of the world population, imported by immigrant users wherever they settle, and is the fourth most widely used addictive substance. This plant is traditionally used



to overcome varied ailments including worm disease condition, stomach-ache, jaundice and malaria like fevers. This study is an attempt to assess AC as antimicrobial and antimalarial plant. Therefore, crude extract and fractions from AC nuts were tested against *Plasmodium falciparum* 3D7 and 11 strains of bacteria.

Methods & Materials: Extract from AC nuts was obtained by Soxhlet extraction using methanol as solvent. Fractions viz. hexane, chloroform, ethylacetate, butanol and water were obtained by partitioning methanol extract in water and different solvents in order of increased polarity. Antimalarial activity of extract and fractions from AC was performed through SYBR green method whilst antimicrobial activity was assessed through Disc Diffusion Assay (DDA). The antimicrobial potential was further confirmed quantitatively by determination of the Minimum Inhibitory Concentration (MIC) of extract and fractions from AC.

Results: Extract and fractions from AC showed remarkable antimalarial activity against *P. falciparum*, the most potent being butanol fraction with an IC₅₀ of 18 µg/ml. Significant antimicrobial activity of methanol extract, ethylacetate, butanol and water fraction towards four bacterial strains viz. *Staphylococcus Aureus* 96 (SA96), *Staphylococcus Aureus* 2940 (SA2940), *Streptococcus mutans* (SM) and *Mycobacterium smegmatis* (MS) was recorded. The most potent being butanol fraction with DDA of 14 mm. The MIC values were 125, 250, 62.5 and 250 µg/ml for methanol extract, ethylacetate, butanol and water fractions towards SA96.

Conclusion: AC demonstrated to possess antimalarial and broad antimicrobial activities which might be prospected as potential source for the development of new therapeutic agents.

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Proline residue at NS3₂₄₉ is a primary determinant of West Nile virus virulence in mammals and birds



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Background: West Nile virus (WNV) is a neurotropic flavivirus transmitted through mosquito bites and whose reservoir hosts are wild birds. Equids and humans are incidental dead end hosts and can develop severe neurological symptoms. Despite enhanced reporting of WNV outbreaks in Europe since 2008, much remains to be explored about the virulence level and determinants of WNV strains circulating in Europe. Of note, recently expanding lineage 2 virus has gained a proline residue at position 249 in the non structural 3 (NS3) protein and has caused the worst epidemics ever experienced in central and Southern Europe. Interestingly, Brault *et al.* (2007) identified NS3_{249P} as being crucial for the virulence of WNV in American crows.

Methods & Materials: An infectious clone, based on WNV lineage 1 IS-98-ST1, a highly neuroinvasive strain, harbou-

ring NS3_{249P}, was constructed (Bahuon *et al.*, 2012) and a NS3_{P249T} mutant was generated by directed mutagenesis.

We aimed at deciphering the properties of recombinant viral particles *in vitro* and *in vivo*, in mammalian and bird models (Dridi *et al.*, 2013).

Results: In Vero cells, virus with a NS3_{249T} protein proved to replicate at a slower rate than the parental NS3_{249P} virus. When injected intraperitoneally in adult female Balbc/J mice, parental virus was found to be highly virulent (LD50 < 1 pfu), while only 4 out of 20 animals infected with the NS3_{249T} virus succumbed, regardless of the initial infecting dose (1-10³ pfu). Mice infected with NS3_{249T} virus experienced milder clinical and virological outcomes, characterized by delayed weight loss and decreased viremia 4 days pi (1.4x10³ vs 3.2x10⁴ viral copies/mL blood). Birds, one-day old chicks and young corvids (*Corvus corone*), also indicated that NS3_{249T} virus was attenuated for model and susceptible European birds. In particular, in young crows, 16.7% (1/6) animals died after subcutaneous infection with NS3_{249T} virus whereas a 100% lethality (7/7) was observed with NS3_{249P} virus.

Conclusion: The presence of a proline residue at position 249 in NS3 appears as a primary determinant for WNV virulence in wild birds, as well as in mammals and could be a genetic factor accounting for enhanced reporting of WNV neuro-invasive cases in humans in Europe.

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Genetic Diversity of West Nile virus Isolated from the tick, *Rhipicephalus pulchellus*, in Kenya



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Background: West Nile virus is a re-emerging infectious disease that has a wide geographical distribution in Africa, parts of Europe, the Middle East, Asia, Australia and the Americas where it causes outbreaks. Although WNV has been isolated in mosquitoes in Kenya, paucity of genetic information exists. Mosquitoes are the traditional vectors for WNV however; the virus has also been isolated from some tick species in North Africa and Europe which could be a means of introduction and spreading of the virus over long distances through migratory birds. North-Eastern province of Kenya has been found to be a major hot spot for arbovirus circulation where arboviruses such as Rift Valley fever (RVFV), WNV and Crimean-Congo hemorrhagic fever have been isolated from vectors and humans. Moreover, some of these viruses such as RVFV has been reported to have caused outbreaks in the province.