Methods & Materials: This mixed method study extracted data from adult malaria inpatient records of the hospital from 2010-2015, and assessed drug supply at pharmacies. Physicians' practices and perspectives were explored by in-depth interviews. Compliance was assessed by severity, type of species and pregnancy status. Thematic analysis was done for the qualitative data.

Results: A total of 247 case files were reviewed. Vivax malaria (41.0%) was more common than falciparum malaria (37.2%). The majority (90.8%) of cases were severe malaria. Overall compliance for use of schizonticidal drug was 73.0% in severe malaria and was only 9.5% in uncomplicated malaria. Compliance for use of gametocidal drug (primaquine) was 15.3%. Schizonticidal drugs were available in all pharmacies except the public one. Primaquine was available in only one. The main themes emerging in the thematic network analysis were physicians' misconceptions, physician-related factors, and hospital-related and drug access factors.

Conclusion: The degree of compliance for severe malaria treatment was reasonably good but low for radical cure. Raising knowledge and awareness among health care providers, by using written treatment protocols and continuing medical education would improve compliance.

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Ongoing activity of invasive aedes species in Northern Anatolia: lack of Chikungunya despite West Nile virus circulation

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Purpose: In order to screen for invasive mosquito species and associated viruses, we performed a field survey for mosquitoes in the Black Sea region of Anatolia where Aedes aegypti and Aedes albopictus were previously recorded.

Methods & Materials: Mosquitoes were collected from 31 sites in Artvin, Trabzon and Rize provinces during 2016-2017. The specimens were identified morphologically and pooled according to collection site and species. Selected specimens were processed for DNA barcoding via cytochrome oxidase I amplification and sequencing, for confirmation of the morphological species identification. Virus screening was carried out using polymerase chain reaction (PCR) assays targeting alpha and flaviviruses, as well as recently-described novel rhabdovirus Merida-like virus Turkey (MERDLVT), followed by sequencing for characterization.

Results: A total of 756 mosquitoes that comprise Ae. albopictus (675, 89,2%), Ae. aegypti (61, 8,1%) and Culex pipiens sensu lato (20, 2,6%) were collected and grouped in 65 pools. No amplification was observed in any pool via generic alphavirus PCR. Generic flavivirus PCR was reactive in 7 and 8 pools collected in 2016 and 2017, respectively. Cell fusing agent virus (CFAV) sequences were characterized in 4 pools (6,1%) of Ae. albopictus (n = 2) and Ae. aegypti (n = 2), collected in 2016. Aedes flavivirus (AFEV) sequences were characterized in 6 pools (9,2%) of Ae. albopictus (n = 5) and and Ae. aegypti (n = 1), collected in 2016 (n = 3) and 2017 (n = 3). Sequences of West Nile virus (WNV) was detected in 5 pools (7,6%) of Ae. albopictus (n = 4) and and Cx. pipiens s.l. (n = 1), collected in 2017. In phylogenetic analyses, the WNV sequences clustered with local and global lineage 1 clade 1a strains. Moreover, partial L and N gene sequences of MERDLVT were identified in the Cx. pipiens s.l. pool, coinfected with WNV.

Conclusion: This is the initial detection of WNV and MERDLVT in field-collected mosquitoes from the Black Sea region. Although no alphavirus sequence could be demonstrated, presence of Ae. albopictus and Ae. aegypti indicates ongoing risk for potential spread.

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Clinico- bacteriological study and molecular detection of campylobacter in childhood diarrhoea

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Purpose: Campylobacter enteritis is rapidly becoming the most commonly recognized cause of bacterial gastroenteritis in man and causes 5–14% of diarrhea, worldwide. High incidence of Campylobacter diarrhoea, as well as its duration and possible sequelae, make it important from a socio-economic perspective. Diagnoses of Campylobacter infections are challenging because the organism is difficult to isolate, grow and identify. Guidelines for Clinical and laboratory diagnosis are inadequate.

Methods & Materials: A Hospital based Cross sectional descriptive study conducted in JSS tertiary care hospital, Mysuru. Study included 55 stool samples of children aged between 1 to 60 months who presented to Department of Pediatrics, JSS hospital, both as in and out patients with complaints of diarrhea and dysentery. All stool samples were inoculated on to selective and non-selective media with filtration using a 0.45 μm membrane filters and incubated in microaerophilic conditions using the candle jar at temperatures 37 °C and 42 °C. The culture isolates were confirmed by standard phenotypic tests. A simplex polymerase chain reaction (PCR) with universal Campylobacter primers and primers specific for C.jejuni and C.coli, was performed on the DNA extracted from the stool filtrates.

Results: Campylobacter was isolated in 5(9.1%) out of 55 stool samples using culture and the isolate were confirmed to be Campylobacter jejuni by phenotypic tests. Campylobacter Genus level PCR was positive for 10 samples (18.2%), rest of the samples were negative. The positive samples were subjected to species level PCR and all were positive for C.jejuni (100%) and negative for C.coli (0%).

Conclusion: The implication of this study is that culture is less sensitive for use in diagnosis of Campylobacter infection in our settings. Nucleic acid based diagnostics offer increased sensitivity, can determine both the presence and burden of infection, and can distinguish between Campylobacter infections at the species level. We therefore recommend PCR, if feasible, as the preferred diagnostic modality for detection of Campylobacter infection. However, the role of culture in the diagnosis of Campylobacter infections is that it allows precise identification of bacteria and testing