

## 21.161

### A metagenomic survey of ticks reveals pathogenic rickettsia and francisella/coxiella-like endosymbionts in Anatolia

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**Purpose:** We investigated tick-borne bacteria in field-collected ticks via a metagenomic approach using high throughput sequencing.

**Methods & Materials:** A total of 210 ticks, collected from various regions of Anatolia, were identified morphologically and processed in 39 pools. Homogenization, nucleic acid purification and library preparation in pools were performed using standard assays and protocols, followed by sequencing using the Illumina MiSeq system.

**Results:** A near-complete Rickettsial genome of 1.485.148 nucleotides with 89.5% identity to Rickettsia felis strain URRWX-Cal2 was assembled from a pool of Haemaphysalis parva ticks. The identical pool further provided a 5690-nucleotide sequence of the Rickettsial conjugative plasmid. Varying lengths of 16S, OmpA, Sca1 and gltA sequences were obtained from 7 tick pools (17.9%) comprising Haemaphysalis parva, Rhipicephalus bursa, Rhipicephalus sanguineus sensu lato and Hyalomma marginatum ticks. The sequences were characterized as Rickettsia felis and Rickettsia hoogstraalii in 5 pools whereas strain identification remained obscure in two pools. 16S rRNA sequences of Coxiella-like endosymbionts were detected in 15 pools (38.4%) of Haemaphysalis parva, Rhipicephalus bursa, Rhipicephalus sanguineus s. l., Hyalomma marginatum, Hyalomma excavatum and Dermacentor marginatus ticks. These sequences formed three phylogenetically-distinct clusters with previously-characterized Coxiella-like endosymbionts from Rhipicephalus, Ixodes and Dermacentor species. Finally, Francisella-related 16S sequences were characterized in 9 pools (23%) of Rhipicephalus sanguineus s. l., Hyalomma marginatum, Dermacentor marginatus and Hyalomma aegyptium ticks. These sequences formed two distinct clusters and grouped with Francisella-like endosymbionts of Dermacentor ticks, sharing a common ancestor with Francisella persica.

**Conclusion:** Rickettsia of the spotted fever - Rickettsia akari group were characterized in this preliminary tick screening study, with detailed sequence information obtained for various strains. Widespread infection of ticks with Francisella- and Coxiella-like symbionts were also identified. The impact of these endosymbiotic bacteria on the circulation and detection of pathogenic strains in ticks requires further investigation.

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## 21.162

### Falciparum predominant malaria outbreak in Hunkund taluk, Bagalkote District, Karnataka, India, 2015 to 2016

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**Purpose:** India accounts for 58% of malaria cases in South East Asia region. Four villages of Hungund taluk, Bagalkote district in Karnataka state, India reported clustering of malaria cases on 15<sup>th</sup> of November, 2015. We investigated to describe the outbreak and to give recommendations.

**Methods & Materials:** Our study population included residents of all four villages, Hirekodagalli, Gugglemaari, Gudur and Hanumna. We surveyed fever cases in fever clinic, between 20<sup>th</sup> of November, 2015 and 31 of March, 2016. We defined a confirmed case of Malaria as any patient whose blood smear was positive for malarial parasites, Plasmodium falciparum and Plasmodium vivax. We collected line list of confirmed malaria cases from fever clinics in the four villages. We calculated attack rates by village, age groups and gender.

**Results:** There were 601 falciparum cases and 213 vivax cases. Sixteen cases had mixed infections. The epidemic curve showed that falciparum cases started on 26<sup>th</sup> October, 2015, with peak between 27<sup>th</sup> and 29<sup>th</sup> October and started coming down after 1<sup>st</sup> of December, 2015. Last case occurred on 18<sup>th</sup> of February, 2016. Overall attack rate of Falciparum cases was 15% (601/4111). Median age was 22 years (range: 1.5 – 81 years). Falciparum incidence was highest (24% in Gugglemaari village). Vivax cases started on 26<sup>th</sup> of October peaked between 27<sup>th</sup> October and 16<sup>th</sup> of November and last case occurred on 21<sup>st</sup> of December, 2015. Median age was 22 years (3 to 80 years). Overall attack rate of vivax cases was 5% (213/4111). Attack rates among females {5%, (103/2133)} and males {6%, (110/1978)} were almost equal. Highest attack rate (7%) was in Gugglemaari (69/959) and Gudur (45/668) while attack rate was 4% in Hirekodagalli (83/2024) and 3% in Hanumna (15/460).

**Conclusion:** There was malaria outbreak between 26<sup>th</sup> October, 2015 and 18<sup>th</sup> February, 2016 in four villages of Hungund taluk. Falciparum accounted for majority of cases and Gugglemaari village was most affected. We recommend identifying entomological and environmental factors for the outbreak.

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## 21.163

### Enhanced surveillance and integrated approach reduced dengue incidence, Namakkal, Tamilnadu, India, 2017

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**Purpose:** Highest burden of dengue is in India, accounting for 34% of global cases. Dengue cases started increasing in Namakkal district of Tamilnadu, India from July and peaked in October, 2017. District surveillance unit planned interventions to control the outbreak. After two months, we evaluated the impact of interventions.

**Methods & Materials:** We did an experimental study between October and December, 2017 in all the 15 blocks of Namakkal

