at least 4 weeks in 5% CO_2 with high humidity. Indirect fluorescence assay (IFA) was done for the detection of IgM antibodies in the serum using a commercial kit. Whole blood was used to perform Polymerase chain reaction (PCR) for the citrate synthase gene (*glt A*).

Results: IFA was positive in 11 (8.46%) patients and PCR was positive in 3 (2.3%) patients. Culture was negative in all the cases. Out of the eleven IFA positive cases, seven presented with fever and lymphadenopathy. Five of these were diagnosed as having Pyrexia of Unknown Origin (PUO), one with Cat Scratch Disease (CSD) and one with Granulomatous Disease (CD). Among the four IFA positive ophthalmology cases, one was a case of Parinaud Oculoglandular syndrome and the rest showed symptoms of neuroretinitis. A higher incidence of Bartonella infection was seen in patients with fever and lymphadenopathy i.e. 9/39 (23.07%) eight of whom were children.

Conclusion: The present study shows that the threat of Bartonella infection is very much a reality in India. It is also an important treatable cause of fever and lymphadenopathy in children. Serology and PCR are useful tests for its diagnosis. Clinicians should consider Bartonella infection in the differential diagnosis of febrile illnesses and chronic diseases.

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20.083 Middle East Respiratory Syndrome Coronavirus (MERS-CoV): A systematic literature review

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Purpose: Since the detection of Middle East Respiratory Syndrome Coronavirus (MERS-CoV) among humans in 2012, questions remain unanswered regarding the virus's origins; clinical, epidemiological, and virological characteristics; and potential therapeutics. A systematic literature review was conducted to synthesize current knowledge and identify critical knowledge gaps.

Methods & Materials: We conducted a systematic review on MERS-CoV using PRISMA guidelines and identified 312 relevant, peer-reviewed publications from Embase, Google Scholar, and PubMed. Of these, 206 were selected for inclusion based on their contributions to four pre-defined themes (virology, epidemiology/clinical characteristics, origins/reservoirs, and therapeutics/prevention).

Results: Virological research identified the functional human receptor (CD26/DPP4) and shed light on MERS-CoV's broad species tropism. A variety of molecular and serological assays have been developed for surveillance and research. The epidemiologic profile is incomplete, although initial data suggest values for the basic reproductive rate, proportion of primary cases, case fatality rate, and demographic and geographic distributions. There have been sustained outbreaks in Saudi Arabia and South Korea, and potential risks for infection include camel contact, nosocomial exposures, and close contact to active cases, but not Hajj pilgrimage. The primary mechanism of transmission in health care settings appears to be environmental contamination of medical devices and surfaces from respiratory secretions. MERS and MERS-like CoVs have been detected in bat species in numerous countries, and MERS-CoV is genetically similar to bat coronavirus HKU-4, which contains cell surface-expressed CD26/DPP4. Dromedary camels have demonstrated MERS-CoV seropositivity throughout the Middle East and Africa and there is preliminary evidence of camel-to-human MERS-CoV transmission events. Various potential therapeutic agents have been identified from high-throughput screening and other methods, but none have been clinically evaluated in human trials. At least one candidate vaccine has progressed to Phase I human trials.

Conclusion: Although there has been substantial MERS-CoV research since 2012, significant knowledge gaps persist. Uncertainties remain about the zoonotic origin, clinical characteristics, risk factors for infection, asymptomatic transmission, effective therapeutics, and vaccine candidates. These areas merit urgent attention by the global community to better understand, detect, and control MERS-CoV using a unified One Health approach.

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20.084

Mammalian haploid genetic screen to identify host factors essential for Rift Valley fever virus

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Purpose: Rift Valley fever virus (RVFV, family *Bunyaviridae*, genus *Phlebovirus*) is currently referenced by the WHO as one of the 8 emerging pathogens likely to cause serious outbreaks in the near future and for which few medical countermeasures exist. Transmitted by mosquitoes, RVFV causes large and devastating epidemics in Africa and Arabia, leading to hemorrhages and massive abortions in livestock ruminants, and hepatitis and hemorrhages in 10-20% of human hospitalized patients.

While some RVFV proteins are known to interfere with apoptosis and antiviral signalling, a knowledge gap exists concerning the host cellular factors required for the virus cycle. Using a forward genetic screen, we aim to identify those host genes and pathways essential for RVFV entry, transcription and replication.

Methods & Materials: Haploid organisms allow the study of gene knockouts, since recessive mutations will show a clear phenotype due to the absence of a second gene copy. Combined with the pluripotency of embryonic stem cells, the effect of the knockout on viral cycle can be assessed in any disease-relevant cell type. We used the recently developed mammalian haploid embryonic stem cells (mESCs) (Elling, 2011, Cell stem cell), which were mutagenized with a revertible genetrap vector, for infection with the RVFV MP-12 vaccine strain.

Results: While wild-type cells massively died upon infection, a higher number of cells survived within the mutagenized cells. Surviving cells were submitted to next generation sequencing, and statistical analysis gave a list of 5 genes potentially involved in RVFV MP-12 cycle, but not essential for normal cell life. Those genes will be validated by infection of specific knockout mESCs clones (and their reverted version) by different strains of RVFV.

Conclusion: Such an approach allows the identification with a great confidence of important host cofactors to RVFV, increasing our knowledge on the viral cycle, and giving access to several potential targets for antiviral design.

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