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**Antiviral activity and possible mechanisms of action of *Acacia nilotica* against influenza A virus**Mona Timan Idriss<sup>1</sup>, Malik Suliman Mohamed<sup>2</sup>, Sarawut Khongwichit<sup>3</sup>, Natthida Tongluan<sup>3</sup>, Duncan R Smith<sup>3</sup>, N H Abdurahman<sup>4</sup>, N H Azhari<sup>4</sup> and Alamin Ibrahim Elnima<sup>2</sup><sup>1</sup>Sudan International University, Sudan<sup>2</sup>Khartoum University, Sudan<sup>3</sup>Mahidol University, Thailand<sup>4</sup>University Malaysia Pahang, Malaysia

We investigated the anti-influenza virus activity of *Acacia nilotica* and possible mechanisms of action in vitro. We found that *Acacia nilotica* has anti-influenza-virus activity and both pre-incubation of virus prior to infection and post-exposure of infected cells with *Acacia nilotica* extract significantly inhibited virus yields. Influenza-virus-induced hemagglutination of chicken red blood cells was inhibited by *Acacia* extract treatment, suggesting that *Acacia* can inhibit influenza A virus infection by interacting with the viral hemagglutinin. Furthermore, *Acacia* extract significantly affect nuclear transport of viral nucleoprotein (NP). To best of our knowledge, this study revealed for the first time that *Acacia nilotica* extract can inhibit both viral attachment and replication and offers new insights into its underlying mechanisms of antiviral action. The fruit husk of *Acacia nilotica* collected from Sudan and extracted with 70% methanol. The crude extract was screened for its cytotoxicity against MDCK cell line by alamarBlue assay and WST-1 assay. Antiviral properties of the plant extract were determined by cytopathic effect inhibition assay and virus yield reduction assay (plaque assay). Time of addition assay and nuclear export mechanism were also performed.

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**Genetic analysis of Crimean Congo hemorrhagic fever virus in Iran**Nariman Shahhosseini<sup>1</sup> and Sadegh Chinikar<sup>2</sup><sup>1</sup>Bernhard Nocht Institute for Tropical Medicine, Germany<sup>2</sup>Pasteur Institute of Iran, Iran

**Background:** Crimean Congo Hemorrhagic Fever (CCHF) caused by CCHF virus, belongs to Nairovirus genus and *Bunyaviridae* family. The route of transmission is through the bite of infected ticks, handling of infected blood or organs of livestock and nosocomially. The virus has a negative and three segments (S, M and L) RNA genome. The initial phylogeny study on CCHFV in Iran showed that isolated Iranian strain (ArTeh193-3) was similar to Senegalese strain.

**Methods:** The CCHFV-RNA was extracted from human sera and tick samples collected from different parts of Iran during 15 years. The virus genome was examined by RT-PCR. Positive samples were sequenced and sequences were analyzed by Geneious.

**Results:** Phylogenetic investigations on CCHFV sequences obtained from human and tick samples showed that clade IV (Asia-1 and 2), clade V (Europe) and clade VI (Greece) are circulating genomic variants of CCHFV in Iran.

**Conclusion:** Interestingly, all phylogeny studies during the last 15 years indicated that CCHFV strain Iran/ArTeh 193-3 is likely fade away from Iran and it has been never reported since 35 years ago when it was reported as the first CCHFV strain from Iran. Since understanding the molecular epidemiology of CCHFV is the sine qua non to develop and implement surveillance strategies for its control, phylogenetic analysis of CCHFV is worthy of note. As endemic countries for CCHF surround Iran, high genetic diversity for CCHFV could be expected.

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