

### 306/ZOP

#### Serological and molecular epidemiology of Crimean-Congo hemorrhagic fever in Ghaemshahr county in the Mazandaran province of Iran

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**Introduction:** Crimean-Congo Hemorrhagic Fever (CCHF) is a tick-borne viral hemorrhagic fever disease. During the transmission cycle of the disease, ticks play both vector and reservoir roles for the CCHF virus (CCHFV). CCHF is an endemic disease in different provinces within Iran.

**Materials and Methods:** This study describes CCHFV in Ghaemshahr county of Mazandaran Province, a province in the northern part of Iran. By using an ELISA method, IgG antibodies against CCHFV were detected in 4 (4.8%) of 84 sheep sera samples collected from 4 villages.

**Results:** Forty sera were obtained from human in contact with the examined sheep, none of which had IgG antibodies against CCHFV. Molecular analysis on the ticks by RT-PCR detected the CCHFV genome in 1.7% of hard tick samples. Sequence analysis demonstrated that the CCHFV genomes isolated from ticks were 100% identical to those isolated from corresponding livestock.

**Conclusion:** This study confirms the circulation patterns of the virus in this region, so people in close contact with livestock and health care workers should be alerted.

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### 307/ZOP

#### Crimean-Congo Hemorrhagic Fever: A Molecular Survey in Damqan district, Semnan Province, Iran

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**Introduction:** Crimean Congo Hemorrhagic Fever (CCHF) is an arboviral zoonotic disease that is asymptomatic in infected animals, but a serious threat to humans. Numerous genera of ticks serve as both vector and reservoir of CCHF virus. CCHF is an endemic disease in different provinces of Iran.

**Material and Methods:** We tried to catch ticks persisting livestock (Camel, Sheep, Cow and Goat) in Damqan district in spring 2013.

**Results:** We discovered presence of Rhipicephalus and Hyalomma genera of ticks in studied district with 5 species. The most frequent tick was *Rh. sanguineus*. We also found *Hy. marginatum*, *Hy. dromedarii*, *Hy. anatolicum* and *Hy. schulzei*. Reverse Transcription-polymerase Chain Reaction (RT-PCR) showed CCHFV in 17 hard tick samples including all identified species.

**Conclusion:** This study confirms the circulation of the virus in the afore-mentioned region and so, humans of this region who are in close contact with livestock including health-care workers should

be alerted. Additional information will be presented in near future.

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### 308/ZOP

#### Isolation and characterization of lytic bacteriophages specific for enterohemorrhagic *Escherichia coli* of serotype O104:H4

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**Introduction:** Enterohemorrhagic *Escherichia coli* (EHEC), a highly pathogenic subgroup of intestinal pathogenic *E. coli* (IPEC), can cause hemolytic uremic syndrome (HUS) as severe post-infective complication. In 2011 the so far biggest foodborne European HUS epidemic occurred in Northern Germany. It was caused by an unusual enteroaggregative *E. coli* (EAEC) of serotype O104:H4 that produces Shiga toxin (Stx) 2. Since antibiotic treatment of EHEC infections is not recommended due to an undesirable release of Stx, an interruption of the infection chain via contaminated food is a conceivable approach. In this context, lytic bacteriophages have been shown to eliminate or strongly reduce contaminating EHEC on various foods such as fresh-cut fruits, vegetables, and lettuce.

**Aim:** Objective of this study is the isolation of *E. coli* O104:H4-specific lytic phages out of water samples from different origin as well as the selection and characterization of candidate phages that could be used for the eradication of this highly pathogenic strain from the food chain.

**Methods:** Lytic bacteriophages were isolated from sterile filtered water samples by selective cultural enrichment with a stx-negative derivative of the outbreak strain from 2011 and *E. coli* MG1655 (K-12) as positive control following a protocol of Merabishvili *et al.* (PLoS One, 2012;7(12):e52709). Candidate lytic phages were isolated, purified and characterized by sequencing. Furthermore, their specificity was evaluated with representative *E. coli* reference strains of different serotypes. Future experiments will elucidate if the phages eliminate or reduce contaminating *E. coli* O104:H4 in water and various foods.

**Results:** In this ongoing project we analyzed 95 water samples of different origin so far (waste water, n=2; water from swimming pools/ponds, n=3; well water, n=6; groundwater, n=13; surface water, n=38; drinking water, n=33). Lytic phages were isolated from wastewater and surface water exclusively (2/2 and 13/38 samples, respectively). As expected, the presence of *E. coli* in water samples correlated with the presence of corresponding lytic phages. Preliminary results indicate, that the specificity of phage isolates varies as shown by their ability to infect the aforementioned indicator strains: a single phage isolate was lytic for *E. coli* O104:H4 exclusively, whereas 10 isolates infected only MG1655 and four phage isolates infected both indicator strains.

**Conclusion:** Lytic Bacteriophages that are able to infect *E. coli* O104:H4 can be isolated from water samples that are contaminated with *E. coli*. Current experiments will help to characterize the isolates in more detail on a genomic and phenotypic level.

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