

**Results:** We identified multiple introductions of clade 2.2 from Europe and of clade 2.3.4.4-B from South and North-Central Asia into the African continent, while a single virus spread from South Asia to Africa seems to have been responsible of the 2.3.2.1c incursion. Our results identify West Africa as the most important area of virus introduction into the continent. A joint analysis of host dynamics and continuous spatial diffusion indicates that the incursion of the H5 clades into Africa is driven by wild *Anseriformes* and domestic *Galliformes* hosts, suggesting that both migratory birds and live poultry trade may have played an important role in the spread of the virus into Africa.

**Conclusion:** This study shows that viral sources are not stable over time in the African continent, but can change at each epidemic wave, making it difficult to predict the source for the next incursion. In addition, our results indicate a strategic role of West Africa in the virus spread within the continent, which may be considered as a hotspot for H5 HPAIV surveillance.

<https://doi.org/10.1016/j.ijid.2018.11.041>

08.009

### Changing epidemiology of *Listeria* outbreaks and recalls: a review of ProMED reports from 1996–2018

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**Purpose:** Given emerging data regarding large-scale outbreaks of listeriosis, the purpose of this study is to identify trends in global *Listeria* epidemiology using ProMED reports. ProMED is an informal, global outbreak reporting system, that, in the context of *Listeria* outbreaks, reports atypical findings such as larger than average case counts, events from unusual sources, and multinational outbreaks.

**Methods & Materials:** Keywords “*listeria*,” and “*listeriosis*,” were utilized in the ProMED search engine from 1996–2018. Issue date, countries involved, source, suspected and confirmed case counts, and fatalities were extracted. Data unique to each outbreak including commentary by content experts were evaluated. Three independent investigators manually reviewed the database. When multiple reports regarding the same outbreak were obtained, the last report pertaining to that outbreak was utilized. Number of events and countries involved over time were normalized to the total number of *Listeria* ProMED events each year and compared using a two sided t-test;  $p < 0.05$  was considered statistically significant.

**Results:** From 1996 to 2018, 91 outbreak events and 29 recalls from 27 countries were identified. The implicated food source was identified in 105 events. 27/105 events (26%) were associated with atypical food sources and 2 events were associated with pet foods. Events associated with unusual food sources increased over the study period with 7 events reported from 1997–2007 to 20 events reported from 2008–2018 ( $p < 0.05$ ). Event size did not differ significantly over the two time periods. 17/120 reports described international events with more than one country involved in the outbreak or recall, most of which (14/17; 82%) occurred from 2008–2018 ( $p < 0.05$ ). 34 events (28%) resulted in large-scale recalls of food items. 8 outbreaks (6.6%) were hospital-acquired.

**Conclusion:** This study demonstrates that the epidemiology of *Listeria* infections has been changing over time. More events are now associated with atypical food sources. Informing high-risk

individuals such as pregnant women and immunocompromised individuals of safe food handling practices is warranted. To ensure timely recall of contaminated sources, open data sharing and communication across borders is critical. Changes in food production and distribution and improved diagnostics may contribute to the observed changes.

<https://doi.org/10.1016/j.ijid.2018.11.042>

08.010

### Hantavirus *Puumala* genetic variation in the patients with HFRS in Tatarstan, Russia

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**Purpose:** Background: *Puumala* hantavirus (PUUV) can cause hemorrhagic fever with renal syndrome (HFRS), an acute infection characterized by hemorrhages and kidney insufficiency. The Volga Federal District, including the Republic of Tatarstan (RT), is the most active zoonotic region where HFRS accounts for 83.3% of all zoonotic registered cases. Although PUUV is identified as the main infectious agent, little is known about the genetic variability of PUUV in the RT.

**Methods & Materials:** Total RNA was extracted from 49 HFRS blood samples diagnosed in RT during 2015 and 2016 outbreak. RNA was used for RT-PCR analysis of the PUUV S-segment RNA. PCR products were sequenced using ABI Prism<sup>®</sup> 3730XL DNA Analyzer (ABI, USA) and analyzed using LaserGene software packet (DNASTAR, USA).

**Results:** Phylogenetic tree analysis revealed high similarity (99.4%) between PUUV S-segment RNA isolated during 2015–2016 period. Also, PUUV RNA from 11 cases collected during 2015 outbreak clustered together with the Finish lineage with 93.0–100.0% identity. The remaining 14 PUUV RNA S-segment sequences closely resembled that of Russian lineage with 91.0–96.0% identity. Interestingly, 23 out of total 24 samples collected during the 2016 outbreak clustered with Finish lineage (93.6–99.4% identity) and only one sample clustered with Russian lineage (92.0–93.6% identity). The proportion of FIN lineage strains found in HFRS patients far exceeds the share of this lineage strains detected in populations of their native host (bank voles) in RT. Therefore, PUUV strains of the FIN lineage might be more virulent for human than the RUS lineage strains.

**Conclusion:** This data suggest the co-circulation of two PUUV lineages FIN and RUS in the patients diagnosed with HFRS in Tatarstan.

The Russian Government Program of Competitive Growth of Kazan Federal University supported this study. Also, Albert Rizvanov was supported by state assignment 20.5175.2017/6.7 of the Ministry of Education and Science of the Russian Federation.

<https://doi.org/10.1016/j.ijid.2018.11.043>

