from 6 to 77 years (Median: 17). Clinical manifestations were abdominal pain (26, 90%), fever (16, 55%), and diarrhea (14, 48%). One (3%) had lymphadenopathy. Interview revealed that a dead water buffalo was butchered and sold amongst the villagers. All 11 serum specimens and five soil samples were negative for *Bacillus anthracis*. After multivariate analysis, eating uncooked meat of dead animal (Adj.OR = 6, 95% CI: 1.7–18.4) was a risk factor.

Conclusion: The epidemic curve indicates a point source outbreak of gastrointestinal Anthrax. We found valid statistical and temporal association of eating by-product of dead water buffalo and gastrointestinal Anthrax. Though, bacterial isolation were both negative for human specimen and environmental sample, all clinical manifestations were consistent with *Bacillus anthracis* rather than other foodborne bacterial pathogens. Hence, we conducted massive information education campaign sick or dead animal by-product should not be sold or eaten and properly handled and disposed.

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Purified Vero cell rabies vaccine (PVRV, Verorab): A review of intradermal use between 1985 and 2019

T. Moulenat [1], V. Bosch Castells [2], G. Houillon [2,*]

[1] *University Claude Bernard, Pharmacy, Lyon, France*
[2] *Sanofi Pasteur, Medical Affairs, Lyon, France*

Background: Worldwide, rabies continues to kill roughly 59,000 individuals per year. Rabies vaccine types and regimens have changed over time, including the recent World Health Organization (WHO) update to include intradermal (ID) administration for rabies post-exposure prophylaxis (PEP). A trend has developed in the rabies field in which both the dose number and dose volume is reduced to accommodate patients and vaccine supply constraints, especially in underserved endemic regions.

Methods & Materials: In light of this critical health issue and an evolving environment of vaccination, we sought to perform a full literature review of PEP and pre-exposure prophylaxis (PrEP) PVRV vaccination via ID administration. The ID route endorsed by WHO was already included in Verorab product insert since 1996 in several Asian countries, whereas the intramuscular (IM) route was first registered worldwide over 30 years ago. The review searched 7 databases (including the terms: rabies vaccine, PrEP, PEP, and ID) and was enriched with non-published data, thus covering a variety of schedules including company-sponsored or externally-conducted studies.

Results: A total of 34 studies out of 136 original references were identified, including over 3000 subjects and related to no less than 10 PrEP and 17 PEP regimens, including booster administration. In all studies, seroconversion rate (SCR) was assessed by the proportion (%) of vaccines with RVNA titers $\geq$0.5 IU/mL. SCR was assessed from day (D) 0 to Year (Y) 5, including in general D14, D28 and Y1 and Y1 + D7 and/or D14 data for schedules with booster. For PrEP, 10 studies including around 900 subjects were identified and documented schedules from 1D to 3 visits, through 1 month resulting in SCR higher than 90%. PEP was documented in 24 studies including more than 2150 subjects. D14 SCR ranged from 70% (in HIV CD4 <200 mm^3 patients) to 100%. All schedules including booster(s) at Y1 resulted in 100% SCR 7 and/or 14 days after it.

Conclusion: ID administration of rabies vaccination is efficacious and future studies will help confirm this regarding PVRV PrEP ID delivery through abbreviated, updated WHO schedules.

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Puumala orthohantavirus genome sequence variations in the Republic of Tatarstan, Russia

E. Kabwe [1,*], Y. Davidyuk [2], A. Shamsutdinov [2], S. Morzunov [3], E. Martynova [2], E. Garanina [2], R. Ismagilova [2], A. Belyaev [2], E. Shuralev [2], G. Isaeva [4], S. Khaiboullina [5], A. Rizvanov [2]

[1] *Kazan Federal University, Kazan, Russia*
[2] *Kazan (Volga Region) Federal University, Kazan, Russia*
[3] *University of Nevada, Reno, Nevada, USA*
[4] *Kazan Research Institute of Epidemiology and Microbiology, Kazan, Russia*
[5] *W.P. Institute, Reno, USA*

Background: Hemorrhagic fever with renal syndrome (HFRS) is endemic in Republic of Tatarstan (RT), where *Puumala orthohatavirus* (PUUV) is identified as the main cause of infection. Eight genetic lineages of PUUV were shown to circulate in Eurasia; however, the diversity of PUUV variants in RT remains largely unknown.

Methods & Materials: Total RNA extracted from lung tissues of bank voles captured in multiple location in RT was used for RT-PCR analysis. More than hundred PCR products containing partial S, M and L segments coding regions (566/1057, 1014 and 665 bp, respectively) were sequenced and used to determine genome variations.

Results: Most of PUUV sequences revealed low divergence as compared to previously identified in Udmurtia, Bashkortostan and Samara. All these samples belong to the Russian lineage. Interestingly, in addition to the Russian lineage, three RT PUUV strains were part of the Finnish lineage, suggesting co-circulation of two PUUV lineages in some RT locations.

Phylogenetic analysis revealed that RT PUUV partial S, M and L segments of RUS lineage formed six subclades, corresponding to their geographic locations in RT districts. Subclades I–IV contained strains from Pre-Kama area, subclade V strains are distributed in Trans-Kama area, while strains from subclade VI are found in Pre-Volga area.

Subclades IV and V clustered together on the S and M segment trees, while subclade IV located as a separate group of the L segment. Also, subclade III clustered with subclade II for the S segment, with subclades IV–V for the M segment and with subclades I–II for the L segment. These differences in tree topologies suggest the reassortment or/and recombination origin of some PUUV strains circulating in the RT.

Conclusion: Collected data improves our understanding of PUUV diversity and distribution in different regions of RT, which help better control the epidemiological situation in the region.

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