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Predicting Rodent Population Dynamics as Early Warning for Zoonotic Disease Transmission

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Purpose: Rodent borne diseases, including those indirectly transmitted by vectors, represent an increasing threat for public health. The provisioning of early warning indicators of the changing hazard is of great utility for the improvement of prevention and control strategies.

Climate can affect tree seed production, which represents the major food resources for several rodent species including *Apodemus flavicollis*, a very common forest rodent species and an important reservoir for different zoonotic pathogens (as Hantavirus, TBEV and *Borrelia burgdorferi* s.l). We thus investigate how climatic data alone might be useful to predict rodent population dynamics which in turn affect rodent borne disease risk as seen in previous studies.

Methods & Materials: Rodents were monitored for 20 years (2000-2020) using Capture-Mark-Recapture method. Four grids with 8×8 multiple live traps and intertrap distance of 15 m were located in the Province of Trento, northern Italy. At each session a set of standard parameters were recorded (for example: species, sex, body mass, etc..) and animals were individually tagged with a subcutaneous transponder. Animal abundance was obtained using the Jolly-Seber method and then averaged over study sites and year of sampling. Temperature and precipitation data were obtained from a weather station close to the study area. Linear models were implemented to assess how yearly average mice abundance was associated with previous years weather conditions.

Results: We found that warmer summers two years before sampling are positively related to *A. flavicollis* average population densities in forests dominated by beech belonging to European alpine biomes. On the other hand, precipitation occurring during the autumn before sampling negatively influenced mice abundance. We thus hypothesized that wetter conditions during this season could reduce mice survival.

Conclusion: To the best of our knowledge, this is one of the first attempts at investigating how rodent abundance might be predicted using climatic data obtained from local weather stations in the alpine region. Our results highlight important correlations, which eventually might be used for estimating risk of transmission of rodent borne zoonotic pathogens.

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Natural SARS-CoV-2 infection in two cats in Spain

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Purpose: SARS-CoV-2 is a zoonotic pathogen able to infect humans, pets and other animal species, mustelids and felids being highly susceptible. Experimentally, it has been shown that SARS-CoV-2 replicates efficiently in cats, inducing humoral immunity and causing a variable clinical presentation. Here we report the case of two cats (G1 and G2) naturally infected with SARS-CoV-2 after contact with their COVID-19 positive owner diagnosed in September 2020.

Methods & Materials: Oral swabs soaked in PBS were collected daily from 1 to 16 days after the owner tested positive for SARS-CoV-2. Urine and feces were taken several times during this period. Samples were analyzed by in-house real-time RT-PCR (based on CDC 2019-nCoV_N1). Serum samples, collected at day 30, were tested by IDVet multi-species ELISA. Vero E6 cells was used for virus isolation. Partial spike gene was sequenced by Sanger and compared with the owner sequence and the reference Wuhan 2019 (NC_045512.2).

Results: G1 showed apathy, anorexia, lack of grooming and mild respiratory symptoms (tearing and sneezing) for 5 days and then recovered gradually. G2 remained clinically asymptomatic. Viral RNA peak in oral swabs was detected in both cats at day 2 showing similar Ct value (25). SARS-CoV-2 was consistently shedding in G1 for 9 days, after sporadically detected until day 16. Viral shedding in G2 decreased quickly during the first 6 days. Faeces were positive to SARS-CoV-2 until 9 (G1) or 12 (G2) days post-viral detection. Viral RNA in urine was sporadically detected in G2 with high Ct values. Specific antibodies were detected in both cats one month after infection. Virus isolation was not successful. Cats and owner sequences of the spike protein were homologous with two mutations (A222V and D614G) that classify the virus within the 20A.EU1 clade.

Conclusion: SARS-CoV-2 natural infection of two cats occurred after close contact with their infected owner. Both cats developed humoral immune response but they showed different clinical presentation and viral shedding pattern. Oral swabs and feces are proper samples for SARS-CoV-2 detection in cats. Variant 20A.EU1 detected in this study emerged in early summer 2020, presumably in Spain, and subsequently spread throughout Europe.

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Molecular Analysis of Puumala orthohantavirus Strains in Hemorrhagic Fever with Renal Syndrome Patients in Tatarstan

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Purpose: *Puumala* hantavirus (PUUV) is the main causative agent of hemorrhagic fever with renal syndrome (HRFS) in the Republic of Tatarstan (RT). The natural host of PUUV is the bank vole (*Myodes glareolus*), where virus establishes life-long infection. The goal of this work was to identify the PUUV strains in HFRS patients from Kazan and search for related strains circulating in the bank vole populations in RT.

Methods & Materials: Total RNA was extracted from HFRS blood samples. The overlapping PCR-products were obtained by RT-PCR using S segment specific primers and automated sequencing.

Results: The PUUV RNA was detected in three HFRS samples. Analysis of a complete PUUV S segment coding region (1302 bp) revealed high genetic identity (99.7%) between GL436 and GL437 HFRS strains. Sequence identity between these two strains and GL427 strain was within 92.2-92.3% range. Strains GL436 and