aculopapular elements still present on left lower leg, day 10 after admission.

Multiple eschars including primary eschar (top right) on right leg 10 days after admission.

Conclusion: Purpuric rash is previously described in rickettsia conorii infection in two immunodeficient patients. To our knowledge we are the first to present an ATBF case with multiple eschars on three limbs presenting more than 12 days after leaving the endemic area. The eschars seemed to develop metastatic rather than from multiple tick bites. Awareness of late developing eschars in immunosuppressed patients may be important in order to alert physicians to initiate early treatment on clinical suspicion of rickettsial infection in patients with relevant exposure.

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Q fever: The importance of surveillance in the Autonomous Province of Bolzano (Italy)

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Background: Q fever caused by Coxiella burnetii is mainly an occupational disease in agriculture, cattle, sheep, and goats, being the primary reservoirs. Usually animal hosts are asymptomatic. The zoonosis is transmitted primarily through inhalation of aerosols or contact with specific tissues and fluids of shedding animals; rarely by tick bites, ingestion of unpasteurized milk or dairy products, and from person-to-person. Only half of the infections develop in acute Q fever with self-limited, influenza-like febrile symptoms, at times complicated by pneumonia and hepatitis. Chronic Q fever patients mainly show endocarditis with negative culture findings and seropositivity. Animal cases, routinely seen in the Autonomous Province of Bolzano (ABP), supported the hypothesis of local disease transmission to people. However, no national data concerning human cases were available, as Q fever only recently requires compulsory, official notification in Italy.

Methods & Materials: Between 2008 and 2012 active veterinary surveillance was implemented. This consisted in the use of various diagnostic methods to analyse bovine, ovicaprine samples (CBR, ELISA, PCR). For the same period, retrospective case finding, at health district level, was carried out. Criteria for including cases: compatible clinical symptoms and laboratory confirmation by immunofluorescent assay (IFA).

Results: In ABP, for the 5-year period considered, Q fever’s annual diagnostic rate in humans was 1/100.000 inhabitants. A total of 5 cases were identified, 4 of them autochthonous. Four patients with complications had been hospitalised and three of the autochthonous cases were exposed to livestock.

9700 blood samples in total, gave an overall prevalence of 13.6% for cattle; 11.7% for sheep and 7.9% for goats. For confirmation, PCR was carried out on organ tissues and swabs. Overall, PCR-Test on milk from shedding animals contributed to the timely prevention of zoonosis transmission.

Conclusion: At present, in Italy, Q fever is not considered a major health problem; however, this disease may have an unexpected impact at local level, especially in areas with intense animal production and countryside tourism activities. More research is needed to understand the epidemiology of Q fever in ABP. The interdisciplinary approach is essential and will be pursued in future in order to fill the knowledge gaps.

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Surveillance for arboviruses in ticks sampled from wildlife in Ijara District, Kenya

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Background: Tick-borne viruses cause significant morbidity, economic loss and mortality to both human and animals in the world. Tick vectors have been implicated as important routes for virus transmission and dissemination where one host may act as a reservoir of infection, pass this infection via the tick to a more vulnerable host which then suffers disease and reduced survival. This study aimed at determining the prevalence of arboviruses among ticks sampled from wildlife in Ijara district, Kenya.

Methods & Materials: A total of 504 ticks were sampled from wildlife: warthogs (Phacochoerus delamerei), lesser Kudu (Ammelaphus imberbis), common zebra (Equus quagga) and giraffe (Giraffa camelopardalis). The sampled ticks were processed in 151 pools of up to 8 ticks per pool and classified to species using morphological keys. Virus screening was performed by a combination of virus isolation, RT-PCR and amplicon sequencing.

Results: The tick species sampled included: Rhipicephalus pulchellus, Hyalomma truncatum, Amblyomma gemma, Amblyomma lapedum, Amblyomma hebraeum and Boophilus annulatus. Bunyamwera- (2), NDumu- (1), Semiliki forest- (2), Thogoto- (1), and West Nile (WNV)- (2) virus strains were identified.

Conclusion: The highest prevalence of virus-positive ticks was recorded in warthogs. Viruses were only isolated from giraffe (Bun-
Understanding human–bat interactions to enhance Australian bat lyssavirus risk communication

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Background: Australian Bat Lyssavirus Virus (ABLV) is known to infect megabats (i.e. flying foxes) and to a lesser extent microbats (i.e. insectivorous bats) in Australia. The virus can be transmitted to humans from the saliva of the infected bat, usually via a bite or scratch. Human disease with the virus is almost always fatal, unless prior vaccination and/or post-exposure treatment (PET) are given. Despite ongoing public health messages across Australia about the risks associated with bat contact, evidence demonstrates that from 2007 to 2011 the rate of people receiving PET for bat contact increased fourfold in Hunter New England (HNE) a regional area of Australia. The study aims to better understand human–bat interactions and why people come in contact with bats, so that more targeted risk communication strategies can be developed.

Methods & Materials: The Notifiable Conditions and Incident Management System (NCIMS) in NSW was used to identify all people in the HNE region who received PET for bat exposure during the period 2011–2013 (n=25). A 20min semi-structured phone interview then explored with participants the experience of contact with the bat and reasons why the contact occurred. In addition, the appropriateness of current public health messaging regarding bats and ABLV was explored. Interviews were digitally recorded and transcribed for coding and thematic analysis by two independent investigators.

Results: The results of the study will increase our understanding of the reasons why people come into contact with bats in a regional area of Australia. Preliminary analysis reveals a dissociation between exposure (i.e. scratches in particular) and risk of ABLV infection, low levels of awareness and understanding about the risk from bats and ABLV, confusion with Hendra virus, fear of what exposure might mean and for animal welfare and a ‘humane’ need for people to “rescue” bats in need of help.

Conclusion: The final results will be used by the regional health service, as well as other government (e.g. Department for Primary Industries) and non-government stakeholders (e.g. Australian Wildlife Health Network) to help develop new public health risk communication and educational materials regarding ABLV.

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Genetic diversity of velogenic Newcastle disease virus isolates from Ukraine

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Background: Three velogenic Newcastle disease viruses (NDV) isolates obtained from pigeons and chicken in Ukraine were characterized by analyses of full F and HN genes. The sequence analysis demonstrated the same deduced amino acid sequence, 112R/K-R-Q-K-R-F117 cleavage site, which is typical for velogenic strain of NDV and they were closely related to the strains, which were isolated in Russia and China. As known, Ukraine has unique geographical location in the center of Europe and through its great territory passes transcontinental migration routes of wild birds.

Methods & Materials: The NDV isolates NDV/Chicken/Ivano-Frankivsk/58/2007: Pigeon/Dnipropestrovsk/1-18-11 and Pigeon/Ukromne/3-26-11, were propagated in specific pathogen free (SPF) embryonated chicken eggs. Total RNA was extracted from allantoic fluids using RNA extraction kit “Ribosorb” (Russia) following the manufacturer’s instructions. The full F and HN genes nucleotide sequences were determined by using a RT-PCR/sequencing approach (Diel et al., 2011). The phylogenetic analysis was performed with the software MEGA5 (Tamura et al., 2011) and the evolutionary history was inferred by using the Maximum likelihood methods (Tamura and Kumar 2002), with standard errors being calculated based on 500 bootstrap replicates. Genotypes and sub-genotypes were assigned based on the phylogenetic topology and on the evolutionary distances between different taxonomic groups. (Diel et al., 2012).

Results: Phylogenetic analysis indicated that isolate NDV/Chicken/Ivano-Frankivsk/58/2007 showed similarities to the subtype VIIId. Genotype VII is the genotype most frequently associated with outbreaks of ND in the Middle East and Asia (Miller et al., 2010).

Two strains Pigeon/Ukromne/3-26-11 and Pigeon/Dnipropestrovsk/1-18-11, which were isolated from pigeons, were placed in genotype VI. They have demonstrated 98% homology in nucleotide according to new published in GenBank sequences from Russian isolates. Genotype VI contains only virulent viruses and are the predominant genotypes circulating worldwide (Miller et al., 2009). All of the sequences from the fusion protein cleavage site have 112R/K-R-Q-K-R-F117 motifs, which is typical for highly virulent NDV (Alexander, 1997).

Conclusion: This study has shown that velogenic NDV of VII, VI genotypes circulate in Ukraine. To estimate the risk for interspecies transmission and to provide control strategies it needs to continue the monitoring over possible circulating of NDV strains in Ukraine.

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