Patients were febrile several days before admission, had dull and some of them severe abdominal pain, decreased urine output, diarrhoea (53%) visual troubles (48%) and arthromyaligiae. Bleeding was moderately expressed and rarely abundant (cavity organ hemorrhages in 30%). Jaundice was mild and not frequent.

Blood tests showed metabolic acidosis, increased serum creatinine (784 ± 72 mmol/l), blood urea nitrogen (37 ± 5 mmol/l), potassium (5.9 ± 0.5 mmol/l), ALT (67 ± 8.1 U/l), AST (89 ± 7.4 U/l) and decreased PLT (78 ± 18 × 10^9/l), haemoglobin (7.4 ± 2.2 mmol/l) and fibrinogen (1.98 ± 0.34 mmol/l) levels. Urinalysis showed considerable proteinuria, leukocyuria and degenerated renal epithelial cells with so-called fat corpuscles. Ultrason: enlarged kidneys with acute parenchymal lesions. One of our patients with 8-fold increased antibody titer to Hanta-virus developed hemolytic anemia, decreased haptoglobin levels and exhibited transitional neurological signs, mimicking thrombocytopenic-thrombotic syndrome. In the last years lethal exit is very rare. Only one patient (4.76%), admitted in infectious shock state and abundant bleeding died four hours after admission.

Conclusion: Deep changes in the social-economic standards of last decades affected the spreading of HFRS and respective morbidity and mortality in this case.

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76.013
The complete genome sequence and analysis of the betaproteobacterium *Laribacter hongkongensis*

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**Background:** *Laribacter hongkongensis* is a newly discovered, facultative anaerobic, Gramnegative, motile, sea gull-shaped bacillus of the *Neisseriaceae* family associated with freshwater fish-borne gastroenteritis and traveler’s diarrhea.

**Methods:** The genome sequence of *L. hongkongensis* HLHK9 was determined with the whole-genome shotgun method. Shotgun sequences were assembled with Phrap. Gene prediction was performed by Glimmer version 3.02, and results post-processed using TICO for improving predictions of translation initiation sites.

**Results:** *L. hongkongensis* HLHK9 recovered from an immunocompetent patient with severe gastroenteritis, possesses a single chromosome of 3,169-kb chromosome with G+C content of 62.35%. Genome analysis reveals different mechanisms potentially important for its adaptation to diverse habitats of human and freshwater fish intestines and freshwater environments. The gene contents support its phenotypic properties and suggest that amino acids and fatty acids can be used as carbon sources. We identified extensive variety of transporters, including multidrug efflux and heavy metal transporters as well as genes involved in chemotaxis, which may make *L. hongkongensis* possible to survive in different environmental niches. A pool of genes encoding urease, bile salts efflux pump, adhesin, catalase, superoxide dismutase, and other putative virulence factors such as hemolysins, RTX toxins, patatin-like proteins, phospholipase A1, and collagenases are present. Proteomes of *L. hongkongensis* HLHK9 cultured at 37 degrees C (human body temperature) and 20 degrees C (freshwater habitat temperature) showed differential gene expression, including two homologous copies of *argB*, *argB*-20, and *argB*-37, which encode two isoenzymes of N-acetyl-L-glutamate kinase (NAGK)-NAGK-20 and NAGK-37-in the arginine biosynthesis pathway. NAGK-20 showed higher expression at 20 degrees C, whereas NAGK-37 showed higher expression at 37 degrees C. NAGK-20 also had a lower optimal temperature for enzymatic activities and was inhibited by arginine probably as negative feedback control. Similar duplicated copies of *argB* are also observed in bacteria from hot springs such as *Thermus thermophilus*, *Deinococcus geothermalis*, *Deinococcus radiodurans*, and *Roseiflexus castenholzii*, suggesting that similar mechanisms for temperature adaptation may be employed by other bacteria.

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76.014
The 2008 dengue epidemic on Curacao: Correlation with climatological factors

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**Background:** Dengue fever is a common disease on Curacao, a small Caribbean island close to Venezuela, with tens to hundreds of proven cases during the rain period each year. However, 2008 showed an unexpected and dramatic rise in incidence of dengue fever with almost 1200 serologically proven cases. We studied the correlation between climatological factors and the incidence of dengue fever.

**Methods:** The statistical correlation between the incidence of serologically proven cases of dengue fever and
several climatological factors, such as rainfall, mean-, maximum- and minimum temperature, wind velocity, sun hours, cloud coverage, evaporation rate and air pressure in the past ten years was investigated by using the non-parametric Spearman’s correlation test.

**Results:** Lower average temperature, lower absolute maximum temperature, lower absolute minimum temperature and lower average maximum temperature all showed a strong correlation with the incidence of dengue fever \((r = -0.228, p = 0.01; r = -0.225, p = 0.01; r = -0.235, p = 0.01\) and \(r = -0.268, p = 0.003\) respectively). A less strong, but significant correlation with rain (positive correlation) and evaporation rate (negative correlation) could be observed \((r = 0.192, p = 0.04\) and \(r = -0.192, p = 0.04\) respectively).

**Conclusion:** In 2008, an unexpected and dramatic peak in incidence of dengue fever in Curacao was observed. In the same year, average- as well as absolute minimum and maximum temperature were significantly lower than in the previous years and were strongly correlated with dengue incidence. As expected from earlier studies, rainfall and evaporation rate were also significantly correlated to dengue incidence.

However, temperature changes showed a stronger correlation with the incidence of dengue fever than rainfall and evaporation rate, suggesting that lower temperatures are an important factor in the development of higher dengue incidence in Curacao and not merely an epiphenomenon, concurring with the rain period. This is in contrast with results from earlier studies conducted in Mexico and Trinidad.

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**76.015**

Cross-reactive neutralizing antibody response to enterovirus 71 infection in Taiwanese young children

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**Background:** Enterovirus 71 (EV71) is causing life-threatening hand-foot-mouth disease (HFMD) involving neurological and cardiopulmonary complications in Asian children. Phylogenetically, EV71 viruses can be classified into 3 genogroups (A, B and C) and 11 genotypes (A, B1—B5 and C1—C5). In Taiwan, nationwide EV71 epidemics with different predominant genotypes occurred in 1998 (C2), 2000—2001 (B4), 2004—2005 (C4) and 2008 (B5) but the mechanism is not clear. In early 2007, genotype C5 viruses were isolated sporadically and EV71 epidemic did not begin until genotype B5 viruses were detected in late 2007. This study was conducted to measure cross-reactive neutralizing antibody response to EV71 Infection in Taiwanese young children to explore the mechanism of the genotype replacement in Taiwan, which is critical to the selection of vaccine strains.

**Methods:** We prospectively conducted cohort study to follow up healthy neonates starting from June 2006 and sera were collected from participating children for measuring EV71 neutralizing antibody titers at birth and at 6, 12, 24, and 36 months of age. Throat swabs were collected from participating children developing herpangina or HFMD for virus isolation. Isolated EV71 viruses were genotyped using VP1 gene sequences.

**Results:** In 2008—09, 24 children developed EV71 neutralizing antibody seroconversion, including 11 symptomatic and 13 asymptomatic infections. Five EV71 viruses were isolated from the symptomatic cases and all belongs to genotype B5. These B5 viruses are phylogenetically related to B5 viruses circulating in the South-Eastern Asia recently. Thirty-one post-infection sera collected from the 24 seroconverted children were measured neutralizing antibody titers against genotype A, B4, B5, C2, and C4 viruses. Geometric mean (95% confidence intervals) of neutralizing antibody titers against these viruses were 52 (38—72), 150 (109—205), 234 (176—311), 114 (82—158), and 105 (76—144), respectively. Serological tests show that children infected with B5 viruses have lower neutralizing antibody titers against A, C2 and C4 viruses than B5 virus \((p < 0.05\), t-test).

**Conclusion:** Antigenic differences could be detected between enterovirus 71 viruses in different genogroups but not in the same genogroup using children post-infection sera. Significant antigenic differences between B5 and C4 viruses may explain the genogroup replacement occurring in the 2008 epidemic.

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**76.016**

‘One World One Health’ in practice: Integrating public health and veterinary curricula on emerging infectious diseases in Africa

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**Background:** Research indicates that up to 65% of emerging infectious diseases are zoonotic. This has contributed to the ‘One World One HealthTM’ paradigm which highlights interactions between humans, domestic and wild animals in a shrinking environment. Though the OWOH theme has gained support within the scientific community, formal training integrating medical, veterinary and public health practices addressing emerging zoonotic disease is rare.

The USAID-funded Stamping Out Pandemic and Avian Influenza (STOP AI) global project is designed to prepare those responsible for the planning, surveillance, response to and prevention of highly pathogenic avian influenza (HPAI). Since inception, STOP AI has drawn upon veterinary and human medicine disciplines, public health, and the social sciences to design its training programs. Through practical field experience, STOP AI determined that effective training required the integration of veterinary, medical and public health aspects.

**Methods:** STOP AI training modules on HPAI epidemiology, risk assessment, surveillance, outbreak response, bio-safety and bio-security were subsequently integrated by teams of