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 arthromyalgiae. 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. Urinanalysis showed considerable proteinuria, leukocy turia and degenerated renal epithelial cells with so-called fat corpuscles. Ultrasound: 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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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, adhesins, 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.

Conclusion: The genome sequence and analysis of L. hongkongensis revealed novel mechanisms for adaptations to survival at different temperatures and habitats.

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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