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Editorial

Infectious diseases: A never-ending threat

Infectious diseases are a constant threat caused by pathogens or alien forms that enter the body and multiply. Due to the (re-) emergence as well as the persistence of old and new infectious diseases, they remain the leading causes of death worldwide, despite remarkable advances in basic research and clinical treatment during the 20th century. We at *BioMedicine* have therefore chosen "infectious diseases" as the focus of this issue.

Bacteria such as *Staphylococcus aureus*, *Vibrio vulnificus*, and *Helicobacter pylori* cause diseases by disrupting vital processes in hosts. Methicillin-resistant *S. aureus* (MRSA) is one major multidrug-resistant pathogen in hospitals. Following the emergence of community-acquired MRSA, traditional MRSA was designated hospital-acquired MRSA. Comparing the genetic nature and virulence of community-acquired- and hospital-acquired MRSA, Yamamoto's laboratory indicates that the MRSA epidemic, including invasive diseases, in the community is dynamic. The marine Gram-negative bacterium *V. vulnificus* invades and damages tissue in hosts. Its two cytotoxins, $MARTX_{Vv}$ and VvhA, have been identified and characterized. While $MARTX_{Vv}$ is required for the survival of *V. vulnificus*, VvhA plays a minor role in its pathogenesis. Persistent infection by *Helicobacter pylori*, a spiral Gram-negative microaerophilic bacterium, correlates with clinical outcomes: gastritis, peptic ulcer, and gastric adenocarcinoma. Utilization of lipid rafts promotes its inhabitation. Dissecting mechanisms underlying the orchestration between membrane cholesterol and *H. pylori* might yield novel approaches to controlling *H. pylori*-mediated diseases.

Mounting evidence reveals that cellular and viral long noncoding RNAs (lncRNAs) are linked with viral infection. The interactions and functions of several cellular lncRNAs (XIST, HOTAIR, NEAT1, BIC and virus-encoded lncRNAs) are surveyed, summarized, and discussed. Severe acute respiratory syndrome (SARS) is caused by coronavirus (CoV). Depending on the strain, manifestations of human CoV (HCoV) infection can either be self-limiting in healthy adults or severe in hosts with poor immunity. Recently, a novel HCoV strain has been designated as SARS-CoV, and another novel human betacoronavirus, 2C EMC2012, has been reported. Phylogenetic analysis between SARS-CoV and EMC2012 has revealed similarities and differences that might provide insights in the development of therapeutic agents for HCoV infection cases.

Candida albicans is a prevalent fungal opportunistic pathogen in humans. Its penetration and traversal of the epithelial barrier to gain entry into the bloodstream can cause systemic and invasive infections. Tsai et al summarize the knowledge that has been gained from the use of experimental tools developed in the post-genomic era to understand *C. albicans* pathogenesis and its interactions with the host.

The availability of pathogens' genomic sequences and the development of genome-wide technology portends a thorough understanding of the pathogen–host relationship during infection. This no doubt will provide novel strategies to prevent, control, and treat infectious diseases that challenge global health.

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