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Note generali	Description based upon print version of record.
Nota di bibliografia	Includes bibliographical references.
Nota di contenuto	Workshop overview -- Contributed manuscripts -- The microbial forensics pathway for use of massively parallel sequencing technologies -- Microbial virulence as an emergent property: consequences and opportunities -- Microbial genome sequencing to understand pathogen transmission -- Presence of oseltamivir-resistant pandemic A/H1N1 minor variants before drug therapy with subsequent selection and transmission -- Design considerations for home and hospital microbiome studies -- Sequencing errors, diversity estimates, and the rare biosphere -- Phylogeography and molecular epidemiology of <i>Yersinia pestis</i> in Madagascar -- Big data in biology: pitfalls when using shotgun metagenomics to define hypotheses about microbial communities -- High-throughput bacterial genome sequencing: embarrassment of choice, a world of opportunity -- Evidence for several waves of global transmission in the seventh cholera pandemic -- Multi-partner interactions in corals in the face of climate -- Change genomic transition to pathogenicity in chytrid fungi -- Natural and experimental infection of <i>Caenorhabditis</i> nematodes by novel viruses related to nodaviruses -- Genomic approaches to studying the human

microbiota -- Sequence analysis of the human virome in febrile and afebrile children.

Sommario/riassunto

"On June 12 and 13, 2012, the Institute of Medicine's (IOM's) Forum on Microbial Threats convened a public workshop in Washington, DC, to discuss the scientific tools and approaches being used for detecting and characterizing microbial species, and the roles of microbial genomics and metagenomics to better understand the culturable and unculturable microbial world around us. Through invited presentations and discussions, participants examined the use of microbial genomics to explore the diversity, evolution, and adaptation of microorganisms in a wide variety of environments; the molecular mechanisms of disease emergence and epidemiology; and the ways that genomic technologies are being applied to disease outbreak trace back and microbial surveillance. Points that were emphasized by many participants included the need to develop robust standardized sampling protocols, the importance of having the appropriate metadata, data analysis and data management challenges, and information sharing in real time. The Science and Applications of Microbial Genomics summarizes this workshop."--Title homepage.
