A Novel Mode of Transmission for Human Enterovirus Infection Is Swimming in Contaminated Seawater: Implications in Public Health and in Epidemiological Surveillance

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(See the article by Begier et al. on pages 616–23)

Enteroviruses (EVs; Picornaviridae) are among the most common viruses infecting humans worldwide [1]. These positive-RNA viruses possess a high genetic diversity (89 serotypes), and they can evolve through genetic mutations or recombination events that are associated with the potential emergence of new epidemic serotypes [2, 3]. Although the majority of human EV infections remain asymptomatic, these viruses are associated with a large diversity of clinical syndromes, ranging from minor febrile illness to severe and potentially fatal pathologies, including aseptic meningitis, encephalitis, myopericarditis, acute flaccid paralysis, and severe neonatal sepsis-like disease [1, 4]. The primary mode of direct or indirect transmission of EV remains the fecal-oral route [4]. However, other efficient modes of transmission, such as respiratory or eye mucosal routes, have been reported [5, 6].

Patterns such as direct person-to-person contact seem to be important in many outbreaks of EV infection. However, because human EVs are enteric viruses, water-related transmission remains of primary importance for indirect viral transmission and represents a potentially significant human health risk [7, 8]. Consequently, the information regarding the detection of EV in water, such as epidemiological data related to waterborne diseases, is crucial to modern public health surveillance systems [8].

In this issue of Clinical Infectious Diseases, Begier et al. [9] present an epidemiological and virological analysis of an outbreak of concurrent echovirus 30 (E30) and coxsackievirus A1 (CVA1) infections associated with sea swimming among a group of travelers to Mexico in 2004. This study reports, for the first time to our knowledge, an important public health problem: swimming in contaminated seawater as a novel mode of transmission of EVs. Previous studies reported potential transmission of EVs through clams or oysters, drinking water, and recreational hot spring waters but never through contaminated seawater [10–13]. In the study by Begier et al. [9], the authors identified cases of concurrent E30 and CVA1 infections associated with swimming in seawater. They used partial viral capsid protein 1 (VP1) gene analysis to perform direct genotyping identification, which revealed the presence of E30 in CSF samples and the presence of E30 and CVA1 in stool samples [14]. For the 29 symptomatic travelers, the clinical and epidemiological parameters related to this epidemic event were recovered and analyzed; some clinical syndromes were statistically significantly associated with EV contamination through swimming in seawater. The originality of this article also resides in the description of the first potential outbreak of CVA1 infection reported among immunocompetent patients since the only published outbreak of CVA1 gastroenteritis among immunocompromised children (bone marrow transplant recipients) was previously reported [15, 16].

Because EVs are easily dispersed, display serotypic and genetic diversity, and can tolerate extreme conditions (naked viruses), they are ubiquitous and can easily contaminate water [4, 17]. The presence of these waterborne enteric pathogens in recreational water presents a potentially significant human health risk [12]. Although major outbreaks of waterborne disease are comparatively rare, there is
substantial evidence that human EVs are frequently present in recreational waters and are responsible for a low incidence of waterborne microbial disease [8, 10]. Usually, these diseases are associated with low morbidity rates among healthy adults [8]. However, it is possible that new recombinant EV strains may escape the immune system or demonstrate high fitness or infectivity levels and, therefore, may cause severe clinical syndromes, even in immunocompetent persons, as observed in the study by Begier et al. [9]. Moreover, EVs can cause severe illness and even death in young children, the elderly, or persons with compromised immune systems [1, 4].

As the epidemiology of waterborne diseases is changing, there is growing global public health concern about new and reemerging infectious diseases, which are occurring through a complex interaction of social, economic, evolutionary, and ecological factors [17, 18].

A relatively small number of viruses have been proven to be true etiologic agents in outbreaks of waterborne disease in humans; these viruses include rotavirus, calicivirus, astrovirus, and some enteric adenoviruses [19]. Etiologic agents in outbreaks of waterborne disease have frequently been identified because of inadequate diagnostic technology, but many outbreaks of infection of unknown etiology that have been recently reported were likely attributable to viral agents [19].

In the study by Begier et al. [9], the integration of new molecular techniques for identification of EVs provides an important complement to the field investigation, as shown by the identification of CVA1, an EV rarely identified in outbreaks of EV disease [1]. It is evident that new molecular tools are useful and of major interest to detect and to quantify the levels of EV genomes in recreational water [10]. Genetic identification of the EV serotype by partial sequencing of VP1 and 3Dpol genes can allow identification of recombinant or mosaic EV strains [3]. Moreover, it is necessary to use new, integrated cell culture and molecular systems to determine the infectivity of the EV strains detected in water samples [20]. The combination of these systems is now necessary to detect infectious EV strains, to observe the levels of contamination in recreational water, and to genetically identify and compare serotypes or strains incriminated as causes of cases or outbreaks of waterborne disease.

Prevention of an epidemic of waterborne EV infection could be efficiently performed by prospective virological surveillance to indicate the infectivity of the strains and the levels of contamination [7, 8]. However, this approach should be associated with a public health surveillance system, such as the US Outbreak Surveillance System, for data collection and reporting of outbreaks of waterborne disease [21–24]. Moreover, sewage has to be treated to achieve efficient inactivation of the viral agents before it is poured in seawater, especially in tourist areas [10]. In the context of an increasing tourist population, it is of major importance to establish specific epidemiological and virological measures aimed at reducing the risk of viral waterborne infectious diseases. Moreover, recent studies identified links between climate variability and the occurrence of microbial agents in water. These relationships need further evaluation in the present context of ecological stresses.

In conclusion, the detection of EVs and other enteric viruses in seawater and the determination of the epidemiology of waterborne diseases are crucial to modern public health and epidemiological survey systems. These measures for the epidemiological and virological control of recreational seawater may become additional stresses.

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References


