

Introduction

In 2016, 5.5 million children aged 17 and under were admitted to hospitals, with an average stay of 4.0 days. Respiratory infection, such as pneumonia, acute bronchiolitis, and asthma, is the most common reason for inpatient pediatric hospitalization. Appendicitis, seizures, infections, and dehydration are all major reasons for pediatric hospital hospitalizations. Although many of these patients can be properly cared for in the community, a balance must be struck between family convenience, safe health care, and resource utilization [1]. It is widely accepted that a minimum case volume is required to maintain competence and is linked to better outcomes; as a result, health care administrators and professionals must assess their ability to care for the unique needs of the pediatrics population, as well as determine whether they have the diagnostic and treatment capabilities, as well as the equipment and staffing, to provide high-quality and safe health care for these patients [1]. Hospitals should assess their resources carefully, and they may decide to be proactive in stabilizing and then transferring pediatric patients to hospitals with larger pediatric inpatient volumes and more resources.

COVID-19 has impacted and continues to touch practically every facet of pediatric and adolescent healthcare. Because of the pandemic, pediatricians must be knowledgeable about a variety of areas, including infection prevention and control, epidemiology, laboratory diagnostics (molecular and otherwise), and vaccines. COVID-19 has also demonstrated the value of pediatrician's advocacy for patients as persons and in the context of public health. It focuses on the components of COVID-19 prevention, diagnosis, outpatient management, and advocacy that are most important to pediatric and adolescent primary care clinicians. This review does not cover inpatient management options or the consequences of pediatric COVID-19 infection, such as MIS-C [2].

Coronaviruses are single-stranded RNA viruses that are enclosed. Six coronavirus species were known to cause infections in humans prior to the identification of SARS-CoV-2 (the virus that causes COVID-19). HCoV-229E, HCoV-NL63, HCoV-OC43, and HCoV-HKU1 are endemic to this region and are known to cause mild to moderate respiratory disease. Bats are believed of being a key ancestral source of the other two species, much as they are for SARS-CoV-2 (SARS-CoV and MERS-CoV) [2, 3].

Since the start of the pandemic, SARS-CoV-2 has been developing. Genetic mutations have resulted in the emergence of variants of the original virus, some of which have improved transmissibility and infectivity. The Pango nomenclature system (which allocates a series of letters, numbers, and dots to signify variant ancestry based on viral genome sequencing features) and the World Health Organization (WHO) technique (which employs letters of the Greek alphabet) are used to classify SARS-CoV-2 variations [4, 5]. The lay public is more likely to use the WHO classification terminology. For example, the Pango system's B.1.1.529 version is most commonly referred to as the Omicron variant by the WHO.

SARS-CoV-2 is spread mostly by contact with an infected person's respiratory secretions, either directly through respiratory droplets

or indirectly through inhalation of infectious aerosols. The virus's longevity on fomites and surfaces is uncertain, however it is considered