Letter to Editor

Adenoviruses are cause of ocular morbidity worldwide in the form of Epidemic Keratoconjunctivitis (EKC). The EKC consequences in patients, such as reduced vision and corneal erosion, can last between weeks and months. Besides, many adenoviruses are characterized by high infectivity and structural stability that enable their easy spread by direct contact with infected patients or with contaminated surfaces, creating high risks of nosocomial outbreaks [1]. Additionally, the EKC infections by emergent novel recombinant adenoviral types point to a growing number of EKC threats [2-5]; therefore, efficient and proper diagnosis of adenoviral infections and the subsequent accurate type identification are challenges for clinicians. The spotting of the early symptoms of EKC, its timely treatment, and its swift containment are challenges to be overcome. Although there is no available commercial remedy against EKC, promising research is being performed to develop clinical treatments [6]. Likewise, bioinformatics analyses comparing genomic variation across adenoviral types aim to better understanding the cellular pathways affected by the adenoviral infections [7]. The characterization of host-pathogen interactions will lead us to the improvement of treatment and prevention practices. In short, despite our growing knowledge about adenoviral EKC, much remains to be clarified to convert this understanding into practical applications to alleviate the health and economic burden of EKC in our society.

References