**Genome Sequencing Reveals Molecular Epidemiological Characteristics and New Recombination of HAdV in Beijing**

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**Objective:** To investigate the molecular epidemiological characteristics and genetic variation of HAdV in acute respiratory tract infection in Beijing.

**Methods:** Whole genome sequencing and phylogenetic analyses were performed for 83 strains of HAdV with different types in Beijing from 2014 to 2019.The clinical characteristics of HAdV infection were analyzed statistically.

**Results:** Our study found that the genome diversity of species C was the highest in Beijing from 2014 to 2019, while the types of species B and species E were relatively single. In species C, 9 recombinant adenovirus strains were identified in type 1, accounting for 64.3% (9/14) of the detected type 1 adenovirus, and 7 recombinant strains were found in type 2 adenovirus, accounting for 53.8% (7/13) of the detected type 2 adenovirus. In type 1, we found three newly emerged recombinant strains (A47, A48 and A52) from 2017 to 2019, whose common parent is MK041227. Further study showed that the three newly emerged recombinant strains all had antigenic changes. The Penton and Hexon gene of A47 and A48 were more similar to most adenoviruses in northern China and Singapore. The three antigen genes of A52 were linked to HAdV found in Yunnan and Hunan. The other six recombinant strains in type 1 (A3, A40, A41, A44, A45, and A46) have nearly identical recombinant structure to the recombinant strain MH183293 found in SARI infants with severe acute respiratory infection in Shanghai, China. In type 2, two recombinant strains A60 and A63 were the closest to the strain MK883607 found in Shanghai in 2012. Five additional recombinant adenovirus strains (A55, A56, A57, A59, and A65) showed the highest similarity to a recombinant strain found in Beijing in 2013. These reported recombinant strains have been circulating in Beijing for a long time. Adenovirus types 3, 4, 7, 14 and 55 in Beijing showed little change in their genomes, but two strains of adenovirus type 4 contained Nuclear Factor I sequences. Analysis of clinical features shows that recombinant strains of type 1 have more disease severity than other HAdV, causing severe pneumonia in both the elderly and children.

**Conclusion:** This is the first study to analyze the genome and infection characteristics of HAdV in Beijing using large-scale genome-wide data and clinical features of HAdV. Phylogenetic analysis of these sequences revealed the diversity of HAdV epidemics in Beijing. New recombinations and previously discovered recombinations were also found in our study, indicating the continuous emergence of recombinant strains in Beijing. Analysis of clinical features shows recombinations tend to cause severe respiratory symptoms. Continuous population-wide molecular epidemiological surveillance of HAdV is essential for the prevention and control of respiratory infectious diseases.