One of the most frequent causes of infections in humans is Human Rhinovirus (HRV), a member of the viral family Picornaviridae. More than 100 different HRV serotypes are known to circulate in humans, and this diversity is thought to be a cause of the high frequency of infection. Two species, HRV-A and HRV-B, have been described, but otherwise the genetic diversity and variability of HRV are only partially known. Another unknown is the exact relationship of HRV to the closely related genus Enterovirus (HEV), although it has already been suggested that HRV-B is in fact closer to HEV than to HRV-A. These two picornavirus genera have the same genomic structure but their phenotypes are distinct (e.g. in cell tropism, acid lability, and optimal temperature), and phenotypically HRV-A is closer to HRV-B.

The complete genomes of 12 new prototype serotypes have been sequenced and compared to available sequences. Maximum-likelihood phylogenetic analysis confirms that HRV-B is globally more closely related to HEV than to HRV-A. This is also supported by the conservation of a 2C cis-acting replication element (cre) in HRV-B and HEV, but not in HRV-A. The capsid and 3B-C genes, however, exhibit closer relatedness between HRV-B and HRV-A. This observation may explain similar HRV phenotypes. In contrast to HEV viruses, HRV-A and HRV-B share also markedly lower GC content along the whole genome length. This might reflect their different biological properties.