

Objective:

The human parvovirus B19 (B19) is a non-enveloped, single-stranded DNA virus and belongs to the genus *Erythrovirus*, within the *Parvoviridae* family. B19 usually causes a subclinical infection in immunocompetent individuals. Whereas immunocompromised individuals who fail to produce neutralizing antibodies and do not eradicate virus, may develop a state of chronic anemia, arthropathies, hepatitis and a variety of other diseases. Previous studies reported persistent B19 infection with anemia in immunocompromised individuals like human immunodeficiency virus (HIV) infected patients. Anemia related B19 virus is very important in HIV infected subjects, because it is a treatable cause of anemia in this population.

Three distinct genotypes of B19 have been determined; genotype 1, with subtypes 1a and 1b, genotype 2 and genotype 3, with subtypes 3a and 3b.

Few studies have been carried out on distribution and genotype of B19 in Iran. Therefore, we aimed to determine the molecular epidemiology of B19 among Iranian patients infected with HIV and explore their molecular characterization.

Methods:

We conducted a cross sectional survey on 99 HIV patients and 64 healthy controls. IgG and IgM antibodies against B19 were detected by ELISA and B19 DNA was assessed by nested PCR. PCR products were subjected to direct sequencing and classified after phylogenetic analysis.

Results:

The prevalence of B19 immunoglobulin was 11.1% for IgG and 1% for IgM. B19 DNA was detected in 13.1% of cases. No samples were found to be positive for both antibodies while 3 cases showed B19 IgG and viremia simultaneously. The prevalence of B19 IgG, IgM and DNA in control group was 25%, 1.6% and 9.4% respectively.

B19 viremia and IgG found concurrently in 4.7% of control cases. B19 IgG was significantly lower in HIV group than in normal controls. There was no significant difference regarding anemia between cases and controls.

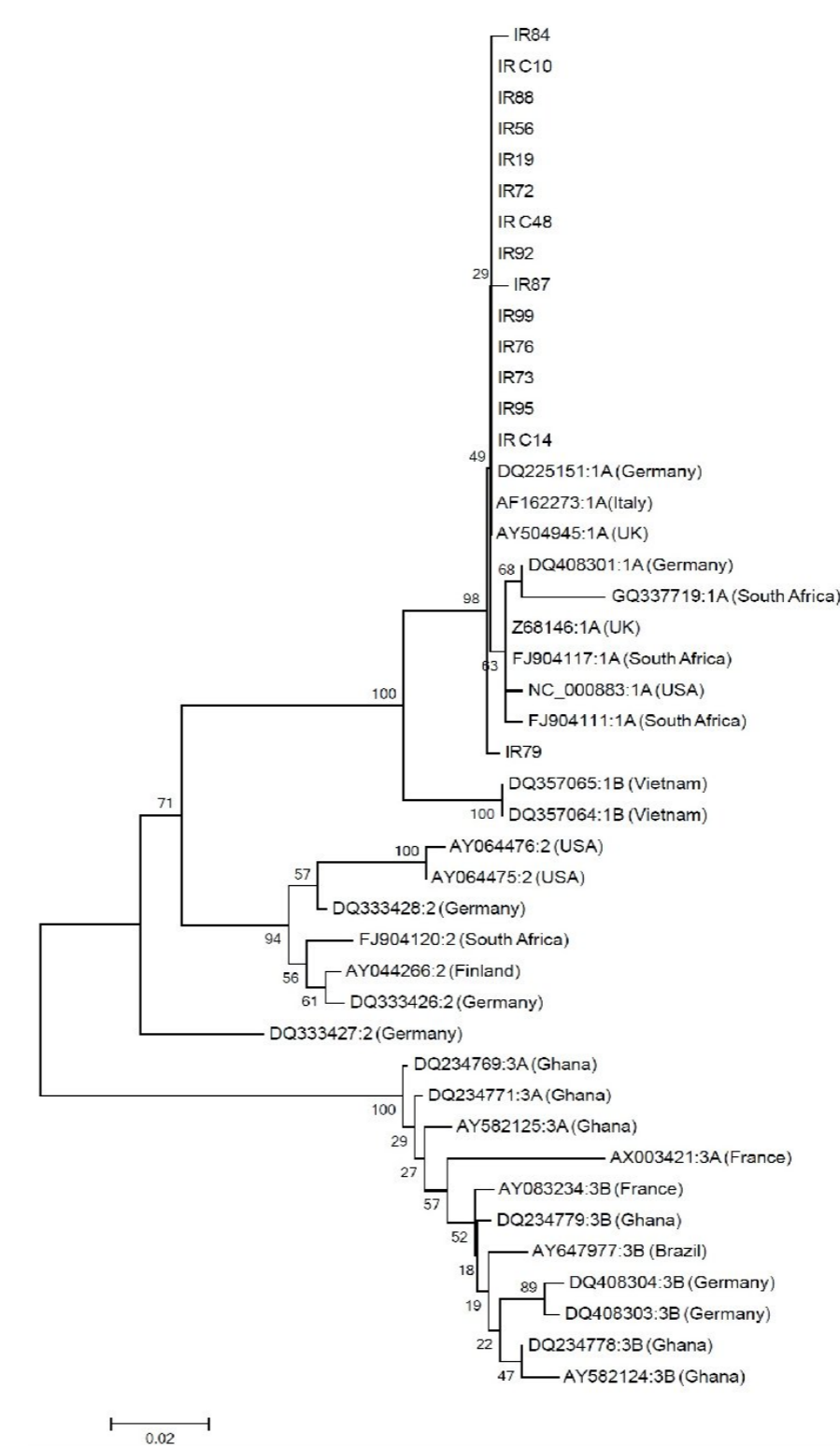
No associations with B19 serology or viremia were found with respect to CD4 count and route of HIV transmission in patients group. But, the prevalence of B19 viremia was significantly higher in naïve patients than cases under HAART treatment (30.4% vs. 8.1%, p<0.012).

All sequenced B19 isolates in case and control groups belonged to genotype 1, and classified as subtype B19-1A.

We also determined the magnitude of nucleotide and amino acid divergence between Iranian strains. By comparison of the nucleotide sequences, the mean variation was 0.0013 (range 0.00-0.006) and in respect to amino acid divergence, mean was 0.004 with range of 0.00 to 0.02. The mean intra-genotypic nucleotide distance within Iranian isolates and other 1A isolates was 0.004 (range 0.000-0.02724).

The mean inter-genotypic nucleotide distance between group 1A and all other groups was 0.095 (range: 0.00-0.2215).

Fig. 1. Phylogenetic tree was constructed by the neighbour-joining method of 15 B19 strains isolated from 12 Iranian HIV patients and 3 healthy controls. Iranian sequences determined in this study are indicated by the IR prefix for HIV patients and as IRC for control cases.



The maximum distance obtained between AX003421 (France) from genotype 3A with IR84 (study strain) and FJ904117 (South Africa) from genotype 1A. The mean inter-genotypic amino acid variation between group 1A and all other groups was 0.229 (range: 0.00-0.525) and within Iranian isolates and other 1A isolates was 0.01312 (range: 0.000-0.07490)

Conclusion:

This is the first study in Iran which investigates the genotype of B19 in normal population and HIV patients. The prevailing B19 genotype 1A in this study groups concurred with reports from most parts of the world and B19-1A is the only detectable genotype in our study cohort from Iran.

In our survey, a low degree of nucleotide and amino acid diversity among B19 strains was observed which is in agreement to other report by some authors which found a low genetic variation among B19 strains (<2%). Additionally, our findings indicated that in the HAART era, the importance of B19 infections in HIV patients may be limited whereas persistent B19 viremia in the circulation of healthy controls raises a potential concern in blood donations.