

## Polymorphism and functional properties of the LMP1 gene of the Epstein-Barr virus in patients with lymphoproliferative diseases

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### ABSTRACT

Phylogenetic analysis of LMP1 variants isolated from tumor tissue of patients with EBV-associated pathologies in different geographic regions revealed the accumulation of a number of mutations in this gene, indicating a high degree of its polymorphism. Currently, three main mechanisms of LMP1 variability are considered: the occurrence of point mutations leading to the substitution of individual amino acids; the formation of deletions and duplications; and homologous recombination as a result of coinfection of lymphoid or epithelial cells with two different EBV strains. The study of individual mutations of this gene revealed the ability of some of them to affect the biological properties of the LMP1 molecule, which probably plays an important role in the etiopathogenesis of diseases caused by EBV. Of greatest interest are mutations of the C-terminal cytoplasmic domain, which, as shown earlier, affect the immunogenicity and half-life of LMP1, which ultimately contributes to the enhancement of its transforming effect on the cell. No less important role in changes in the properties of the protein is played by point mutations localized in the transmembrane domain of LMP1, and it has been shown that some of them lead to a significant decrease in the cytotoxic effect of the viral protein on the cell, which possibly affects the transforming potential of this oncoprotein.

**Keywords:** LMP1 gene, Polymorphism, Epstein-Barr virus, lymphoproliferative diseases

**Funding information**  
Self-funded

**Conflict of interest**  
None declared by author

### Citation:

Aditya R. Kiran, Neha U. Diya. Polymorphism and functional properties of the LMP1 gene of the Epstein-Barr virus in patients with lymphoproliferative diseases. AJMS 2025; 11 (3): 89-96

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