Cloning of the matrix gene of measles virus (Hallé strain)

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We report the nucleotide and predicted amino acid sequence of the matrix (M) gene of the Hallé strain of measles virus cloned from a pcD library (1). The analysis shows that the sequence is highly conserved compared with the prototype Edmonston sequence (2), containing only three amino acid changes (underlined). In contrast, other SSPE strains have been shown to contain high nucleotide mutation rates (3), especially T to C. Three of the six nucleotide changes in Hallé are also T to C and interestingly one of these gives rise to proline substituting serine. The Hallé strain is still lytic but T to C mutation by a process such as RNA editing could give rise to multiple changes to proline with drastic consequences in terms of protein structure and viral persistence. At 1418 a G is deleted as in strain Hu2 (4) which is also lytic but is not SSPE-derived.

REFERENCES

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