Molecular analysis of measles virus genome derived from SSPE and acute measles patients in Papua, New Guinea

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Abstract

A very high annual incidence of 56 per million population below the age of 20 years for subacute sclerosing panencephalitis (SSPE) has been reported from Papua New Guinea (PNG). In a more recent study, we have confirmed this unusual high incidence for Eastern Highlands Province (EHP) of PNG. In the study, it was observed that the vaccination rate among SSPE patients registered at Goroka Base General Hospital (GBGH) in EHP was higher than that of other infants in the province in recent years. To identify the measles virus (MV) responsible for SSPE in EHP, sequence analysis of hypervariable region of the N gene was performed from 13 MV genomes: 2 amplified from clinical specimens of SSPE patients and 11 from acute measles patients. In 2 cases among the 11 with acute measles, nucleotide sequence of the entire H gene derived from isolated viruses was determined. Both nucleotide sequence and phylogenetic tree analyses showed that the amplified MV cDNAs were closely related to one another and belonged to the D3 genotype though they were different from any previously reported MV sequences. No genome sequences of vaccine strains were detected. These findings suggest that the MV strains prevailing in the highlands of PNG belong to genotype D3 of the MV and this wild-type MV rather than the vaccine strains was likely to be responsible for SSPE in these patients. J. Med. Virol. 68:105–112, 2002. © 2002 Wiley-Liss, Inc.