

Analisis genetik dan antigenik beberapa virus campak liar dan virus vaksin campak di Indonesia

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Abstrak

ABSTRACT

Measles immunization has been introduced since 1960, thereby markedly reducing the number of cases in developed countries. However, measles epidemics still occur even in developed countries. In the United States, in 1988-1992 an increase in the number of measles cases reaching 50,000 cases was reported. Some of these cases occurred in previously immunized patients. This was thought to be caused by genetic mutation of the measles virus, aside from weaknesses of the vaccine and low immunization coverage. Since measles immunization was employed in Indonesia, the number of measles patients has decreased. However, epidemics are still frequently reported. About 15-30% of reported cases occurred in those previously immunized, raising the question of whether a genetic difference exists between the wild-type measles virus circulating in Indonesia and the vaccine virus being used. Such a difference may lead to the differences in the antigenicity of the wild-type and vaccine viruses, rendering the resulting antibody incapable of neutralizing the wild-type viruses. Based on the above, this study is aimed to demonstrate the extent of genetic and antigenic differences between the wild-type and vaccine measles viruses.

We conducted an experimental laboratory study to sequence the N, H, and F genes of the wild-type measles viruses (G2, G3, and D9) and the CAM-70 vaccine virus. To show antigenic differences, the wild-type viruses (G2, G3, and D9) and the CAM-70 and Schwarz viruses were injected to BALB/c mice. Serum antibodies of the mice were analyzed using ELISA, cross-neutralization test, and immunoblotting using antigens from the respective viruses.

Results of this study showed that the wild-type and the vaccine viruses differ in the sequence of the N gene by 73-79 nucleotides, resulting in amino acid substitution of 17-24 residues; the H gene by 60-99 nucleotides, resulting in amino acid substitution of 13-29 residues; the F gene by 71-88 nucleotides, resulting in amino acid substitution of 4-3 I residues. Differences between the wild-type and the CAM-70 and Schwarz vaccine viruses were also found in the epitope site of the CTL and antibodies, which are important to virus antigenicity.

We conclude that a significant difference in antigenicity exists between the wild-type measles viruses circulating in Indonesia with the CAM-70 measles virus. We also found the immunogenicity of the CAM-70 and Schwarz vaccine viruses to be lower than that of the wild-type viruses.