

## **Selected references on measles virus genotypes and sequencing, 1991-2004**

### *Publications 2004 (including in press and submitted manuscripts)*

Nakayama, T., Fujino, M., and Yoshida, N. Molecular epidemiology of measles virus in Japan. *Pediatr Int.* 2004;46:214-223.

Rota, P.A., Rota J.S., Redd, S.B., Papania, M.J., and Bellini, W.J. Genetic analysis of measles viruses isolated in the United States between 1989 and 2001: Absence of an endemic genotype since 1994. *J. Infect. Dis.* 2004;189:S160-164.

Tipples, G.A., Gray, M., Garbutt, M., Rota, P.A. and the Canadian Measles Surveillance Program. Genotyping of measles virus in Canada: 1979-2002. *J. Infect. Dis.* 2004;189:S171-176.

### *Publications 2003*

Chibo, D., Riddell, M., Catton, M., Lyon, M., Lum, G., and Birch, C. Studies of measles viruses circulating in Australia between 1999 and 2001 reveals a new genotype. *Virus Res.* 2003;91:213-221.

Horm, S.V., Dumas, C., Svay, S., Feldon, K., and Reynes, J-M. Genetic characterization of wild-type measles viruses in Cambodia. *Virus Research* 2003;97:31-37.

Kubo, H., Iritani, N., and Seto, Y. Co-circulation of two genotypes of measles virus and mutual change of the prevailing genotypes every few years in Osaka, Japan. *J. Med. Virol.* 2003;69:273-278.

Mbugua, F.M, Okoth, F.A., Gray, M., et al. Molecular epidemiology of measles virus in Kenya. *Jrl. Med Virol.* 2003;71:599-604.

Na, B-K., Shin, J-M., Lee, J-Y., et al. Genetic and antigenic characterization of measles viruses that circulated in Korea during the 2000-2001 epidemic. *J. Med. Virol.* 2003;70:649-654.

WHO. Update of the nomenclature for describing the genetic characteristics of wild-type measles viruses: new genotypes and reference strains. *Wkly Epidemiol. Rec.* 2003;78:229-232.

Zhou, J., Fujino M., Inou, Y., et al. H1 genotype of measles virus was detected in outbreaks in Japan after 2000. *J. Med. Virol.* 2003;70:642-648.

### *Publications 2002*

Alla, A., Liffick S.L., Newton, B.N., Elaouad, R., Rota, P.A., and Bellini, W.J. Genetic analysis of measles viruses isolated in Morocco. *J. Med. Virol.* 2002;68:441-444.

Chibo, D., Riddell, M., Catton, M., and Birch, C. Novel measles virus genotype, East Timor and Australia. *Emerg. Infect. Dis.* 2002;8:735-37.

Christensen, LS, Scholler S, Schierup MH, et al. Sequence analysis of measles virus strains collected during the pre- and early-vaccination era in Denmark reveals a considerable diversity of ancient strains. *APMIS* 2002;110(2):113-22.

Coughlan, S., Connell, J., Cohen B. et al. Suboptimal measles-mumps-rubella vaccination coverage facilitates an imported measles outbreak in Ireland. *Clin. Infect. Dis.* 2002;35:84-6.

El Mubarak, H.S., vande Bildt, M.W.G., Mustafa, O.A., et al. Genetic characterization of wild-type measles viruses circulating in suburban Khartoum, 1997-2000. *J. Gen Virol.* 2002;83:1437-1443.

Jin, L., Beard, S., Hunjan R., Brown, D., and Miller, E. Characterization of measles virus strains causing SSPE: A study of 11 cases. *J. Neurovirol.* 2002; 8(4):335-344.

Kouomou, D.W., Nerrienet, E., Mfoupouendoun, J., Tene, G., Whittle, H., and Wild, T.F. Measles virus strains circulating in central and West Africa: Geographical distribution of two B3 genotypes. *J. Med. Virol.* 2002;68:433-440.

Kubo, H., Iritani, N., Murakami, T., and Haruki, K. Isolation of a wild type measles virus classified as genotype H1 in Osaka City. *Jpn. J. Infect. Dis.* 2002;55:177-79.

Miki, K., Komase K., Mgone, C.S., Kawanishi, R., Iijima, M., Mgone, J.M., Asuo, P.G., Alpers, M.P., Takasu, T., and Mizutani, T. Molecular analysis of measles virus genome derived from SSPE and acute measles patients in Papua, New Guinea. *J. Med. Virol.* 2002;68:105-112.

Oliveira, M.I., Rota, P.A., Curti, S.P., Figueiredo, C.A., Afonso, A.M.S., et al. Genetic homogeneity of measles viruses associated with a measles outbreak, São Paulo, Brazil, 1997. *Emerg. Infect. Dis.* 2002;8(8):808-813.

Rota, P.A., Liffick, S.L., Rota, J.S., Katz, R.S., Redd, S., Papania, M., and Bellini, W.J. Molecular epidemiology of measles viruses in the United States, 1997-2001. *Emerg. Infect. Dis.* 2002;8(9):902-908.

Santibanez. S., Tischer, A., Heider, A., Siedler, A., and Hengel, H. Rapid replacement of endemic measles virus genotypes. *J. Gen. Virol.* 2002;83:2699-2708.

Wairagkar, N., Rota, P.A., Liffick, S., Shaikh, N., Padbidri, V.S., and Bellini, W.J. Characterization of measles sequences from Pune, India. *J Med Virol.* 2002;68:611-614

### *Publications 2001*

Liffick, S, Thoung, N, Xu, W. et al. Genetic characterization of contemporary wild-type viruses from Vietnam and China: identification of two genotypes within clade H. *Virus Res.* 2001;77:81-7.

Na, B-K., Lee, J-S., Shin G-C., et al. Sequence analysis of hemagglutinin and nucleoprotein genes of measles viruses isolated in Korea during the 2000 epidemic. *Virus Res.* 2001;81:143-149.

Nigatu, W., Jin, L., Cohen, B.J., Nokes, D.J., Etana, M., Cutts, F.T. and Brown, D.W.G. Measles virus circulating in Ethiopia during 1998-1999: identification of a new genotype. *J. Med. Virol.* 2001;65:373-380.

Siqueira, M.M., Castro-Silva, R., Cruz, C., Oliveira, I.C., Cunha, G.M.C., Mello, M., Rota, P.A., Bellini, W.J., and Friedrich, F. Genomic characterization of wild-type measles viruses that circulated in different states in Brazil during the 1997 measles epidemic. *J. Med. Virol.* 2001;63:299-304.

Truong, T.A., Mulders, M.N., Gautam, D.C., Ammerlaan, W., De Swart, R., Chwan-Chuen, K., Osterhaus, A.D.M.E., and Muller, C.P. Genetic analysis of Asian measles virus strains-new endemic genotype in Nepal. *Virus Res.* 2001;76:71-78.

WHO. Nomenclature for describing the genetic characteristics of wild-type measles viruses (update)- part II. *Wkly. Epidemiol. Rec.* 2001;76:249-251.

WHO. Nomenclature for describing the genetic characteristics of wild-type measles viruses (update)-part I. *Wkly. Epidemiol. Rec.* 2001;76:242-247.

### *Publications 2000*

Barrero, P.R., de Wolff, C.D., Passeggi, C.A., and Mischenko, A.S. Sequence analysis of measles virus hemagglutinin isolated in Argentina during the 1997-1998 outbreak. *J. Med. Virol.* 2000; 60:91-96.

Baumeister, E, Siqueira, M.M., Savy, V., and Friedrich, F. Genetic characterization of wild-type measles viruses isolated during the 1998 measles epidemic in Argentina. *Acta Virologica* 2000;44:169-174.

Canepa, E., Siqueira, M.M., Hortal, M., and Friedrich, F. Recent measles viral activity in Uruguay: serological and genetic approaches. *Acta Virol.* 2000;44:35-39.

Chibo, D., Birch, C.J., Rota, P.A., and Catton, M.G. Molecular characterization of measles viruses isolated in Victoria, Australia, between 1973 and 1998. *J. Gen. Virol.* 2000;81:2511-

2518.

de Swart, R.L., Wertheim-van Dillen P.M., van Binnendijk, R.S., Muller, C.P., Frenkel, J., and Osterhaus, A.D. Measles in a Dutch hospital introduced by an immunocompromised infant from Indonesia with a new virus genotype. *Lancet* 2000;355:201-202.

Hanses F., van Binnendijk, R., Ammerlaan, W., Truong, A.T., de Rond L., Schneider, F., and Muller, C.P. Genetic variability of measles viruses circulating in the Benelux. *Arch. Virol.* 2000;145:541-551.

Rota, P.A., Liffick, S., Rosenthal, S., Heriyanto, B., and Chua, K.B. Measles genotype G2 in Indonesia and Malaysia. (Letter) *Lancet* 2000;355:1557-1560.

Rota, J.S., Bellini, W.J., and Rota, P.A. Measles. In: Thompson, R.C.A. (Ed.). *Molecular Epidemiology of Infectious Diseases*. London: Arnold Publishers; 2000; 168-180.

Takahashi, M., Nakayama, T., Kashigawi, Y., Takami, T., Sonoda, S., Yamanaka, T., Ochiai, H., Ihara, T., and Tajima, T. Single genotype of measles virus is dominant whereas several genotypes of mumps virus are co-circulating. *J. Med. Virol.* 2000;62:278-285.

#### *Publications 1999*

Hanses, F., Truong, A.T., Ammerlaan, W., Ikusika, O., Adu, F., Oyefolu, A.O., Omilabu, S.A., and Muller, C.P. Molecular epidemiology of Nigerian and Ghanaian measles virus isolates reveals a genotype circulating widely in western and central Africa. *J. Gen. Virol* 1999;80:871-877.

Santibanez, S., Heider, A., Gerike, E., Agafonov, A., and Schreier, E. Genotyping of measles virus isolates from central Europe and Russia. *J. Med. Virol.* 1999;58:313-320.

Truong, A.T., Ammerlaan, W., Hartter, H.K., Adu, F., Omilabu, S.A., Ovefolu, A.O., Berbers, G.A., and Muller, C.P. Genotypic and antigenic characterization of hemagglutinin proteins of African measles virus isolates. *Virus Res.*1999;62:89-95.

#### *Publications 1998*

Ayata, M., Kimoto, T., Hayashi, K., Toshiyuki, S., Murata, R., and Ogura, H. Nucleotide sequences of the matrix protein gene of subacute sclerosing panencephalitis viruses compared with local contemporary isolates from patients with acute measles. *Virus Res.*1998;54:107-115.

Bellini, W.J., and Rota, P.A. Genetic diversity of wild-type measles viruses: Implications for global measles elimination programs. *Emerg. Infect. Dis.* 1998;4:29-35.

Giraudon, P., Jacquier, M.F., and Wild, T.F. Antigenic analysis of African measles virus field isolates: identification and localisation of one conserved and two variable epitope sites on the NP protein. *Virus Res.* 1998;18:137-152.

Jin, L., Knowles, W.A., Rota, P.A., Bellini, W.J. and Brown, D.W.G. Genetic and antigenic characterisation of the haemagglutinin protein of measles virus strains recently circulating in the UK. *Virus Res.* 1998;55:107-113.

Jin, L., Sun, U.J., Ge, L., and Brown, D.W.G. Characterization of a new genotype of measles virus detected in China and England. *Epidemiol. Infect.* 1998;121: 691-697.

Oliveira, I., Curti, S.P., Figueiredo, C.A., et al. Genetic analysis of measles virus in Sao Paulo, Brazil. *Virus Rev. Res.* 1998;3:7-8.

Rota, J.S., Rota, P.A., Redd, S.B., Redd, S.C., Pattamadilok, S., and Bellini, W.J. Genetic analysis of measles viruses isolated in the United States, 1995-1996. *J. Infect. Dis.* 1998;177:204-208.

WHO. Standardization of the nomenclature for describing the genetic characteristics of wild-type measles viruses. *Wkly. Epidemiol. Rec.* 1998;73:265-272.

Xu, W.B., Tamin, A., Rota, J.S., LiBi, Z., Bellini, W.J., and Rota, P.A. New genetic group of measles virus isolated in the People's Republic of China. *Virus Res.* 1998;54:147-156.

#### *Publications 1997*

Heider, A., Santibanez, S., Tischer, A., Gerike, E., Tikhonova, N., Ignatyev, G., Enders, G., Mrazova, M., and Schreier, E. Comparative investigation of the long non-coding M-F genome region of wild-type and vaccine measles viruses. *Arch. Virol.* 1997;142:2521-2528.

Jin, L., Brown, D.W.G., Ramsay, M.E.B., Rota, P.A. and Bellini, W.J. The diversity of measles virus in the UK, 1992-1995. *J. Gen. Virol.* 1997;78:1287-1294.

Katayama, Y., Shibahara, K., Kohama, T., Homma, M. and Hotta, H. Molecular epidemiology and changing distribution of genotypes of measles virus field isolates in Japan. *J. Clin. Microbiol.* 1997;35:2651-2653.

Kreis, S., and Whistler, T. Rapid identification of measles virus strains by the heteroduplex mobility assay. *Virus Res.* 1997;47:197-203.

Kreis, S., Vardas, E., and Whistler, T. Sequence analysis of the nucleocapsid gene of measles virus isolates from South Africa identifies a new genotype. *J. Gen. Virol.* 1997;78:1581-1587.

Outlaw, M.C., Jaye, A., Whittle, H., and Pringle, C. Clustering of hemagglutinin sequences of measles viruses isolated in the Gambia. *Virus Res.* 1997;48:125-131.

Rima, B.K., Earle, J.A.P., Baczko, K., ter Meulen, V., Liebert, U., Carstens, C., Carabana, J., Cabellero, M., Celma, M., and Fernandez-Muñoz, R. Sequence divergence of measles virus hemagglutinin during natural evolution and adaptation to cell culture. *J. Gen. Virol.* 1997;78:97-106.

Yamaguchi, S. Identification of three lineages of wild measles virus by nucleotide sequence analysis of N, P, M, F, and L genes in Japan. *J. Med. Virol.* 1997;52:113-120.

*Publications 1996*

Rota, J.S., Heath, J.L., Rota, P.A., King, G.E., Celma, M.L., Carabana, J., Fernandez-Muñoz, R., Brown, D., Jin, L., and Bellini, W.J. Molecular epidemiology of measles virus: Identification of pathways of transmission and the implications for measles elimination. *J. Infect. Dis.* 1996;173:32-37.

*Publications 1995*

Kobune, F., et al. Characterization of measles viruses isolated after measles vaccination. *Vaccine* 1995;13:370-372.

Nakayama, T., Mori, T., Yamaguchi, S., et al. Detection of measles virus genome directly from clinical samples by reverse transcriptase-polymerase chain reaction and genetic variability. *Virus Res.* 1995;35:1-16.

Outlaw, M.C., and Pringle, C.R. Sequence variation within an outbreak of measles virus in the Coventry area during spring/summer 1993. *Virus Res.* 1995;39:3-11.

Rima, B.K., Earle, J.A.P., Yeo, R.P., Herlihy, L., Baczko, K., ter Meulen, V., Carabana, J., Caballero, M., Celma, M.L., and Fernandez-Munoz, R. Temporal and geographical distribution of measles virus genotypes. *J. Gen. Virol.* 1995;76:1173-1180.

Rima, B., Earle, J.A.P., Baczko, K., Rota, P.A., and Bellini, W.J. Measles virus strain variations. *Curr. Topics Microbiol. Immunol.* 1995;191:65-84.

Rota, P.A., Rota, J.S., and Bellini, W.J. Molecular epidemiology of measles virus. *Semin. Virol.* 1995;6:379-386.

Saito, H., Nakagomi, O. and Morita, M. Molecular identification of two distinct hemagglutinin types of measles virus by polymerase chain reaction and restriction fragment length polymorphism (PCR-RFLP). *Molecular and Cellular Probes* 1995;9:1-8.

*Publications 1991-1994*

Baczko, K., Brinckmann, U., Pardowitz, I., Rima, B.K. and ter Meulen, V. Nucleotide sequence of the genes encoding the matrix protein of two wild-type measles virus strains. *J. Gen. Virol.* 1991;72:2279-2282.

Kobune, F., Sakata, H. and Sugiura, A. Marmoset lymphoblastoid cells as a sensitive host for isolation of measles virus. *J. Virol.* 1990;64:700-705.

Rota, J.S., Hummel, K.B., Rota, P.A., and Bellini, W.J. Genetic variability of the glycoprotein

genes of current wild-type measles isolates. *Virology* 1992;188:135-142.

Rota, P.A., Bloom, A.E., Vanchiere, J.A., and Bellini, W.J. Evolution of the nucleoprotein and matrix genes of wild-type strains of measles viruses isolated from recent epidemics. *Virology* 1994;198:724-730.

Rota, J.S., Wang, Z.D., Rota, P.A., and Bellini, W.J. Comparison of sequences of the H, F and N coding genes of measles virus vaccine strains. *Virus Res.* 1994;31:317-330.

Sakata, H., Kobune, F., Sato, T.A., Tanabayashi, K., Yamada, A., and Sugiura, A. Variation in field isolates of measles virus during an 8-year period in Japan. *Microbiol. Immunol.* 1993;37:233-237.

Saito, H., Sato, H., Abe, M., et al. Isolation and characterization of the measles virus strains with low hemagglutination activity. *Intervirology* 1992;33:57-60.

Schulz, T.F., Hoad, J.G., Whitby, D., Tizard, E.J., Dillon, M.J., and Weiss, R.A. A measles virus from a child with Kawasaki disease: sequence comparison with contemporaneous isolates from classical cases. *J. Gen. Virol.* 1992;73:1581-1586.

Taylor, M.J., Godfrey, E., Baczko, K., ter Meulen V., Wild, T.F., and Rima, B.K. Identification of several different lineages of measles virus. *J. Gen. Virol.* 1991;72:83-88.

Whitby, D., Hoad, J.G., Tizard, E.J., et al. Isolation of measles virus from child with Kawasaki disease. (Letter) *Lancet* 1991;338:1215.