

## REFERENCES

- Abdullah, N. A. M. H., Dom, N. C., Salleh, S. A., Salim, H., & Precha, N. (2022). The association between dengue case and climate: A systematic review and meta-analysis. *One Health (Amsterdam, Netherlands)*, 15, 100452. <https://doi.org/10.1016/j.onehlt.2022.100452>
- Añez, G., Heisey, D. A., Volkova, E., & Rios, M. (2016). Complete genome sequences of Dengue virus type 1 to 4 strains used for the development of CBER/FDA RNA reference reagents and WHO international standard candidates for nucleic acid testing. *Genome Announcements*, 4(1), e01583-15. <https://doi.org/10.1128/genomeA.01583-15>
- Araf, Y., Ullah, M. A., Faruqui, N. A., Mowna, S. A., Prium, D. H., & Sarkar, B. (2021). Dengue outbreak is a global recurrent crisis: Review of the literature. *Electronic Journal of General Medicine*, 18(1), e267. <https://doi.org/10.29333/ejgm/8948>
- ATCC. (n.d.). Dengue virus type 1 VR-1856 ™. <https://www.atcc.org/products/vr-1856>
- Baer, A., & Kehn-Hall, K. (2014). Viral concentration determination through plaque assays: Using traditional and novel overlay systems. *Journal of Visualized Experiments : JoVE*, (93), e52065. <https://doi.org/10.3791/52065>
- Barr, K. L., & Anderson, B. D. (2013). Dengue viruses exhibit strain-specific infectivity and entry requirements in vitro. *Virus Adaptation and Treatment*, 1-9.
- Bolívar-Marin, S., Bosch, I., & Narváez, C. F. (2022). Combination of the focus-forming assay and digital automated imaging analysis for the detection of Dengue and Zika viral loads in cultures and acute disease. *Journal of Tropical Medicine*, 2022, 2177183. <https://doi.org/10.1155/2022/2177183>
- Chin-Inmanu, K., Suttipethumrong, A., Sangsrakru, D., Mairiang, D., Tangphatsornruang, S., Malasit, P., & Suriyaphol, P. (2019). Complete genome sequences of four serotypes of Dengue virus prototype continuously maintained in the laboratory. *Microbiology Resource Announcements*, 8(19), e00199-19. <https://doi.org/10.1128/MRA.00199-19>

- Crossley, B. M., Bai, J., Glaser, A., Maes, R., Porter, E., Killian, M. L., Clement, T., & Toohey-Kurth, K. (2020). Guidelines for Sanger sequencing and molecular assay monitoring. *Journal of Veterinary Diagnostic Investigation : Official Publication of the American Association of Veterinary Laboratory Diagnosticians, Inc.*, 32(6), 767–775. <https://doi.org/10.1177/1040638720905833>
- Cruz, C. D., Torre, A., Troncos, G., Lambrechts, L., & Leguia, M. (2016). Targeted full-genome amplification and sequencing of dengue virus types 1–4 from South America. *Journal of Virological Methods*, 235, 158-167.
- Dang, T. T., Pham, M. H., Bui, H. V., & Van Le, D. (2020). Whole genome sequencing and genetic variations in several dengue virus type 1 strains from unusual dengue epidemic of 2017 in Vietnam. *Virology Journal*, 17(1), 1-10.
- Datu, A. M., Natzir, R., Yustisia, I., Wahid, I., Soraya, G. V., & Kadir, S. (2023). Molecular detection and analysis of dengue virus genetic diversity in North Sulawesi, Indonesia during 2022. *Biodiversitas Journal of Biological Diversity*, 24(6). doi: 10.13057/biodiv/d240636
- Dewi, B. E., Nainggolan, L., Sudiro, T. M., Chenderawasi, S., Goentoro, P. L., & Sjatha, F. (2021). Circulation of various dengue serotypes in a community-based study in Jakarta, Indonesia. Japanese. *Journal of Infectious Diseases*, 74(1), 17-22. <https://doi.org/10.7883/yoken.JJID.2019.431>
- Diamond, M. S., Edgil, D., Roberts, T. G., Lu, B., & Harris, E. (2000). Infection of human cells by Dengue virus is modulated by different cell types and viral strains. *Journal of Virology*, 74(17), 7814-7823.
- Du, M., Jing, W., Liu, M., & Liu, J. (2021). The global trends and regional differences in incidence of dengue infection from 1990 to 2019: an analysis from the global burden of disease study 2019. *Infectious Diseases and Therapy*, 10(3), 1625-1643.
- European Centre for Disease Prevention and Control. (2023). 12-month dengue virus disease case notification rate per 100 000 population, July 2022–June 2023 [Data file]. Retrieved from

[https://www.ecdc.europa.eu/en/publications-data/12-month-dengue-virus-disease-case-not  
ification-rate-100-000-population-july-2022](https://www.ecdc.europa.eu/en/publications-data/12-month-dengue-virus-disease-case-notification-rate-100-000-population-july-2022)

Gomes, A., & Korf, B. (2018). Genetic testing techniques. *Pediatric Cancer Genetics*, 47–64.

doi:10.1016/b978-0-323-48555-5.00005-3

Guzman, M. G., & Harris, E. (2015). Dengue. *The Lancet*, 385(9966), 453–465.

doi:10.1016/s0140-6736(14)60572-9

Hagemann, I. S. (2015). Overview of technical aspects and chemistries of next-generation sequencing. *Clinical Genomics*, 3–19. doi:10.1016/b978-0-12-404748-8.00001-0

Hamel, R., Surasombatpattana, P., Wichit, S., Dauvé, A., Donato, C., Pompon, J., ... & Missé, D. (2019).

Phylogenetic analysis revealed the co-circulation of four dengue virus serotypes in Southern Thailand. *PLoS One*, 14(8), e0221179.

Harapan, H., Michie, A., Sasmono, R. T., & Imrie, A. (2020). Dengue: A minireview. *Viruses*, 12(8), 829.

<https://doi.org/10.3390/v12080829>

Hendra, A., Heriani, W., & Perdani, A. L. (2020). Practice of dengue prevention among school-aged children in Indonesia. *International Summit on Science Technology and Humanity (ISETH) 2020*.

Hitakarun, A., Ramphan, S., Wikan, N., & Smith, D. R. (2020). Analysis of the virus propagation profile of 14 dengue virus isolates in *Aedes albopictus* C6/36 cells. *BMC Research Notes*, 13, 1-6.

<https://doi.org/10.1186/s13104-020-05325-6>

Hwang, E. H., Kim, G., Oh, H., An, Y. J., Kim, J., Kim, J. H., Hwang, E. S., Park, J. H., Hong, J., & Koo, B. S. (2020). Molecular and evolutionary analysis of dengue virus serotype 2 isolates from Korean travelers in 2015. *Archives of Virology*, 165(8), 1739–1748.

<https://doi.org/10.1007/s00705-020-04653-z>

Ishige, T., Itoga, S., & Matsushita, K. (2018). Locked nucleic acid technology for highly sensitive detection of somatic mutations in cancer. *Advances in Clinical Chemistry*, 53–72.

doi:10.1016/bs.acc.2017.10.002

- Jonduo, M., Neave, M. J., Javati, S., Abala, D., Bilo, E., Kini, A., Kumbu, J., Laman, M., Robinson, L. J., Makita, L., Susapu, M., Pomat, W., Abdad, M. Y., Williams, D. T., & Horwood, P. F. (2022). Genomic sequencing of Dengue virus strains associated with Papua New Guinean outbreaks in 2016 reveals endemic circulation of DENV-1 and DENV-2. *The American Journal of Tropical Medicine and Hygiene*, 107(6), 1234–1238. <https://doi.org/10.4269/ajtmh.21-1292>
- Kementerian Kesehatan Republik Indonesia. (2023). *Informasi Dengue 2023*. <https://p2pm.kemkes.go.id/publikasi/infografis/info-dbd-minggu-ke-33-tahun-2023>
- Kennedy M. (2005). Methodology in diagnostic virology. *The Veterinary Clinics of North America. Exotic Animal Practice*, 8(1), 7–26. <https://doi.org/10.1016/j.cvex.2004.09.009>
- Khan, M. B., Yang, Z. S., Lin, C. Y., Hsu, M. C., Urbina, A. N., Assavalapsakul, W., ... & Wang, S. F. (2023). Dengue overview: An updated systemic review. *Journal of Infection and Public Health*, 16(10), 1625-1642. <https://doi.org/10.1016/j.jiph.2023.08.001>
- Ko, H. Y., Salem, G. M., Chang, G. J. J., & Chao, D. Y. (2020). Application of next-generation sequencing to reveal how evolutionary dynamics of viral population shape dengue epidemiology. *Frontiers in Microbiology*, 11, 1371.
- Kok, B. H., Lim, H. T., Lim, C. P., Lai, N. S., Leow, C. Y., & Leow, C. H. (2022). Dengue virus infection—A review of pathogenesis, vaccines, diagnosis and therapy. *Virus Research*, 324, e199018. <https://doi.org/10.1016/j.virusres.2022.199018>
- Kutle, I., Sengstake, S., Templin, C., Glaß, M., Kubisch, T., Keyser, K. A., ... & Messerle, M. (2017). The M25 gene products are critical for the cytopathic effect of mouse cytomegalovirus. *Scientific Reports*, 7(1), 15588.
- Martinez, D. R., Yount, B., Nivarthi, U., Munt, J. E., Delacruz, M. J., Whitehead, S. S., ... & Baric, R. S. (2020). Antigenic variation of the dengue virus 2 genotypes impacts the neutralization activity of human antibodies in vaccines. *Cell Reports*, 33(1).
- Masyeni, S., Yohan, B., Somia, I. K. A., Myint, K. S., & Sasmono, R. T. (2018). Dengue infection in international travellers visiting Bali, Indonesia. *Journal of Travel Medicine*, 25(1), tay061.

- Maula, A. W., Fuad, A., & Utarini, A. (2018). Ten-years trend of dengue research in Indonesia and South-east Asian countries: A bibliometric analysis. *Global Health Action*, 11(1), 1504398.
- Megawati, D., Masyeni, S., Yohan, B., Lestarini, A., Hayati, R. F., Meutiawati, F., Suryana, K., Widarsa, T., Budiyasa, D. G., Budiyasa, N., Myint, K. S. A., & Sasmono, R. T. (2017). Dengue in Bali: Clinical characteristics and genetic diversity of circulating dengue viruses. *PLoS Neglected Tropical Diseases*, 11(5), e0005483. <https://doi.org/10.1371/journal.pntd.0005483>
- Mo, L., Shi, J., Guo, X., Zeng, Z., Hu, N., Sun, J., ... & Hu, Y. (2018). Molecular characterization and phylogenetic analysis of a dengue virus serotype 3 isolated from a Chinese traveler returned from Laos. *Virology Journal*, 15, 1-13. <https://doi.org/10.1186/s12985-018-1016-5>
- Nadjib, M., Setiawan, E., Putri, S., Nealon, J., Beucher, S., Hadinegoro, S. R., Permanasari, V. Y., Sari, K., Wahyono, T. Y. M., Kristin, E., Wirawan, D. N., & Thabran, H. (2019). Economic burden of dengue in Indonesia. *Plos Neglected Tropical Diseases*, 13(1), e0007038. <https://doi.org/10.1371/journal.pntd.0007038>
- Niu, C., Huang, Y., Wang, M., Huang, D., Li, J., Huang, S., ... & Zhang, R. (2020). Differences in the transmission of Dengue fever by different serotypes of Dengue virus. *Vector-Borne and Zoonotic Diseases*, 20(2), 143-150. <https://doi.org/10.1089/vbz.2019.2477>
- Owens, A., Shifflett, J., Radhakrishnan, S., Langenbach, K., & Baker, R.O. (2009). Comparison of Dengue virus type 1 growth characteristics in Vero and C6/36 cell lines [Poster presentation]. BEI Resources. Manassas, VA, United States. <https://www.beiresources.org/Portals/2/Comparison%20of%20Dengue%20Virus%20Type%201%20Growth%20Characteristics.pdf>
- Parkash, O., & Hanim Shueb, R. (2015). Diagnosis of dengue infection using conventional and biosensor based techniques. *Viruses*, 7(10), 5410-5427. <https://doi.org/10.3390/v7102877>
- Pavel, S. T. I., Yetiskin, H., Aydin, G., Holyavkin, C., Uygut, M. A., Dursun, Z. B., Celik, İ., Cevik, C., & Ozdarendeli, A. (2020). Isolation and characterization of severe acute respiratory syndrome

coronavirus 2 in Turkey. *PLoS One*, 15(9), e0238614.

<https://doi.org/10.1371/journal.pone.0238614>

Phadungsombat, J., Vu, H. T. T., Nguyen, Q. T., Nguyen, H. T. V., Nguyen, H. T. N., Dang, B. T., ... & Pham, T. N. (2023). Molecular characterization of dengue virus strains from the 2019–2020 Epidemic in Hanoi, Vietnam. *Microorganisms*, 11(5), 1267.

<https://doi.org/10.3390/microorganisms11051267>

Poltep, K., Phadungsombat, J., Nakayama, E. E., Kosoltanapiwat, N., Hanboonkunupakarn, B., Wiriarat, W., ... & Leaungwutiwong, P. (2021). Genetic diversity of dengue virus in clinical specimens from Bangkok, Thailand, during 2018–2020: Co-circulation of all four serotypes with multiple genotypes and/or clades. *Tropical Medicine and Infectious Disease*, 6(3), 162.

Rahim, R., Hasan, A., Phadungsombat, J., Hasan, N., Ara, N., Biswas, S. M., Nakayama, E. E., Rahman, M., & Shioda, T. (2023). Genetic analysis of Dengue virus in severe and non-severe cases in Dhaka, Bangladesh, in 2018-2022. *Viruses*, 15(5), 1144. <https://doi.org/10.3390/v15051144>

Rodríguez-Manzano, J., Chia, P. Y., Yeo, T. W., Holmes, A., Georgiou, P., & Yacoub, S. (2018). Improving dengue diagnostics and management through innovative technology. *Current Infectious Disease Reports*, 20, 1-8.

Rodríguez-Aguilar, E. D., Martínez-Barnetche, J., & Rodríguez, M. H. (2022). Three highly variable genome regions of the four dengue virus serotypes can accurately recapitulate the CDS phylogeny. *MethodsX*, 9, 101859.

Roy, S. K., & Bhattacharjee, S. (2021). Dengue virus: Epidemiology, biology, and disease aetiology. *Canadian Journal of Microbiology*, 67(10), 687-702.

Santiago, G. A., González, G. L., Cruz-López, F., & Muñoz-Jordan, J. L. (2019). Development of a standardized Sanger-based method for partial sequencing and genotyping dengue viruses. *Journal of Clinical Microbiology*. doi:10.1128/jcm.01957-18

- Sasmono, R. T., Wahid, I., Trimarsanto, H., Yohan, B., Wahyuni, S., Hertanto, M., ... & Schreiber, M. J. (2015). Genomic analysis and growth characteristic of dengue viruses from Makassar, Indonesia. *Infection, Genetics and Evolution*, 32, 165-177.
- Sasmono, R. T., Santoso, M. S., Pamai, Y. W., Yohan, B., Afida, A. M., Denis, D., ... & Frost, S. D. (2020). Distinct dengue disease epidemiology, clinical, and diagnosis features in Western, Central, and Eastern Regions of Indonesia, 2017–2019. *Frontiers in Medicine*, 7, 582235.
- Shepard, D. S., Undurraga, E. A., Halasa, Y. A., & Stanaway, J. D. (2016). The global economic burden of dengue: A systematic analysis. *The Lancet Infectious Diseases*, 16(8), 935-941.
- Sirisena, P. N., Noordeen, F., & Fernando, L. K. (2016). Delayed appearance of virus induced morphological changes in cultures derived from dengue and dengue haemorrhagic fever patients. *International Journal of Infectious Diseases*, 45, 458. doi:10.1016/j.ijid.2016.02.971
- Storch, G. A. (2000). Diagnostic virology. *Clinical Infectious Diseases*, 31(3), 739-751.  
<https://doi.org/10.1086/314015>
- Suppiah, J., Ching, S. M., Amin-Nordin, S., Mat-Nor, L. A., Ahmad-Najimudin, N. A., Low, G. K. K., ... & Chee, H. Y. (2018). Clinical manifestations of dengue in relation to dengue serotype and genotype in Malaysia: A retrospective observational study. *PLoS Neglected Tropical Diseases*, 12(9), e0006817.
- Tatura, S. N., Denis, D., Santoso, M. S., Hayati, R. F., Kepel, B. J., Yohan, B., & Sasmono, R. T. (2021). Outbreak of severe dengue associated with DENV-3 in the city of Manado, North Sulawesi, Indonesia. *International Journal of Infectious Diseases*, 106, 185-196.
- Tian, N., Zheng, J. X., Guo, Z. Y., Li, L. H., Xia, S., Lv, S., & Zhou, X. N. (2022). Dengue incidence trends and its burden in major endemic regions from 1990 to 2019. *Tropical Medicine and Infectious Disease*, 7(8), 180. <https://doi.org/10.3390/tropicalmed7080180>
- Upadhyay, S. (2023). Testing viral infections. In *Viral Infections and Antiviral Therapies* (pp. 99-120). Academic Press. <https://doi.org/10.1016/B978-0-323-91814-5.00003-9>

- Utama, I. M. S., Lukman, N., Sukmawati, D. D., Alisjahbana, B., Alam, A., Murniati, D., ... & Parwati, K. T. M. (2019). Dengue viral infection in Indonesia: Epidemiology, diagnostic challenges, and mutations from an observational cohort study. *PLOS Neglected Tropical Diseases*, 13(10), e0007785.
- Uttam, G., Kumari, A., & Singh, K. (2023). Epitope prediction and designing of receptor inhibitor of Dengue Envelope Protein: An in silico approach. *Journal of Vector Borne Diseases*, 60(2), 161-171.
- Vicente, C. R., Herbinger, K. H., Fröschl, G., Malta Romano, C., de Souza Areias Cabidelle, A., & Cerutti Junior, C. (2016). Serotype influences on dengue severity: A cross-sectional study on 485 confirmed dengue cases in Vitória, Brazil. *BMC Infectious Diseases*, 16(1), 1-7.
- Wang, W. H., Urbina, A. N., Chang, M. R., Assavalapsakul, W., Lu, P. L., Chen, Y. H., & Wang, S. F. (2020). Dengue hemorrhagic fever: A systemic literature review of current perspectives on pathogenesis, prevention and control. *Journal of Microbiology, Immunology and Infection*, 53(6), 963-978.
- Wardhani, P., Aryati, A., Yohan, B., Trimarsanto, H., Setianingsih, T. Y., Puspitasari, D., ... & Sasmono, R. T. (2017). Clinical and virological characteristics of dengue in Surabaya, Indonesia. *PLoS One*, 12(6), e0178443.
- Wardhani, P., Yohan, B., Tanzilia, M., Sunari, E. P., Wrahatnala, B. J., Hakim, F. K. N., Rohman, A., Husada, D., Hayati, R. F., Santoso, M. S., Sievers, J. T. O., Aryati, A., & Sasmono, R. T. (2023). Genetic characterization of dengue virus 4 complete genomes from East Java, Indonesia. *Virus Genes*, 59(1), 36–44. <https://doi.org/10.1007/s11262-022-01942-4>
- Yamada, K. I., Takasaki, T., Nawa, M., & Kurane, I. (2002). Virus isolation as one of the diagnostic methods for dengue virus infection. *Journal of Clinical Virology*, 24(3), 203-209.
- Yang, X., Quam, M. B., Zhang, T., & Sang, S. (2021). Global burden for dengue and the evolving pattern in the past 30 years. *Journal of Travel Medicine*, 28(8), taab146.

- Yohan, B., Dhenni, R., Hayati, R. F., Yudhaputri, F. A., Denis, D., Pamai, Y. W., ... & Sasmono, R. T. (2018a). Whole genome sequencing of Indonesian dengue virus isolates using next-generation sequencing. *Indonesian Journal of Biotechnology*, 23(2), 74-83.
- Yohan, B., Wardhani, P., Trimarsanto, H., Aryati, A., & Sasmono, R. T. (2018b). Genomic analysis of dengue virus serotype 1 (DENV-1) genotypes from Surabaya, Indonesia. *Virus Genes*, 54(3), 461–465. doi:10.1007/s11262-018-1558-z
- Yu, Y., Liu, Y., Ling, F., Sun, J., & Jiang, J. (2023). Epidemiological characteristics and economic burden of dengue in Zhejiang Province, China. *Viruses*, 15(8), 1731.
- Zeng, Z., Zhan, J., Chen, L., Chen, H., & Cheng, S. (2021). Global, regional, and national dengue burden from 1990 to 2017: A systematic analysis based on the global burden of disease study 2017. *EClinicalMedicine*, 32.
- Zhang, P., Seth, A., & Fernandes, H. (2014). Other post-PCR detection technologies. *Pathobiology of Human Disease*, 4074–4088. doi:10.1016/b978-0-12-386456-7.07707-8