

Evaluating the Transmission Dynamics of Dengue in Taiwan

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Abstract

Background: Dengue fever is a growing concern to Taiwan, with pronounced spatiotemporal heterogeneities with endemic and non-endemic areas. To understand the transmission dynamics, the present study aimed to estimate the effective reproduction number (R) over time and across regions using limited surveillance data.

Methods: Datasets were retrieved from open data of Taiwan CDC, documenting cases classified as local or imported. We arranged cases as monthly data from 1998 to 2024. R was estimated using a maximum likelihood method. Geographic areas included southern Taiwan (Kaohsiung, Tainan, Pingtung), northern Taiwan (Taipei, New Taipei, Taoyuan), and central/eastern regions.

Results: Southern Taiwan regularly had a time period with $R > 1$, while R was mostly below 1 in northern Taiwan despite frequent importations. Time-series analysis revealed that R was associated with temperature and precipitation. Kendall trend test indicated a slow increase in R from 1998–2014 across Taiwan, followed by the absence of trend from 2015–2024.

Discussion: A distinct geographic pattern was observed between north and south, though seasonal patterns were shared between two regions. Southern Taiwan had higher risk, with R more often exceeding 1. Across Taiwan, R tended to take the value below 1 from January–June.