

中文題目：屏東 C 型肝炎流行病學

英文題目：**Genotype distribution, clinical characteristics, and racial differences observed in chronic hepatitis C patients in Pingtung, Taiwan**

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Background: The World Health Organization (WHO) set out to eliminate hepatitis C virus (HCV) infection by 2030, a goal Taiwan might achieve before 2025. Using effective direct antiviral agents (DAAs) against chronic hepatitis C (CHC) in Taiwan, the treatment of CHC has been initiated in rural areas. Here, we aimed to elucidate the clinical and virological characteristics of HCV infection, and the treatment efficacy of DAAs in patients from Pingtung county in southern Taiwan.

Methods: A total of 152 chronic hepatitis patients treated with DAAs were consecutively enrolled. Baseline characteristics and therapeutic efficacy were evaluated.

Results: HCV genotype 2 was the most common viral genotype (39.5 %), followed by 1b (36.8%), 6 (10.5%), and 1a (9.2%). The sustained virological response (SVR) rate was 99.2%. Hakka patients accounted for 22.4 % of the study cohort, of which 14.7% had HCV genotype 6. There were no differences in clinical characteristics between Hakka and non-Hakka patients. Patients with HCV genotype 6 were younger in age (OR/CI: 0.95/0.91-1.00, $P = 0.04$) and comprised of more people who inject drugs (PWID) (OR/CI: 17.6/3.6-85.5, $P < 0.001$), when compared to other patients.

Conclusion: We demonstrated that DAA therapy can achieve a 99.2% SVR rate among CHC patients in Pingtung county of southern Taiwan, with a relative higher prevalence of genotype 6. The most important factor attributed to genotype 6 infection was PWID.

Keywords: CHC, DAA, genotype 6, Pingtung, SVR