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Current Status And Genetic Analysis of Artemisinin Resistance in Malaria

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Abstract

Malaria is still an important public health issue to date. Artemisinin-based combination therapies (ACTs) are highly effective and have been recommended by the World Health Organization as the first-line treatment for *Plasmodium falciparum* infection.

Since 2008, ACT resistance has been reported in the Greater Mekong Subregion. The efficacy of ACTs has gradually decreased with its widespread use. Now the world is deeply concerned with the spreading of artemisinin resistance and ACT multidrug resistance. Mutations in the propeller domain of the *P. falciparum kelch13* (*pfK13*) gene are associated with artemisinin resistance. In order to assess the artemisinin resistance of imported malaria in Taiwan, we sequenced *pfK13* gene of four falciparum malaria cases imported from Kenya, Solomon Islands and Uganda in 2018 and no mutations were found in *pfK13* gene.

To better cope with imported malaria cases, measures such as clinical observations, travel history inquiry, laboratory diagnosis and follow-up should be reinforced. In addition, for patients from Greater Mekong Subregion with parasitemia after therapy

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regimen, the possibility of resistance should be evaluated, and malaria drug resistance genes, such as *pfKelch-13* gene, should be sequenced to assess the resistance of artemisinin for timely adjustment of treatment strategies. These efforts assist in more rational use of antimalarial drugs, delay the development of drug resistance and maintain the effectiveness of artemisinin.

Keywords: Malaria, *Plasmodium falciparum*, artemisinin, resistance