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Surveillance of molecular epidemiology of *Cryptococcus gattii* in Taiwan

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Purpose: *Cryptococcus gattii* species complex is a yeast pathogen causing cryptococcosis mainly in non-HIV infected patients. Studies had discovered various species of trees as ecological niches of *C. gattii* and, therefore, sources of infection. We screened trees and the soil around these trees for *C. gattii* isolation and determined the molecular epidemiology of *C. gattii* in Taiwan.

Method: We screened various trees and rhizosphere soil of trees in parks and schools in Western Taiwan to isolate *C. gattii* from the environment. The multilocus sequence typing (MLST) of the isolates was performed, and the mating type of the isolates was determined.

Results: From November 2017 to May 2018, a total of 82 isolates of *C. gattii* had been isolated from wood debris and soils. The isolation rate was higher in the parks or schools that were established early, especially in Japanese-ruled era. Thirty-three of them were VGI, and the others were VGII. Three domestic sequence types (STs) that had not been reported in other parts of the world were discovered in Taiwan, which were ST328, ST546, and ST548. The diversity of ST is region-dependent. A park in mid-Taiwan had the highest diversity of ST of *C. gattii*. The *Cryptococcus gattii* was isolated in limited species of trees. The top 3 trees that *C. gattii* was most commonly isolated from are *Eucalyptus robusta*, *Pithecellobium dulce*, and *Melaleuca leucadendra*, and the positive rate was 45/116 (38.8%), 22/59 (37.3%), 10/94 (10.6%), respectively.

Conclusion: Isolation of *C. gattii* from the environment can enrich our knowledge of local molecular epidemiology of this yeast. This molecular epidemiology data is helpful in studies of the evolution of *C. gattii*, the determination of the source of infection and disease prevention.