



Molecular variation of *Sporisorium scitamineum* in Mainland China revealed by internal transcribed spacers

Y.Y. Zhang^{1,2*}, N. Huang^{1,2*}, X.H. Xiao^{1,2}, L. Huang^{1,2}, F. Liu^{1,2}, W.H. Su^{1,2} and Y.X. Que^{1,2}

¹Key Lab of Sugarcane Biology and Genetic Breeding, Ministry of Agriculture, Fujian Agriculture and Forestry University, Fuzhou, Fujian, China

²Sugarcane Research & Development Center, China Agriculture Research System, Fujian Agriculture and Forestry University, Fuzhou, Fujian, China

*These authors contributed equally to this study.

Corresponding author: Y.X. Que

E-mail: queyouxiong@126.com

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ABSTRACT. Sugarcane smut caused by the fungus *Sporisorium scitamineum* is a worldwide disease and also one of the most prevalent diseases in sugarcane production in mainland China. To study molecular variation in *S. scitamineum*, 23 *S. scitamineum* isolates from the 6 primary sugarcane production areas in mainland, China (Guangxi, Yunnan, Guangdong, Hainan, Fujian, and Jiangxi Provinces), were assessed using internal transcribed spacer (ITS) methods. The results of ITS sequence analysis showed that the organisms can be defined at the genus level, including *Ustilago* and *Sporisorium*, and can also differentiate between closely related species. This method was not suitable for phylogenetic relationship analysis of different *S. scitamineum* isolates and could not provide support regarding their race ascription at the molecular level. The results of the present study will be useful for studies examining the molecular diversity of *S. scita-*

mineum and for establishing a genetic foundation for their pathogenicity differentiation and new race detection. In addition, our results can provide useful information for the pathogen selection principle in sugarcane smut resistance breeding and variety distribution.

Key words: Internal transcribed spacer; Molecular diversity; *Sporisorium scitamineum*; Sugarcane smut