Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Hemileia vastatrix* (Coffee Leaf Rust) Physiological Races Emergent in Coffee Germplasm Collections in the Coffee-Cropping Regions of China

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Coffee leaf rust (CLR), caused by the obligate biotrophic fungus *Hemileia vastatrix*, is a devastating disease worldwide leading to severe reductions in yield and economic losses in coffee plantations, especially of *Coffea arabica* L. (Talhinhas et al. 2017). The frequent emergence of new *H. vastatrix* races is a major constraint on coffee production due to continuous exertion of selective pressure on the pathogen from pathogen-resistant cultivars under the coevolutionary “arms race” (Silva et al. 2018). More than 50 physiological races of *H. vastatrix* have been described globally (Várzea and Marques 2005), and at least 16 *H. vastatrix* races have been detected in China (Bai et al. 2018; Chen 1998; Zhang et al. 2014). Coffee is an important cash crop in China (Yan et al. 2019). The majority of coffee germplasm collections in China are located in the main coffee-cropping regions, although

documentation on the prevalent *H. vastatrix* races is lacking. A total of 57 CLR samples (each sample contained multiple leaves with 20 to 30 pustules of coffee rust) were collected from four germplasm fields situated in the main coffee-cropping regions during the high seasonal incidence of CLR in 2018 to 2019: field 1, Coffee Germplasm Collection of Malipo County, Wenshan (23°11' N, 104°55' E, 550 m); field 2, Coffee Germplasm Collection I in Puer (22°47'45" N, 100°58'59" E, 1,320 m); field 3, Coffee Germplasm Collection II in Puer (22°37'36" N, 100°59'50" E, 1,010 m); and field 4, Coffee Germplasm Collection in Ruili (24°01' N, 97°51' E, 1,260 m). Uredinospores were recovered on susceptible genotypes 849/1 Matari and 19/1 Caturra and were tested on a set of coffee differentials at the CIFC (Oeiras, Portugal) following a standard race-typing procedure (Várzea and Marques 2005). The coffee trees where the rusts were isolated were used to verify. The infection type criteria determining virulence and avirulence were based on the classification standards for disease resistance (Várzea and Marques 2005). Twenty-seven pure-cultured *H. vastatrix* isolates were derived from single rust pustules taken from distinct sample groups. The predominant race XXXVII (*v*_{2,5,6,7,9}) was present in fields 1, 2, and 3 at high frequency (74.04%) separately derived from the genotypes Catuai, Arabica-Catimor Derivatives, T2, CCC 24, Typica, T8667 Catimor HW 26/5 (F2), and Sarchimor. Race XXXIV (*v*_{2,5,7,9}) was detected in field 4 (3.70%). Races XXXVII and XXXIV had emerged in China during 2011–2015 (Bai et al. 2017, 2018). A new race (*v*_{2,5,6,7}) (7.41%) was isolated from the host DTART 316 and was able to infect the differentiators of physiologic groups D, E, R, 4, 6, 12, and a. Based on its pathological and genetic characteristics, *H. vastatrix* with high evolutionary potential has inevitably overcome the resistance of released coffee cultivars with increase virulence, thereby adapting to new hosts (McCook and Vandermeer 2015; Silva et al. 2018; Talhinhas et al. 2017; Zambolim 2016). The results obtained in this work corroborate the evidence that the emergence of new *H. vastatrix* races occurs preferentially at germplasm fields due to the multiselection pressures from various hosts. Our findings are of considerable importance given the potential of the coffee germplasm collections in coffee regions to promote evolution of new races. The continued emergence of new *H. vastatrix* races places the current commercial cultivars at risk from a loss of resistance. Monitoring the occurrence, dissemination, distribution, and pathogenicity of new races is essential for targeted resistance breeding and CLR control.

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