




A leaf spot of *Tectona grandis* caused by *Xanthomonas fuscans* in Brazil

Rafaela C. F. Borges¹ · Maurício Rossato¹  · Maria do Desterro M. Santos¹ · Cléia S. Cabral¹ · Greecy Mirian R. Albuquerque² · Maria A. Ferreira³ · Maria Esther N. Fonseca⁴ · Leonardo Silva Boiteux⁴

Received: 3 September 2018 / Accepted: 12 November 2018 / Published online: 10 December 2018
© Società Italiana di Patologia Vegetale (S.I.Pa.V.) 2018

Keywords Bacterial spot · *gyrB* · Phylogeny · *rpoD* · Teak

Tectona grandis (teak) is a major timber crop in the North Brazilian region. Necrotic leaf lesions often surrounded by chlorotic halos were observed in teak plants (100 days after germination) in a clonal mini-garden displaying ~15% incidence (of 400,000 plants), in Mato Grosso State (May, 2016). Five bacterial isolates (with yellow-pigmented, mucoid, domed colonies) were obtained by isolation of 15 distinct plants in NA medium (28 °C/72 h) and named Xanteca1 to 5. All isolates were inoculated in four teak clones (TG01 to TG04; 90 days after germination) via cuts (0.5 cm) with scissors at the end of the leaf blades followed by immersion into bacterial suspensions (10^8 CFU ml⁻¹). The symptoms appeared 11 days after inoculation and similar colonies were re-isolated from symptomatic leaves. Two representative isolates (Xanteca3 and Xanteca4) were selected for identification. Genus identification was performed using 16S rRNA region (primers 27F/1492R) (MF033093 to MF033097) in EzBioCloud (Yoon et al. 2017), and recognized as a member of the *Xanthomonas* genus. Further identification of the bacteria was performed by sequencing *gyrB* partial sequence (emigrB1F/emigrB4R) with 864 base pairs (bp) and *rpoD* (emirpo11F/ emirpo13R), also partial, with 873 bp. Phylogenetic analysis of both genes were executed with

Bayesian inference, model GTR + G + I, selected with Akaike Information Criterion (AIC). For use as references, type strains sequences of several species were downloaded from GenBank (Parkinson et al. 2009). *gyrB* (MF034328 to MF034332) and *rpoD* (MH673499 to MH673501) phylogenetic analysis, both clustered XanTeca sequences with *X. fuscans* and *X. fuscans* subsp. *aurantifolii* (isolates ICMP10027, ICMP10030, ICMP8432, NCPPB381) with a value of “1” of posterior probability. Four *X. fuscans* isolates from teak (CCRMXF01, CCRMXF02, CCRMXF03, CCRMXF04) were deposited in the public culture collection “Rosa Mariano” of the Plant Bacteriology Lab (UFRPE, Recife-PE, Brazil). To our knowledge, this is the first worldwide report of *X. fuscans* infecting teak.

References

- Parkinson N, Cowie C, Heeney J, Stead D (2009) Phylogenetic structure of *Xanthomonas* determined by comparison of *gyrB* sequences. *Int J Syst Evol Microbiol* 59:264–274
- Yoon SH, Ha SM, Kwon S, Lim J, Kim Y, Seo H, Chun J (2017) Introducing EzBioCloud: a taxonomically united database of 16S rRNA and whole genome assemblies. *Int J Syst Evol Microbiol* 67: 1613–1617

✉ Maurício Rossato
mauricio.rossato@unb.br

¹ Department of Plant Pathology, Instituto de Ciências Biológicas, Universidade de Brasília, Brasília, DF 70910-900, Brazil

² Department of Agronomy, Universidade Federal Rural de Pernambuco, Recife, PE 52171-900, Brazil

³ Department of Plant Pathology, Universidade Federal de Lavras, Lavras, MG 37200-000, Brazil

⁴ Plant Breeding Lab, Embrapa Vegetable Crops, Brasília, DF 70275-970, Brazil