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ARTICLE

IMA Genome-F 1: *Ceratocystis fimbriata*

Draft nuclear genome sequence for the plant pathogen, *Ceratocystis fimbriata*

P. Markus Wilken[1], Emma T. Steenkamp[2], Michael J. Wingfield[1], Z. Wilhelm de Beer[2], and Brenda D. Wingfield[1]

[1]Department of Genetics, [2]Department of Microbiology and Plant Pathology, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria; corresponding author e-mail: markus.wilken@fabi.up.ac.za

Abstract: The draft nuclear genome of *Ceratocystis fimbriata*, the type species of *Ceratocystis*, is comprised of 29 410 862 bp. *De novo* gene prediction produced 7 266 genes, which is low for an ascomycete fungus. The availability of the genome provides opportunities to study aspects of the biology of this and other *Ceratocystis* species.

Key words:
Ceratocystis fimbriata
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INTRODUCTION

The fungal genus *Ceratocystis* (*Microascales*, *Sordariomycetes*, *Ascomycota*) includes numerous important plant pathogens, some of considerable economic importance. Species in the *C. fimbriata* complex include *C. platani* that causes a serious wilt of *Platanus* trees in Europe (Ocasio-Morales *et al*. 2007), *C. manginecans*, causal agent of Mango wilt disease (van Wyk *et al*. 2007), and *C. fimbriata sensu stricto,* a pathogen of sweet potato (Baker *et al.* 2003). The genus also encompasses several other species complexes that include economically important species (e.g. the thielaviopsis morph, Punja & Sun 1999), agents of blue stain in timber (e.g. *C. polonica,* Christiansen 1985) and saprophytes. These fungi all have intriguing and little-understood associations with insects (Seifert *et al*. 2013).

Recent studies on *Ceratocystis* species have focused on species delimitation (van Wyk *et al.* 2010), reproductive strategies (Harrington & McNew 1997, Witthuhn *et al*. 2000) and links between pathogenicity and host range (Ferreira *et al.* 2011). Although genome sequence information represents an invaluable resource for such studies, whole genome sequences have not yet been determined for *Ceratocystis* species or other members of the *Microascales*. In this study, we report the availability of the nuclear genome sequence for an isolate of *C. fimbriata*. This *Ceratocystis* species was chosen for sequencing because it is the type species of the genus (Seifert *et al*. 2013).

SEQUENCED STRAIN

USA: *North Carolina*: isol. ex *Ipomoea batatas* (sweet potato), December 1998, *D. McNew* (CBS 114723, CMW 14799). Dried culture also preserved in the CBS fungarium, CBS H-21516.

NUCLEOTIDE SEQUENCE ACCESSION NUMBER

The Whole Genome Shotgun project of the *Ceratocystis fimbriata* genome has been deposited in DDBJ/EMBL/GenBank under the accession APWK00000000. The version described in this paper is the first version, CFim_1.0.

METHODS

DNA was extracted and subjected to 454 pyrosequencing (Roche Diagnostics, Mannheim, Germany) at Inqaba Biotechnology (Pretoria, South Africa). The resulting reads were assembled into a draft genome consisting of 3 668 contigs by using the Newbler v. 2.3 genome assembler. The “create detailed mapping report” command of the CLC Genomics workbench package v. 5.0.1 (CLC bio, Aarhus, Denmark) was used to produce statistics for the draft sequence.

RESULTS AND DISCUSSION

The draft genome had an estimated size of 29 410 862 bp (as calculated by summation of all the contig sizes), 20× average coverage, N50 contig size of 42 879 bases and an estimated GC content of 48.06 %. All contigs with a length of > 199 bp were submitted to NCBI’s genome database. To assess the completeness of the genome, contigs of size ≥ 500 bp (2641 contigs) were analysed with the CEGMA pipeline (Parra *et al*.

2007), which produced a 96.77 % indication of completeness. Although we did not produce a complete annotation for the *C. fimbriata* genome, analysis with AUGUSTUS (Stanke *et al*. 2006) identified 7 266 putative ORFs at a gene density of 246 ORFs/Mb. Of the putative protein coding genes, the majority (97 %) had 100 or more amino acids.

The *C. fimbriata* genome is relatively small (29.4 Mb) and harbours fewer genes than other fungal species such as *Fusarium graminearum* (36.1 Mb, 11 640 genes) (Cuomo *et al*. 2007) and *Neurospora crassa* (39.9 Mb, 10 082 genes) (Galagan *et al*. 2003). Whether this difference is linked to the different lifestyles of these fungi requires further research. The availability of this *Ceratocystis* genome sequence will contribute to our understanding of the molecular and cellular mechanisms underlying the biology of these and other fungi.

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