IMA Genome-F 1: Ceratocystis fimbriata

Draft nuclear genome sequence for the plant pathogen, Ceratocystis fimbriata

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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 genome Microascales

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, Punjab & Sun 1999), agents of blue stain in timber (e.g. C. polonica, Christiansen 1985) and saprophyles. 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, Withuhn 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


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), 20x 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. 2003).
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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REFERENCES


