Data in Brief 12 (2017) 644–648

Contents lists available at ScienceDirect

Data in Brief

journal homepage: www.elsevier.com/locate/dib

Data Article

Data on microsatellite markers in Colletotrichum gloeosporioides s.l., polymorphism levels and diversity range

Laurent Penet*, Sophie Briand, Dalila Petro, François Bussière, Sébastien Guyader

INRA, UR1321, ASTRO Agrosystèmes tropicaux, F-97170, Petit-Bourg (Guadeloupe) France

ARTICLE INFO

Article history:
Received 8 March 2017
Received in revised form
12 April 2017
Accepted 4 May 2017
Available online 11 May 2017

Keywords:
Colletotrichum gloeosporioides
Anthracnose disease
Microsatellites
Molecular markers

ABSTRACT

Colletotrichum gloeosporioides is a species complex of fungi belonging to the *Glomerellaceae* family (Ascomycota). It has a global worldwide occurrence and while sometimes described as a plant endophytic commensal, it also often demonstrates pathogenicity on crops and is responsible for anthracnose disease in many cultivated species. Thirty-nine polymorphic microsatellites were isolated and their polymorphism levels were determined in 95 strains from Guadeloupe (Lesser Antilles), mostly isolated from Water Yam (*Dioscorea alata*). The average allele number per polymorphic locus was 12.3 (decreasing to 4.3 at 5% frequency threshold, indicative of dramatic amounts of rare polymorphisms), with a range of 2–29 alleles. The microsatellite markers data will facilitate genetic diversity analyses and population genetics studies for the species complex.

Specifications Table

Subject area	*Biology*
More specific subject area	*Microsatellite markers data (primers and expected diversity levels)*

* Corresponding author.
E-mail address: laurent.penet@inra.fr (L. Penet).

http://dx.doi.org/10.1016/j.dib.2017.05.012

Type of data	*Table*
How data was acquired	ABI PRISM 3730XL automated sequencer (MACROGEN)
Data format	*Raw (primers information) and partially analyzed (diversity indices)*
Experimental factors	Genomic DNA
Experimental features	*Isolation of microsatellite markers and amplification test*
Data source location	*Guadeloupe 4°44.0694′ N 53°46.881′ W*
Data accessibility	*This manuscript (Table 1), primers are also available from probe data bank @ NCBI (www.ncbi.nlm.nih.gov/probe/)*

Value of the data

- Large set of potentially polymorphic microsatellite markers in *Colletotrichum gloeosporioides.*
- Diversity and genetic structure analyses at both fine and broad geographic scales.
- Pathogenic strains genetic profiling.
- Further *Colletotrichum gloeosporioides* species delineation (complimentary to sequencing data).
- Origin of crop inocula and host origin analyses.

1. Data

This dataset is a list of 39 microsatellite markers from the worldwide pathogenic species complex *Colletotrichum gloeosporioides*, including primers and basic information relative to diversity levels expected at each locus. *Colletotrichum* fungi are diversified [1], with species ranging from genuine endophytic commensals to biotrophic parasites or even saprophytic pathogens [2]. Species of this genus are thus often associated with crop diseases, and especially anthracnose in plants [3–5]. Taxonomic studies are currently investigating sequence based delineation of species (DNA barcoding, e.g. [6–8]), but reaching consensus is still undergoing [9]. Defining co-dominant and highly polymorphic molecular markers such as microsatellites available for diversity studies and cross geographical or ecological comparisons would be a valuable tool for the study of this species complex and would allow introducing genetic data complementary to the current genomic approaches [9]. Also, these markers might allow differentiating genetic pools that could reflect host adaptation or even possibly identify new species within strain pools (structuration via reduced gene flow, e.g. [6]). We successfully developed 39 microsatellite markers for this wide geographical and ecological range pathogen (Table 1).

2. Experimental design, materials and methods

Genomic DNA was extracted from seven strains of *Colletotrichum gloeosporioides*. Six microsatellite-enriched genomic libraries were produced following [10]. DNA was digested with RsaI and fragments of 500 bp were ligated into a pCR 4-TOPO vector. These were then used to transform One Shot TOP10 chemically competent Escherichia coli, producing a total of 1158 positives clones and 128 were sequenced on an ABI PRISM 3730XL automated sequencer, using T3 and T7 primers. Consensus sequences were obtained using ChromasPro 1.34 software [11]. Of these sequences, 21 were of poor quality, 24 did not show microsatellite region, 24 were sister clones, and 59 showed microsatellites (motifs of three repetitions or more). Forty-nine primers pairs were thus designed using Primer-3 [12] and PrimerSelect of DNAStar [13].