Data Article

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

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A B S T R A C T

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.

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Specifications Table

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

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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 Rsal 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].
| Locus name | Probe accession reference (NCBI) | Repeat motif | Forward Primer 5’ → 3 | Reverse Primer 5’ → 3 | Amplif. Success | Size range | Nei index |
|------------|---------------------------------|--------------|------------------------|------------------------|----------------|------------|------------|
| Cg12       | Pr032825007                     | tgg          | GCAATGGAGCATGCAACTAA    | TGGGCTACCTCATAACACGG    | 76%            | 150–267    | 0.77       |
| Cg14       | Pr032825015                     | tgg          | TCTATTGGCATCTTACAG      | GCTTCTGCGGCTAGTTTCC     | 37%            | 156–159    | 0.31       |
| Cg16       | Pr032825021                     | cac          | ACAACAGAGTCTCTGCGTCT    | TGATGATGCTGGTAGATCAA     | 85%            | 102–276    | 0.71       |
| Cg19       | Pr032825026                     | gcc          | GTCTTGTTGAAGTTTACGGCT   | AGTTCTAGGCTGATACCTG    | 47%            | 103–224    | 0.69       |
| Cg37       | Pr032825027                     | gac          | TCTCTGAGCAGACTGAGCT     | AGTGGTCTGATGTTTGCGG     | 45%            | 90–103     | 0.64       |
| Cg53       | Pr032825028                     | tgg          | ACACACGAGAAGAATCTGAAA   | GAGACGACGACGAGCACGCA    | 69%            | 231–324    | 0.86       |
| Cg57       | Pr032825029                     | tgg          | CGCCTTATTTTTGGAGTCTGA   | TGCTATGAGTGGATTTGAAG    | 100%           | 197–239    | 0.88       |
| Cg68       | Pr032825030                     | tcc          | TGCTCTGCTCTCAGACTGCT    | AGGCAAGAGACCAAGCAAGA    | 87%            | 109–325    | 0.86       |
| Cg71       | Pr032825031                     | aac          | TGATGCTGCTGAGATTGACT    | GATGATCCTCATAAGGCTC     | 47%            | 91–250     | 0.86       |
| Cg83       | Pr032825032                     | gt           | GGATTTGCTCTGCTGCTAT     | GAGAAGAAGATAGGACAGCA    | 45%            | 122–218    | 0.85       |
| Cg90       | Pr032825033                     | gt           | TACGCTTGGCTGAGACCTT     | AGTGAATGCTAGGAAGGGG     | 74%            | 176–294    | 0.83       |
| Cg91       | Pr032825034                     | ga           | GTTGGGAGAACAAGAGTCC     | GACTGCTGAGAAGAATGCGA    | 56%            | 94–136     | 0.58       |
| Cg92       | Pr032825035                     | tc           | CTTTATTTCACGACACCAAC    | GCAGCAAGGTGTGAGAAGA     | 82%            | 92–250     | 0.94       |
| Cg93       | Pr032825036                     | tgg          | TCTTTGGTTGTGATGAGGAG    | GCCGCAAACTTCTCTACTT     | 45%            | 86–234     | 0.82       |
| Cg95       | Pr032825037                     | ca           | GAGGGTGTGGTCTATGCTT     | GCTGCTTGCTACACACAA      | 80%            | 134–192    | 0.77       |
| Cg96       | Pr032825038                     | ca           | AGCGGGCGGGACCTGACAG     | GAGTACCAATTTGCTGCTA     | 92%            | 102–258    | 0.70       |
| Cg97       | Pr032825039                     | at           | TTGTGTGAAGAAGTAGTTGGA   | AATCCACGGAGAATACATG     | 41%            | 112–152    | 0.53       |
| Cg98       | Pr032825040                     | tg           | CGAGGAACCTGTCAGACTT     | TTGGTCTGCTCTGCTGCTCC   | 56%            | 134–396    | 0.89       |
| Cg100      | Pr032825002                     | ag           | GTGCTCTTGGGAGACAC      | CAATCTTACCGACACACAT     | 77%            | 78–128     | 0.78       |
| Cg109      | Pr032825003                     | gt           | TCAAAAGAAGACCCACCAAG    | GACTGATGCTGAGACCTCAC    | 74%            | 130–190    | 0.75       |
| Cg110      | Pr032825004                     | ac           | TGATACCTGGATGTCACACTG   | GGAAGTGGAGGGACTGACCA    | 94%            | 165–252    | 0.67       |
| Cg115      | Pr032825005                     | cg           | CATTGATGAGATAGGGTTCTT   | GAAAGTGAGACCAAGAAGAG    | 89%            | 92–182     | 0.67       |
| Cg116      | Pr032825006                     | ca           | CATTCTTATCCCCGCTTC      | GCGGCGTATGACAGAGA       | 68%            | 96–196     | 0.89       |
| Cg120      | Pr032825008                     | ac           | ATGTTCCTGTTGATCAGGGC    | GCAGGCAATGACCAAGATG     | 80%            | 86–176     | 0.92       |
| Cg122      | Pr032825009                     | ag           | CTTCTGCGCTCAAGTGGTTG    | GCTGCTTGCTCAAAATCTCC   | 73%            | 78–285     | 0.87       |
| Cg127      | Pr032825010                     | ag           | GTTCTGCTTGGTATACAGGCT   | TTGGCTACCTGATCTGCTG     | 98%            | 208–268    | 0.72       |
| Cg131      | Pr032825011                     | ca           | GACCTAGCAGCAGCAATAGG    | GATGCGCTGTGAGACATG      | 94%            | 72–240     | 0.82       |
| Cg132      | Pr032825012                     | ca           | GATGTCGCTGTCGTTTCTCAT  | AGGGCTGAGTGTCTCTTCA     | 83%            | 92–160     | 0.75       |
| Cg136      | Pr032825013                     | gt           | AATCTCAGGCTGGCTAGTGCTG  | TGACTGACCTGACTGCTTCTT  | 66%            | 86–194     | 0.85       |
| Cg137      | Pr032825014                     | ga           | GAGCAGCTGCTCAAGTGCGAC   | GAGTGGACAGAGTACGCTAG    | 52%            | 162–262    | 0.91       |
| Cg144      | Pr032825016                     | ct           | GCTCCACCATCTACTGAGCT    | GCAGCTAAGTCCGTAAAGGA    | 34%            | 94–112     | 0.81       |
| Cg149      | Pr032825017                     | ga           | ACCAGGAAAGAATACAGGAT    | TGCCATCTGCGGTTGATT      | 78%            | 86–204     | 0.89       |
| Cg150      | Pr032825018                     | gt           | TACGAGGGTTGCAGACCT      | GTCGAGAGAAGATCAGCTG     | 75%            | 90–232     | 0.86       |
| Cg156      | Pr032825019                     | gtt          | AGCCGAGGAGTCTGCTGAGG    | CAGAGAGTGGGGTCTGAGG     | 85%            | 87–285     | 0.79       |
| Cg159      | Pr032825020                     | ctc          | GCTACTTACCCGGCTTCTT    | CGGATACACAAAAAAGGATCA   | 83%            | 79–91      | 0.55       |
| Cg161      | Pr032825022                     | tacc         | GGAAGAACAGAAAGAGCGTA    | GCTGAGGCTGAGGCTAGGAG    | 88%            | 87–267     | 0.69       |
| Cg162      | Pr032825023                     | agtt         | GCTTGTGGTTGCTGAGAGTAC   | TGGCAGGAGATCAGATCAGA    | 46%            | 134–150    | 0.73       |
| Cg163      | Pr032825024                     | accgc        | CAAAGAACAACATACAAAAAC   | AGAGTTGCTGAGCAGCTACC   | 62%            | 142–163    | 0.77       |
| Cg164      | Pr032825025                     | ctaca        | GAGCGAGGAGGAGGAGGAGC    | GACCTGGAAGGCGGTTAAG     | 49%            | 283–298    | 0.66       |
The primers were optimized for amplification, testing annealing temperature (44.5–64.2 °C), MgCl2 concentration (1–3.5 mM), and polymerase chain reaction cycles (25–35). PCR conditions consisted of a denaturation stage at 95 °C for 5 min followed by 40 cycles at 95 °C for 30 s, 59 °C for 30 s, 72 °C for 30 s. Thirty-nine loci successfully amplified, all within expected sizes. In a further sample of 95 strains, polymorphism was assessed. High variability in alleles and Nei index were observed (Table 1). We report amplification success in single PCR runs, to help researchers chose loci more specifically. Indeed, Colletotrichum gloeosporioides demonstrate high phenotypic plasticity, possibly involving flexible DNA methylation, and amplification might vary depending on methylation state. We thus recommend choosing among these loci with a subsample study first.

In this polymorphism assessment, our strains were sampled from Dioscorea alata in Guadeloupe, where anthracnose is the main threat [14] and impacted agro-diversity [15]. Comparisons at wider geographical scales might enlighten important population processes: local dispersal [16], up to migration at greater scales [17], as well as genetic differentiation levels.

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Transparency document. Supporting information

Transparency data associated with this article can be found in the online version at http://dx.doi.org/10.1016/j.dib.2017.05.012.

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