Draft genome sequence of *Venturia carpophila*, the causal agent of peach scab

Chunxian Chen*, Clive H. Bock and Bruce W. Wood

**Abstract**

*Venturia carpophila* causes peach scab, a disease that renders peach (*Prunus persica*) fruit unmarketable. We report a high-quality draft genome sequence (36.9 Mb) of *V. carpophila* from an isolate collected from a peach tree in central Georgia in the United States. The genome annotation is described and a phylogenetic analysis of the pathogen is presented. The genome sequence will be a useful resource for various studies on the pathogen, including the biology and ecology, taxonomy and phylogeny, host interaction and coevolution, isolation and characterization of genes of interest, and development of molecular markers for genotyping and mapping.

**Keywords:** *Cladosporium carpophilum*, *Fusicladosporium carpophilum*, *Prunus persica*, Fungal pathogen, Venturiaceae

**Introduction**

*Venturia carpophila* E.E. Fisher (syn. *Fusicladosporium carpophilum* Partridge and Morgan Jones; *Cladosporium carpophilum* Thüm.; *Megacladosporium carpophilum* Thüm. (Vienn.-Bourg); *Fusicladium carpophilum* Thüm (Oudem.); *Cladosporium americanum* H.C. Greene) is an important fungal pathogen in the family Venturiaceae and is the causal agent of scab in peach (*Prunus persica*) and other species of *Prunus* [1]. Typical symptoms on fruit are black freckles, spots, and/or scabs of variable size, distribution and density (Fig. 1a and b) that render the fruit unfit for market [2]. The pathogen also infects shoots and overwinters in lesions on 1-year-old twigs, which are thought to be the source of primary inoculum in the form of conidia that are both airborne and splash-borne, resulting in infection of young fruit during the spring and early summer [3]. Peach scab generally develops on the most exposed, easily wetted, upper-most portion of the fruit surface, which is consistent with the splash-borne nature of conidia [4]. Multiple fungicide sprays are required to control peach scab at variable costs, which impose a risk of the pathogen developing resistance to certain fungicides. The effect of the fungicide sprays in reducing disease severity and thus improving fruit quality has been demonstrated, but under certain conditions the results are inconsistent [5].

Besides peach, several economically important stone fruit crops, including apricot (*P. armeniaca*), almond (*P. dulcis*), and plum (*P. domestica*), can be infected by *V. carpophila* [1]. Only recently has the taxonomic identity of the pathogens causing scab on stone fruit and other related genera begun to be clarified [6–8]. No complete genome sequence of *V. carpophila* has been reported, although some related species have now been sequenced [9–11]. As with these other species, an annotated genome of *V. carpophila* is a valuable resource for various genomic, genetic, and systematic studies. For example, various genes of interest and importance, such as those related to fungicide resistance, host recognition, or mating type, can be identified for further research to aid in management of the disease. Microsatellites can be developed as informative markers for genetic mapping and diversity studies. Also, the knowledge obtained from the genome can be useful in improving development of resistant cultivars.

In this report, we describe the first high-quality draft genome sequence of *V. carpophila* and provide a phylogenetic analysis of the fungus and other
closely related species. The genome sequence will facilitate further genomic and phylogenetic exploration to understand the pathogen and its relationship with peach.

Organism information
Classification and features
The sequenced strain of *V. carpophila* was isolated from a scab-infected peach fruit (cv. Julyprince) from an 8-year-old tree in June 2014 at the USDA-ARS-SEFTNRL, Byron, Georgia, USA (Table 1). Asexually produced conidia (Fig. 1c) of *V. carpophila* were scraped from a single lesion on the fruit surface using a scalpel, and a dilute spore solution prepared in sterile distilled water. Multiple 0.1 μL aliquots were spread on the surface of replicate water agar plates, amended with lactic acid (0.50 mL/L), streptomycin (0.20 g/L), tetracycline (0.05 g/L) and chloramphenicol (0.05 g/L). Plates were incubated at 27 °C for 48 h under fluorescent light on a 12/12 h day/night cycle. A single germinated spore of *V. carpophila* was excised on an agar plug using a scalpel under a microscope (50×), and was transferred to antibiotic-amended potato dextrose agar, and was grown for 4 weeks under the same conditions described above (Fig. 1d).

The fungus belongs in the Eukaryota, is a member of the Fungal kingdom, phylum Ascomycota, class Dothidiomycetes, and family Venturaceae (Table 1). Several other economically important plant pathogens are members of the Dothidiomycetes, including apple scab (*V. inaequalis*), pear scab (*V. pyrina*), pecan scab (*F. effusum*), rice scald (*Magnaporthe oryzae*), and Septoria leaf blotch of wheat (*Zymoseptoria tritici* syn. *Mycosphaerella graminicola*). *V. carpophila* has been classified based on its host range, morphology and some molecular characteristics [1]. The sexual stage (pseu-dotheecia that produce ascospores) of the fungus has been identified and described from Australia [1], but has not been described elsewhere at any time. Its role in the epidemiology of the disease is unknown.

The phylogenetic relationship of *V. carpophila* to other Ascomycota species based on the 18S rRNA genes shows that it is most closely related to members of the family Venturaceae, particularly the genera *Fusicladium* and *Venturia* (Fig. 2). The 18S rRNA gene was located on scaffold_438 and a 1552 bp sequence aligned with the sequences from the other fungi was used for the analysis. The phylogenetic analysis was performed using the nearest neighbor joining method in CLUSTALX2 [12] with node values based on 1000 replicates. The phylogenetic tree was drawn by TreeView [13]. Members from other genera in the Dothidiomycetes were included as outgroups.

Genome sequencing information
Genome project history
The genome of *V. carpophila* described here was sequenced in 2015 at the ICBR core facility of the

Fig. 1 Scab symptoms caused by *Venturia carpophila* on a immature peach fruit, b a ripe peach fruit, c conidia of *V. carpophila* (400×), and d an 8-week old colony of *V. carpophila* growing on potato dextrose agar
University of Florida, Gainesville, Florida, USA. The genome was assembled and annotated at the USDA-ARS Fruit and Tree Nut Research Laboratory. This Whole Genome Shotgun project has been deposited at DDBJ/ENA/GenBank under the accession MECS00000000 (Bio-project PRJNA321389). The version described in this paper is version MECS01000000. The project data is summarized in Table 2. The project information is in compliance with MIGS version 2.0 [14].

**Growth conditions and genomic DNA preparation**
Culture of *V. carpophila* was on antibiotic-amended potato dextrose agar. The culture was incubated for 4 weeks at 25 °C (12 h light/12 h dark), when the DNA was extracted from the sample using a ZymoResearch DNA extraction kit (ZymoResearch, Irvine, CA), following a slightly modified protocol for DNA extraction from fungi [15]. A Qiagen Tissue Lyser (Qiagen, Valencia, CA) was used to lyse the mycelium. Once obtained, the DNA was quantified using a Nanodrop spectrophotometer (Nanodrop Products, Wilmington, DE) and stored in TE buffer at −20 °C.

**Genome sequencing and assembly**
The genome was sequenced using an Illumina paired-end library (a V3 kit, 2 × 300 cycles) and a MiSeq machine, which generated 400,041,052 raw reads consisting of 12,052,356,652 raw nucleotides. The A5-Miseq assembly pipeline was used automatically to check quality, trim adaptors, filter low-quality reads, to correct sequencing errors using
Fig. 2 (See legend on next page.)
robust error correction (EC) parameters, and generate high-quality genome contigs with additional detection of assembly errors [16]. About 97.54% raw reads and 83.90% nucleotides passed EC; thus a total of 39,057,608 EC reads, containing 10,111,608,273 EC nucleotides, were subject to the final assembly process. A total of 657 contigs, accounting for 36,917,822 bp, were assembled, representing the assembled genome size of the pathogen. Of the assembled nucleotides, 98.58% bases had a PHRED-scale score quality \( \geq 40 \) (Q40) and the average depth of each nucleotide was 263.47, indicating it is a high-quality assembly. Additionally, the longest contig is 1,454,817 bp and the N50 length is 292,586 bp, suggesting the genome was covered mostly by larger contigs. The actual genome size is unknown at this stage, but the 263 × genome coverage likely covers more than 95% of the genome. Therefore we can estimate that the genome size of \textit{V. carpophila} is \( \sim 38.9 \) Mb, which is in the typical size range of genomes in the phylum Ascomycota [17].

**Genome annotation**
The draft genome was annotated using the MAKER pipeline [18]. In summary, repeats were first found and masked using RepeatMasker and the RepBase database [19]; ab initio gene prediction was performed with AUGUSTUS under the parameter \textit{Saccharomyces} [20]; these predicted genes were annotated by BLAST against the NCBI non-redundant (nr) nucleotide database and also by RPSBLAST (Reverse Position-Specific BLAST) batch search in conserved domain database (CDD v3.14) [21, 22]. The CCD is a superset including a total of

### Table 2 Project information

| MIGS ID | Property      | Term                       |
|---------|---------------|----------------------------|
| MIGS-31 | Finishing quality | High-quality draft          |
| MIGS-28 | Libraries used | A paired-end library        |
|         |               | (average insert 518 bp for 2 × 300 cycles) |
| MIGS-29 | Sequencing platforms | Illumina Miseq              |
| MIGS-31.2 | Fold coverage | 263x                       |
| MIGS-30 | Assembler     | AS-MiSeq                   |
| MIGS-32 | Gene calling method | Augustus using Saccharomyces as the species parameter, also COG and BLAST search NCBI nr (non-redundant) database |
|         | Locus Tag     | N/A                        |
|         | Genbank ID    | MEC500000000               |
|         | Genbank Date of Release | 2017-02-10               |
|         | GOLD ID       | N/A                        |
|         | BIOPROJECT    | PRJNA321389                |
|         | BIOSAMPLE     | SAMN04993191               |
| MIGS-13 | Source Material Identifier | N/A                         |
|         | Project relevance | Biotechnology/mycology/disease control |

### Table 3 Nucleotide and gene count levels of the genome

| Attribute                  | Value   | % of Total a |
|----------------------------|---------|--------------|
| Genomic size (bp)          | 36,917,822 |              |
| DNA coding (bp)            | 10,768,752 | 29.17        |
| DNA G + C (bp)             | 17,485,709 | 47.36        |
| DNA scaffolds              | 657     |              |
| Total genes                | 8352    |              |
| Protein coding genes       | 8220    | 98.42        |
| RNA genes                  | 132     | 1.58         |
| Pseudo genes               | Not reported |            |
| Genes in internal clusters | Not reported |            |
| Genes with function prediction | 4632   | 56.35        |
| Genes assigned to COGs     | 1136    | 13.82        |
| Genes with Pfam domains    | 2694    | 32.77        |
| Genes with signal peptides | 390     | 4.74         |
| Genes with transmembrane helices | 2622 | 31.90        |
| CRISPR repeats             | 4       |              |

\( a \) The total is based on either the size of the genome in base pairs or the total number of protein coding genes in the annotated genome.
47,363 position-specific scoring matrix (PSSM) domains curated in the NCBI and imported from Pfam [23], SMART [24], COG [25], PRK [26], and TIGRFAM [27]. The e-value for BLAST and RPSBLAST search in a database was 1e-50 and 0.01, respectively. In addition, CRISPR regions were identified using the CRISPR Recognition Tool (CRT) [28]; tRNAs were identified by tRNAscan-SE-1.23 [29]; rRNAs were identified by RNAmmer [30]; signal peptides and transmembrane helices were predicted using SignalP [31] and TMHMM [32], respectively. According to BLASTN, 107 of the 657 contigs, accounting for 144,247 bp, only had multiple hits of mitochondrial genome sequences at e-10, suggesting they belong to the organelle genome of the pathogen.

**Genome properties**

The properties of the *V. carpophila* genome are summarized in Table 3. The draft genome sequence had 36,917,822 bp in 657 contigs, with a G + C content of 47.36%. The G + C content of the 550 contigs presumable for the nuclear genome is 47.43% and that of the 107 contigs likely belonging to the mitochondrial genome is 30.13%. Of the total 8220 predicted protein-coding genes, 6547 had hits in the nr database. In addition, 4632 had predicted functions, 2694 had Pfam domains, and 3665 were assigned to COGs. The distribution of genes into COG functional categories is presented in Table 4.

**Insights from the genome sequence**

The genome provides a useful resource for identifying genes of interest in *V. carpophila*. Furthermore, the phylogenetic analysis presented earlier confirms the relationship of *V. carpophila* to other members of the Venturiaceae and confirms previous observations on the taxonomic relationships among these members of the Ascomycota. Based on the phylogenetic analysis using the sequence of the 18S rRNA gene (Fig. 2), *V. carpophila* is closely related to other scab-causing fungal pathogens of higher plants, including *V. cerasi*, causing scab on cherry, and also *V. nashicola*, cause of scab on Asian pear.

**Extended insights**

The genome of the peach scab fungus, *V. carpophila*, will be of great value to research on this organism moving forward. Apart from the opportunity it affords for more detailed analysis of individual genes relating to the secretome, we have identified several genes of interest and all microsatellites for further characterization. First, we have located the full open reading frame for one of the mating type idiomorph genes (*MAT1–2*) in scaffold_15 (between 199,706–200,916 bp) with two predicted introns (between 199,953–200,006 bp and between 200,318–200,365 bp), which paves the way for a better understanding of the reproduction of this fungus, particularly in the USA [1]. When fully characterized, the mating type idiomorphs provide the basis not only for a more complete understanding of the epidemiology of the pathogen, but also the potential opportunity for management of the disease through control of the sexual stage, as has been demonstrated with the closely related apple scab pathogen [33]. Secondly, we have also identified the cytochrome b gene in scaffold_347 (between 2149 and 7821 bp), which contains at least two introns. The accurate boundaries of the introns need further determination by PCR and

| Code | Value | % of total | Description |
|------|-------|------------|-------------|
| J    | 200   | 2.43       | Translation |
| A    | 21    | 0.26       | RNA processing and modification |
| K    | 136   | 1.65       | Transcription |
| L    | 208   | 2.53       | Replication, recombination and repair |
| B    | 28    | 0.34       | Chromatin structure and dynamics |
| D    | 172   | 2.09       | Cell cycle control, mitosis and meiosis |
| Y    | 4     | 0.05       | Nuclear structure |
| V    | 63    | 0.77       | Defense mechanisms |
| T    | 122   | 1.48       | Signal transduction mechanisms |
| M    | 142   | 1.73       | Cell wall/membrane biogenesis |
| N    | 19    | 0.23       | Cell motility |
| Z    | 24    | 0.29       | Cytoskeleton |
| W    | –     | –          | Extracellular structures |
| U    | 70    | 0.85       | Intracellular trafficking and secretion |
| O    | 295   | 3.59       | Posttranslational modification, protein turnover, chaperones |
| C    | 240   | 2.92       | Energy production and conversion |
| G    | 249   | 3.03       | Carbohydrate transport and metabolism |
| E    | 270   | 3.28       | Amino acid transport and metabolism |
| F    | 58    | 0.71       | Nucleotide transport and metabolism |
| H    | 134   | 1.63       | Coenzyme transport and metabolism |
| I    | 217   | 2.64       | Lipid transport and metabolism |
| P    | 144   | 1.75       | Inorganic ion transport and metabolism |
| Q    | 117   | 1.42       | Secondary metabolites biosynthesis, transport and catabolism |
| R    | 622   | 7.57       | General function prediction only |
| S    | 110   | 1.34       | Function unknown |
| –    | 4555  | 55.41      | Not in COGs |

*a The total is based on the total number of protein coding genes in the annotated genome*
sequencing of cDNA. This gene is particularly important in plant pathogenic fungi as it plays a critical role in resistance to the quinone outside inhibitor fungicides (also known as strobilurins). Understanding the structure of this gene will form the basis for assessing risk of resistance to the quinone outside inhibitors, as demonstrated in closely related pathogens [34].

Thirdly, we have identified a total of 4021 microsatellites in 322 of the 657 scaffolds. On average, there was about one microsatellite per 10 kb of genome. The tri-type microsatellite was the most abundant. The total length of the largest 101 scaffolds (0 to 100) is 31,436,433 bp, accounting for 85.15% of the total genome size and containing 80.10% of the microsatellites. The count and distribution of microsatellites on scaffold_0 to scaffold_100 are presented (Fig. 3 a and b). Scaffold 9 had the highest count of microsatellites (152), and it was also the longest scaffold. Microsatellites are basic to studying the genetic diversity and population structure of the pathogen, and also have potential to be used for tracking specific genes of interest.

Conclusions
The predicted genes may represent most functional genes in the *V. carpophila* genome and can be used as a new resource for developing molecular markers for genetic diversity studies, and for other research into the biology, ecology, taxonomy and phylogeny of the pathogen, and for research into host/pathogen coevolution.

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Authors’ contributions
CC, CB, and BW conceived the project and drafted the manuscript. CC performed genome bioinformatics and phylogenetic analysis. CB collected
the isolate and extracted the DNA. Each author read and approved the final version of the manuscript.

Competing interests
The authors declare that they have no competing interests.

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