Genome resources for the stem and bark canker pathogens *Corinectria fuckeliana*, *Neonectria hederæ* and *N. punicea*

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Abstract

Corinectria fuckeliana, *Neonectria hederæ*, and *N. punicea* are fungi in the family Nectriaceae that cause canker diseases of numerous hardwood trees, conifers, and woody perennials, often leading to plant mortality. Here, we report draft genome sequences for these three phytopathogenic fungal species. The genome sizes are consistent with those reported for other members of the Nectriaceae (28 to 43 Mb). These are the first genome resources available for *C. fuckeliana*, *N. hederæ*, and *N. punicea*. These genome sequences may provide insights into the mechanisms of virulence and pathogenicity employed by these three destructive plant pathogens, and are resources suitable for the development of molecular markers that could be used for species identification, diagnostic tools and barcodes, and population studies.

Fungal species in the genera *Corinectria* and *Neonectria* are the causal agents of stem and bark canker diseases on a variety of hardwood and coniferous trees such as beech, birch, fir, pine, spruce, and elms, and woody evergreen perennials such as common ivy (Booth 1959; Castlebury et al. 2006; Chaverri et al. 2011; Hirooka et al. 2013). *Corinectria fuckeliana*, *Neonectria hederæ*, and *N. punicea* are primarily wound invaders, requiring natural or artificial wounds for infection and colonization. However, these pathogens also exhibit different levels of virulence depending upon host type and environmental conditions (Crane et al. 2009; Gómez-Cortecero et al. 2016; Uimari et al. 2018). *C. fuckeliana* cause one of the most destructive diseases of young spruce and pine plantations, orchards, and forest stands, resulting in tree mortality and increased pruning and fungicide application costs (Crane et al. 2009). Additionally, *C. fuckeliana* was recently found in systemic association with the moth *Cydia pactolana*, a serious pest of conifer forests and Christmas tree plantations, increasing the impact this disease has on forest health (Uimari et al. 2018). *Neonectria punicea* is often found associated with *Fagus* trees affected by beech bark disease caused by *N. coccinea*/*N. faginata* (Castlebury et al. 2006), or causing collar rots on diseased ash trees affected by *Hymenoscyphus fraxineus* (Langer 2017). The sexual state of *N. hederæ* is often found on cut ends of stems or periderm of ornamental *Hedera helix* (Booth 1959). Although considerable research has been devoted to the cultural management of these diseases, little is known about the population biology or genomes of these and related organisms (e.g., Gómez-Cortecero et al. 2016; Marra and Corwin 2009). Genome resources could advance understanding of disease mechanisms and underlie the development of improved tools for diagnostics, taxonomy, epidemiological, and population studies of these widespread and destructive plant pathogens.

Genomic DNA was extracted from mycelial tissue of *C. fuckeliana* G.J.S 90-31 (syn.= *Nectria fuckeliana*, *Neonectria fuckeliana*) isolated from *Picea* sp. in Switzerland, *N. hederæ*

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Keywords

Nectriaceae, perennial canker, spruce canker

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Table 1. Summary statistics of the draft genome assemblies of *Corinectria fuckeliana*, *Neonectria hederae*, and *N. punicea*

Species	<i>Corinectria fuckeliana</i>	<i>Neonectria hederae</i>	<i>Neonectria punicea</i>
Isolate	G.J.S. 90-31 (= IMI 342667)	CBS 714.97	CBS 119724 (= A.R. 3102)
Herbarium no.	BPI 1107109	BPI 871043, CBS H-6027	BPI 871063
Total length (Mb)	39.0	43.2	41.4
No. scaffolds	1,399	508	1,779
Max. scaffold length (kb) ^a	462.0	802.0	342.6
Avg. scaffold size (kb)	27.8	85.0	23.3
Average coverage	34.3x	52.2x	24.7x
N50 (kb) ^b	95.9	248.9	69.9
GC content (%)	52.3	49.4	52.7
Eukaryote orthologs ^c	95.6%	95.8%	95.3%
Fungal orthologs ^d	99.2%	99.4%	98.2%
Predicted gene models	11,493	11,966	13,180
Transposable elements ^e	1.73%	0.52%	0.39%

^a Minimum scaffold length 500 bp.

^b N50 = scaffold/contig length at which 50% of the total assembly length is covered.

^c Percentage of complete BUSCOs found, 429 total BUSCO groups searched.

^d Percentage of complete BUSCOs found, 1,438 total BUSCO groups searched.

^e Percentage of the nuclear genome containing transposable elements.

CBS 714.97 isolated from *Hedera helix* in the Netherlands, and *N. punicea* CBS 119724 isolated from *Frangula alnus* in Austria, using the OmniPrep DNA kit (G-Biosciences, St. Louis, MO). These three isolates were selected for sequencing because they are well-curated representatives of each species that have been included in major taxonomic studies of the Nectriaceae (Castlebury et al. 2006; Chaverri et al. 2011). Genomic DNA libraries were constructed using the TruSeq DNA PCR-free kit and sequenced on an Illumina MiSeq as 2 × 300 paired-end reads using a MiSeq version 3.0 600 cycle reagent kit (Illumina, San Diego, CA). A total of 5.9, 9.4, and 4.5 million reads were obtained for *C. fuckeliana*, *N. hederae*, and *N. punicea*, respectively, after trimming for quality and to remove sequencing adapters. A de novo genome assembly was performed for all three isolates in CLC Genomics Workbench version 7 (CLC Bio, Boston, MA) using optimal settings determined through empirical testing: default settings (kmer = 20, bubble = 50) for *C. fuckeliana* and *N. punicea*, and kmer = 50, bubble = 36 for *N. hederae*. A summary of the three genome assemblies is provided in Table 1. Assembly sizes of *C. fuckeliana*, *N. hederae*, and *N. punicea* were consistent with the known range of genome sizes reported to date from other species in the Nectriaceae (28 to 58 Mb; Cuomo et al. 2007; Deng et al. 2015; Gómez-Cortecero et al. 2015; Malapi-Wight et al. 2015, 2016; Rivera et al. 2018). BUSCO v3.0 (Simão et al. 2015) analyses to determine the completeness of the assemblies identified 95 to 97% and 98 to 99% of eukaryotic and fungal single-copy orthologs, respectively (Table 1). Transposable element (TE) analysis using REPET version 2.5 (Flutre et al. 2011) following the pipeline described by Rivera et al. (2018) indicated that TEs comprised just a small portion of the three genomes: 1.73% of *C. fuckeliana*, 0.52% of *N. hederae*, and 0.39% of *N. punicea*. Gene model predictions for *C. fuckeliana*, *N. hederae*, and *N. punicea* using the AUGUSTUS web server (Hoff and Stanke 2013) using *Fusarium graminearum* gene models identified a total of 11,493, 11,966, and 13,180 genes for *C. fuckeliana*, *N. hederae*, and *N. punicea*, respectively. Gene orthology analyses using OrthoVenn (<http://www.bioinfogenome.net/OrthoVenn/>; Wang et al. 2015) showed that the predicted proteins of these fungal species formed 10,831 orthologous clusters, of which 8,543 were shared among the three species.

The Whole Genome Shotgun projects described in this paper have been deposited at DDBJ/ENA/GenBank under accession numbers QGQC000000000 (*C. fuckeliana*), QGQB000000000 (*N. hederae*), and QGQA000000000 (*N. punicea*) (BioProject ID PRJNA472761). Voucher specimens of the fungal isolates are available at the US National Fungus Collection (BPI Herbarium) in Beltsville, MD, and the Fungal Biodiversity Institute (CBS) in Utrecht, The Netherlands (Table 1).

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