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1   Resource Announcement

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3   **High quality genome of the tree pathogen *Phytophthora plurivora* - a novel resource for**

4   **epidemiological research**

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19   **Abstract**

20   *Phytophthora plurivora* can affect a range of ecologically and silviculturally important tree species,

21   including European beech (*Fagus sylvatica*), a common late successional tree species native to Europe.

22   Here, we report on the high-quality genome of *P. plurivora* strain TJ71 (CBS 124093). We sequenced it

23   using Oxford Nanopore MinION and PacBio Sequel II long-read sequencing with 80x coverage,

24   chromatin conformation capture (Hi-C) sequencing with 400x coverage and DNBSEQ 150bp paired-end

25   short reads sequencing with 200x coverage. This complex sequencing approach allowed assembly of the

26 genome at the chromosome level. Specifically, the *Phytophthora plurivora* genome resulted in 18

27 scaffolds of 47 Mbp total size with 95% completeness of the eukaryotic gene set as implemented in

28 BUSCO. This is a considerable improvement relative to the previous NCBI reference genomes *P.*

29 *plurivora* (NMPK00000000.1) with ~41 Mbp organized in 1,898 scaffolds with 93.8% eukaryotic

30 BUSCO completeness. This high quality genome provides a valuable resource for further evolutionary,

31 epidemiological and population genomic studies.

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33 **Genome Announcement**

34 A number of broadleaf tree genera are currently threatened worldwide by pathogens in the oomycete

35 genus *Phytophthora* (Goheen et al. 2009; Jung et al. 2016; Lamour 2013). European beech (*Fagus*

36 *sylvatica*) is of special concern among common forest forming tree species in Europe (Houston Durrant

37 et al. 2016). Until the beginning of this century, European beech was considered to be resistant to

38 pathogens and pests. However, we now are observing a widespread decline of juvenile as well as mature

39 trees across Europe and North America caused mainly by two *Phytophthora* species, i.e. *P. plurivora*

40 and *P. x cambivora* (Cleary et al. 2017; Jung and Burgess 2009; Jung et al. 2016; Ruffner et al. 2019).

41 These two pathogens are, however, also associated with oak (*Quercus* spp.) decline and damage to others

42 deciduous trees (Jung et al. 2006; Jung et al. 2016; Mrazkova et al. 2013).

43 Whole genome sequencing enables novel population genomic and epidemiological insights into plant

44 pathogen evolution (Grünwald 2012; Thines and Kamoun 2010). In particular, genome-wide association

45 studies and linkage mapping can identify genomic regions associated with virulence or genes responsible

46 for pathogenic success of newly emerged genotypes (Dalman et al. 2013; Talas and McDonald 2015).

47 Genome scans of regions under diversifying selection in different populations have the potential to

48 identify candidate genes previously unknown to be involved in virulence, host specialization or local

49 adaptation (Cooke et al. 2012; Grünwald et al. 2016). A crucial prerequisite for these studies is a high

50 quality reference genome of disease causing agents and their structural and functional annotation

51 (Grünwald et al. 2017; Grünwald et al. 2016). Novel, high-quality genomes of *P. plurivora* would

52 provide a keystone for further understanding of the underlying patterns leading to the emergence of

53 aggressive genotypes; this would also be of critical importance for biosecurity risk assessment and

54 management of future epidemics of soil-borne *Phytophthora* species.

55 The *P. plurivora* strain TJ71 was isolated from a diseased *Fagus sylvatica* tree in Germany (deposited

56 as CBS 124093) and was first reported in Corcobado et al. (2022). For DNA extraction, the strain was

57 grown at room temperature for one week on Standard Agar Medium (Kruse et al. 2017) supplemented

58 with the antibiotics rifampicin and pimaricin (25 µg ml^{-1} each). A double-sterilized cellophane foil was

59 placed on the agar surface of the inoculated plates. High molecular weight DNA was extracted from the

60 mycelium, which was scratched from the cellophane and immediately frozen in liquid nitrogen. The

61 modified from Francis and Clair (1993) DNA extraction procedure was used. Prior to Oxford Nanopore

62 library preparation, the samples were purified with magnetic beads (Mag-Bind TotalPure NGS, Omega

63 BIO-TEK, USA) using a 0.6x magnetic bead:DNA ratio to remove low molecular DNA fragments and

64 residual inhibitors. The DNA was used for Nanopore library construction using the SQK-LSK110 kit

65 following the manufacturer's instructions (ONT, Oxford, UK) and then sequenced on a MinION Mk1b

66 with a FLO-MIN106 flowcell (both ONT, Oxford, UK). An aliquot of the frozen DNA was sent to the

67 commercial sequencing provider BGI (Hong Kong, China) for DNBSEQ 150bp paired-end reads and for

68 PacBio Sequel II sequencing. In addition, the deep-frozen mycelium was sent to the same the commercial

69 sequencing company for library preparation and Hi-C sequencing.

70 The base calling and processing was done using Guppy version 6.0.1 (Oxford Nanopore Technologies,

71 Oxford, UK) to obtain fastq files with a Phred quality score of more than 7 and length more than 500 bp.

72 The short 150 bp paired-end reads of DNBSEQ were filtered to remove adapters, reads with an average

73 quality less than 25 and shorter than 70 bp using Trimmomatic v0.39 (Bolger et al. 2014). Long-reads

74 were self-corrected, trimmed and assembled using PacBio software Canu v2.1.1 (Koren et al. 2017)

75 separately for Nanopore, PacBio reads and a dataset combining reads from both technologies. Each of

76 the three assemblies were improved using three cycles of subsequent 150 bp paired-end reads alignment

77 using Bwa mem v0.7.17 (Li 2013) and filter for quality level of at least 40. Sorting and indexing was

78 done using Samtools v1.12 and a final assembly correction was achieved with Pilon v1.24 (Walker et al.

79 2014). The completeness and continuity of the raw assemblies was assessed using the BUSCO eukaryotic

80 genes set (Seppey et al. 2019), N50 contigs length, the number and sizes of contigs. The assembly with

81 optimal statistical characteristics was chosen for further assembly of its contigs into chromosome-level

82 scaffolds with the Hi-C reads.

83 HiCUP v0.8.3 (Wingett et al. 2015) was used for filtering and aligning Hi-C reads. Digestion sites of

84 the Hi-C enzymes (ATC, DpnII) were located in the raw assembly, and reads were cleaned by termination

85 at the restriction enzyme recognition sites. Finally, reads were mapped to the raw assembly

86 independently using Bowtie2 with default parameters (Langmead and Salzberg 2012), retaining only

87 reads with both partners of each pair uniquely mapped. Other pairs, i.e. those generated from contiguous

88 sequences, dangling ends, circularization, re-ligation, PCR duplication, and fragments of unexpected size

89 ($\leq$80 bp and $\geq$ 700 bp) were filtered out. The Hi-C alignments and raw assemblies were used for further

90 scaffolding applying the ALLHiC pipeline following Zhang et al. (2019). Apparent problematic regions

91 in the assembly were improved using the juicebox pipelines (Durand et al. 2016). The final assembly

92 was further corrected using three cycles of Pilon polishing with the 150 bp paired-end short reads. The

93 completeness of the assembled genomes were evaluated using benchmarking universal single-copy

94 orthologs (BUSCO) version 5.2.2 (Seppey et al. 2019) with the eukaryota_odb10 (70 genomes, 255

95 genes) database.

96 The BRAKER v 3.0.2 pipeline was used to predict genes (Brůna et al. 2021). The assembly was soft-

97 masked for repeats using RepeatMasker v 4.1.2-p1 (Smit et al. 2015). A custom library for masking was

98 generated by concatenating repeats found *ab initio* with RepeatModeler v 2.0.3 (Smit et al. 2015) and

99 repeats from GIRI RepBase (Bao et al. 2015) in the *Phytophthora* lineage. In addition, proteomes from

100 *Phytophthora spp.* clades 1 to 8 were downloaded from NCBI database and protein hints predicted with

101   ProtHin (Brůna et al. 2020) were supplied to BRAKER (Brůna et al. 2021). Then, genes were predicted

102   using the dataset training with GeneMark-EP+ (Brůna et al. 2020; Lomsadze et al. 2005), AUGUSTUS

103   protein predictions (Stanke et al. 2006), DIAMOND and Spaln2 alignments (Buchfink et al. 2015; Gotoh

104   et al. 2014; Iwata and Gotoh 2012). The resulting gene predictions were subset with BRAKER to three

105   structural annotations: (1) with full proteome support in the assembly, (2) partial findings of the proteins

106   and (3) *de novo* gene annotations. Final gene predictions were converted to gff3, and basic statistics were

107   generated with AGAT v1.0.0 (Dainat 2020), translated to protein files using BRAKER (Stanke et al.

108   2008). Functional annotation of the predicted genes was conducted with Interproscan v5.56-89.0 (Jones

109   et al., 2014).

110   The assembly of the *P. plurivora* genome resulted in 18 pseudo-molecules with 95% BUSCO eukaryotic

111   gene completeness (Table 1) and 22 unscaffolded contigs. Each unscaffolded contig was shorter than

112   0.12 Mbp and had no additional BUSCO genes. The analysis of 21 bp k-mer frequencies and coverage

113   distributions in 150 bp paired-end reads performed with Jellyfish (Marçais and Kingsford 2011) and

114   GenomeScope 2.0 (Ranallo-Benavidez et al. 2020) suggested that *P. plurivora* has a diploid genome

115   with an expected low heterozygosity of 0.06%, similar to other homothallic *Phytophthora* species

116   (Thines et al. 2020; Tsykun et al. 2022) with ~20% repetitive sequences. The last is congruent with the

117   results we obtained with RepeatMasker analysis for the assembled 18 scaffolds (Table 1). The number

118   of genes (12733 - 14888, Table 1) called for the assembly and annotated (Table 2) is congruent to the

119   number (11,741 genes) reported in Vetukuri et al. (2018). However, our genome is a substantial

120   improvement with respect to contiguity and completeness relative to the previously reported genome for

121   *P. plurivora*   (NMPK00000000.1) with ~41 Mbp genome size organized into 1,898 with 93.8%

122   completeness with respect to core eukaryotic genes as implemented in BUSCO (Vetukuri et al. 2018).

123   Furthermore, we achieved a near-chromosome level assembly with oomycete and plant specific

124   telomeric motifs (TTTAGGG)n or/and (TTTAGG)n (Fulnečková et al. 2013) present in both ends of 13

125   scaffolds and in one end of the other 5 scaffolds.

126   The high quality genome of the important tree pathogen *Phytophthora plurivora,* which was *de novo*

127   assembled and annotated here, will serve as a valuable resource for future discovery of virulence factors.

128   This genome provides a novel resource for understanding the recent emergence, evolution, ecology and

129   adaptation of *P. plurivora.* The raw sequencing reads and the genome assembly data are deposited in

130   NCBI BioProject the accession number PRJNA962935.

131   **Acknowledgements**

140   **Table 1.** Genome assembly statistics of *Phytophthora plurivora* strain TJ71 (CBS 124093 isolate)

Statistical characteristic	Value
Genome size in scaffolds (Mbp)	46.88
Scaffolds (counts)	18
Scaffold N50 (Mbp)	3.00
Scaffold count L50 (counts)	6
GC Content, %	51.89
Longest scaffold, Mbp	6.64

Shortest scaffold, Mbp	1.06
Number (% to total size) of unscaffolded contigs	22 (2.2 %)
Complete BUSCOs, % (counts)	94.50 (241 / 241)*
Complete and single-copy BUSCOs (S), % (counts)	92.90 (237 / 237)
Complete and duplicated BUSCOs (D), % (counts)	1.60 (4 / 4)
Fragmented BUSCOs (F), % (counts)	2.00 (5 / 5)
Missing BUSCOs (M), % (counts)	3.50 (9 / 9)
Total BUSCO groups searched (counts)	255
Predicted ploidy	2n
Heterozygosity, %	0.07
Repeats, % among them identified:	21.15
Retroelements	5.70
DNA transposons	4.81

Satellites	0.003
Simple repeats	0.57
Low complexity	0.04
Number of genes (mRNA) among them has matches in the proteome dataset used:	16619 (17321)
Partial	14880 (15484)
Full	10994 (11188)
No	1739 (1837)

141

142　* Numbers of BUSCO genes counted in scaffolds excluding and including unscaffolded contigs are

143　shown in brackets respectively.

144　**Table 2.** Functional annotation of the *P. plurivora* genes with the complete proteome dataset support

Total number of protein families / number of protein sequences	17.84 K / 130 K
Among them related to pathogenicity:	
Aspartyl proteases	9 / 26
Serine carboxypeptidases	7 / 116

Cysteine proteinases	22 / 314
Glycosyl hydrolases	94 / 975
Pectin esterases	7 / 124
Pectate lyases	5 / 110
Lipases	22 / 63
Phospholipases	37 / 180
Protease inhibitors	61 / 583
Cytochrome P450s	10 / 374
ABC transporters	27 / 796
Necrosis inducing proteins	7 / 96
Elicitin-like proteins	5 / 230
Phytotoxin (PcF) protein	1 / 2**
RXLR cytoplasmic effectors	2 / 23 (2 / 27)*
CRN cytoplasmic effectors	1 / 21 (1 / 26)*

145

146   *Functional annotation of genes that has no orthologs (no support) in the protein database used in

147   BRAKER analysis

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