Chromosomal rearrangements but no change of genes and transposable elements repertoires in an invasive forest-pathogenic fungus

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Abstract

Chromosomal rearrangements have been largely described among eukaryotes, and may have important consequences on evolution of species. High genome plasticity have been often reported in Fungi, that may explain their apparent ability to quickly adapt to new environments. *Cryphonectria parasitica*, causing the Chestnut blight disease, is an invasive fungal pathogen species associated with several recent host shifts during its successive introductions from Asia to North America and Europe. Previous cytological karyotyping and genomic studies suggested several chromosomal rearrangements which remains to be described in details for this species. A serious limitation for valid genome comparisons is the access to robust genome assemblies that usually contain genomic regions of low complexity.

We present a new de-novo whole-genome assembly obtained from a high quality DNA extraction and long-reads sequencing Nanopore technology obtained from an isolate sampled in the native Japanese area of the species. The comparison with a recently published reference genome showed no significant variations in gene and transposable elements (TEs) repertoires. We also showed that *C. parasitica* genome is lowly compartmentalized, with a poor association between TEs and some specific genes, such as those potentially involved in host interactions (i.e. genes coding for small secreted proteins or for secondary metabolites). This genome comparison, however, detected several large chromosomal rearrangements that may have important consequences in gene regulations and sexual mating in this invasive species. This study opens the way for more comparisons of high quality assembled genomes, and question the role of structural variations on the invasive success of this fungal pathogen species.

Introduction

Large structural variations of genome (i.e. translocation, insertion, deletions and inversions greater than 100kb) are more and more described in numerous organisms and may have important consequences on species adaptation (Wellenreuther et al., 2019). Filamentous microorganisms (i.e. fungi and oomycetes) have generally small genome sizes, present a large diversity of lifestyles, and many are easy to manipulate in laboratory. These general characteristics make them especially interesting to study genomic evolution in eukaryotes and molecular mechanisms involved in genetic adaptation (Raffaele and Kamoun 2012, Chang et al. 2013, Wang et al. 2020, Yadav et al. 2020). For example, fungal genomic studies have investigated gene repertory associated with specific lifestyles (e.g. Spanu et al. 2010, Duplessis et al. 2011, Riley et al. 2014), evolution of sexual chromosomes (Badouin et al. 2015), signatures of selection along the genome (Badouin et al. 2017), recombination hot-spots (Croll et al. 2015, Laurent et al. 2018), speciation or host specialization (e.g. Stukenbrock et al. 2012, Hou et al. 2014), and cryptic genetic exchanges among genetic lineages (Milgroom et al. 2014, Demené et al. 2019) or between species (Cheeseman et al. 2014, Dhillon et al. 2015). One of the major finding of these studies was the high genomic plasticity observed within and between closely related species, associated with various genetic mechanisms, such as intra- and inter-chromosomal rearrangements (Hou et al. 2014, Frantzeskakis et al. 2018, Plissonneau et al. 2016, Tsushima et al. 2019), gains or losses of genes (Yoshida et al., 2016, Hartmann et al., 2017), variation in chromosome numbers (Ma et al. 2010), or chromosome stretching (Grandaubert et al., 2014). Like single nucleotide polymorphism variations, many of these genomic structural

variations have been considered as fuel for genetic adaptation of fungal species (Raffaele and Kamoun 2012).

These studies have also lead to the development of the « two-speed genome » concept (Grandaubert et al. 2014, Dong et al. 2015) also related to the "genomic island" concept (Fedorova et al. 2008), or also called "genome compartmentalization" (Dutheil et al. 2016, Frantzeskakis et al. 2019), or genomes with "dynamic compartments" (Torres et al., 2020). The general idea behind these concepts is that genomes of many fungal pathogens are composed of two distinct compartments. One compartment, often enriched in transposable elements (TE) and poor in genes, present a high rate of structural variations, copy-number variations, genetic recombination, sequence polymorphisms or genes under strong positive selection (Wang et al. 2017, Faino et al. 2016, Laurent et al. 2018, Sánchez-Vallet et al. 2018, Eschenbrenner et al. 2020, Torres et al. 2020). A second, rich in genes and poor in TEs, is less dynamic. Genes in close physical proximity to these TEs have often been described as genes encoding proteins potentially involved in plant pathogen interactions (Raffaele and Kamoun 2012). Their proximity with TEs has been considered as an advantage for rapid diversification and adaptation to new hosts species or genotypes, because of direct (gene or promoter disruption, introduction of regulatory information) and indirect (induced mutations, ectopic rearrangement mediation, or heterochromatin formation) effects of TEs on neighbour genes (Daboussi and Capy, 2003; Seidl and Thomma, 2017). Consequently, TEs may mediate gain or loss of genes involved in virulence against host (e.g. Castanera et al. 2016, Frantzeskakis et al. 2019). However, this hypothesis has been mainly proposed for fungal pathogens infecting crops for which a need of rapid adaption is often assumed (Brown and Tellier 2011, Raffaele and Kamoun 2012). There is less evidence that this genomic architecture, as well as important variations in gene contents, may be observed in fungal plant pathogens living in more natural ecosystems, and for which selective pressure probably differs (see for example Hartmann et al. 2018). Therefore, the role of TEs in genomic adaptation remains largely debated, certainly because of the scarcity of studies comparing multiple genomes at different evolutionary timescales and lifestyles (Muszewska et al. 2019). As a matter of fact, comparisons of whole-genomes sequences have been rather limited until recently, especially due to the difficulties to assemble regions of low complexity (including TE clusters; e.g. Badouin et al. 2015, Frantzeskakis et al. 2018). The first generation of sequencing technologies (i.e. Sangers technology) are robust for assembling these regions, but their low throughput makes them costly in time, and then in money. By contrast, the second generation of sequencing technology (i.e. Illumina sequencing) has the advantage of yielding high number of short sequences although their efficiency to assemble regions of low complexity remains low, resulting usually in highly fragmented genome assemblies. The recent emergence of the third generation of sequencing technology (e.g. Oxford Nanopore Technologies or Pacific Biosciences sequencing platforms), yielding sequences of several kilobases, allows to solve these limitations (Badouin et al. 2015, Plissonneau et al. 2018). These technological advances are becoming much more accessible for large numbers of taxa, opening new perspectives to investigate the extend and the molecular mechanisms at the origin of genomic structural variations, as well as their phenotypic effects in different ecological and evolutionary contexts.

Cryphonectria parasitica is a devastating forest fungal pathogen infecting chestnut species (*Castanea* sp.) over the world (Anagnostakis 1987). The species originating from Asia has been introduced several times in North America and Europe where it caused serious outbreaks and resulted in the extinction of the mature *C. dentata* in North America (Milgroom et al. 1996, Dutech et al. 2012). The invasive success observed in the two introduced areas, as well as the associated host shifts (*C. crenata* and *C. molissima* in Asia, *C. dentata* in North America and *C. sativa* in Europe, or oaks (*Quercus sp.*) in different countries), asks the question of the adaptative processes associated to these events. For example, change in reproductive mode, a common feature of fungal invasions (Gladieux et al., 2015), has been observed between native and introduced areas (Milgroom et al. 2008, Dutech et al., 2010). It is not clear whether this reproductive shift is a cause or a

consequence of invasive success, and due to genetic incompatibilities among the introduced genetic lineages (Dutech et al. 2010). Recently, a high-quality reference genome of *C. parasitica* was obtained from the laboratory reference strain EP155, originally sampled in North-American from *C. dentata* (Crouch et al. 2020). This reference genome offers the opportunity to study genomic changes that may have occurred during the different introductions of *C. parasitica*. We previously noted that this first reference genome was, in some degrees, different from a new de-novo genome assembly obtained from a French isolate, using a long-reads sequencing technology Demené et al. 2019). This result was consistent with a previous cytological karyotyping study comparing the strain of the reference genome (EP155) with other strains sampled in North America, that suggested several chromosomal rearrangements (Eusebio-Cope et al. 2009). Overall, these results suggest that *C. parasitica* genomes can be quite different and these differences could be linked to its invasion history.

To study putative chromosomal rearrangements and other structural genomic variations (i.e. inversions, duplications, deletions, translocations) that may have occurred between a native and an introduced *C. parasitica* genome, we sequenced a whole-genome of a *C. parasitica* strain, sampled by Liu et al. (2003) in the native Japanese area, and compared the obtained de-novo assembly to the EP155 North-American reference genome (Crouch et al., 2020). The new genome sequence of this strain was produced using a strategy of different sequencing technologies, mixing the use of Oxford Nanopore Technology (ONT) and Illumina sequencing, in order to obtain a robust assembly of regions of low complexity. DNA quality being crucial in the success of ONT sequencing, we developed a new protocol of DNA extraction, yielding high quality DNA with a high molecular weight, and which was successfully applied for other fungal genome sequencing. Using such strategy, we produced a near-chromosome level assembly, which have been manually curated, of the Japanese ESM015 *C. parasitica* isolate. We compared this assembly with the recently published reference EP155 genome (Crouch et al. 2020) to estimate the importance of large structural variations between the two genomes. We produced a gene prediction on the new de-novo assembly, and a manually curated set of TEs representative of both genome assemblies. We looked for possible changes in composition or TEs and gene repertoires which may have occurred during the recent host shift between the Asian *Castanea* species and the North American *C. dentata* species, and may have contributed to the invasive success of the species.

Materials and methods

Sequenced isolate, extraction DNA protocol and sequencing

The sequenced strain ES15 (called ESM015 in this study and in Demené et al., 2009) was sampled in the Japanese Esashi population in 1998 on *Castanea crenata*, and isolated from a single asexual spore (Liu et al. 2003). For this sequencing, this monosporous isolate was multiplied again on potato dextrose agar culture as described in Hoegger et al. (2000). To obtain high quality DNA required for long run sequencing, a new protocol of DNA extraction was developed that aimed to deal with important contents in polysaccharides present in many fungal species (Möller et al., 1992). Briefly, a six-day-old cultivated mycelium (total weight: ~0.4g) was grinded using liquid nitrogen and pre-chilled mortar and pestle. Extraction solution consisted of 10 % Sodium Dodecyl Sulfate lysis buffer with 2 mg of proteinase K at 20 $mg.mL^{-1}$. Grinded mycelium was homogenized with the extraction buffer. No vortexing was applied for maximizing the chance of obtaining a high molecular weight DNA. Two steps of phenol chloroform isoamyl alcohol 25:24:1 have been performed, with an addition of RNAse A for 2% of the final volume. Four ethanol (70%) washes of the DNA pellet have been carefully made to avoid breaking DNA. In order to remove the remaining polysaccharides, a final purification step was performed: the DNA solution was brought to 1.2M NaCl solution, and polysaccharides were precipitated and isolated from DNA using a diethyl ether solution saturated with DNase-free water. The complete protocol is available in the supplementary data (Sup. Mat. 1).

DNA purification was performed using 1.0X magnetic beads (11 % polyethylen glycol), followed by DNA size selection (>1kb) and cleaning, using an optimized solid-phase reversible immobilization according to Fisher et al. (2011), and a bead mixture according to Schalamun et al. (2019). Then, 16µg of purified gDNA was sheared to approximately 40Kb using hydropore-long and megaruptor II (Diagenode, Seraing, Belgium), end-repaired, purified and size selected over 20Kb by using four lanes of a High-pass plus 0,75% agarose-gel cassette and blue pippin instrument (Sage Science, Beverly, MA, USA) and then again purified. A 1D library preparation was performed according to Oxford Nanopore technology recommendations using SQK-LSK109 sequencing kit. Sequencing was performed with a R9.4.1 Flowcell on the GridION device using MinKNOW (version 2.2), and a dedicated basecaller guppy GridION version 1.8.5.1. (Oxford Nanopore technology, Cambridge, UK), at the Genome Transcriptome Facility of Bordeaux (PGTB, University of Bordeaux, France). For increasing the quality of the genome assembly, Illumina reads of the ESM015 isolate produced in Demené et al. (2019) were added to the analysis. These reads were trimmed and filtered using prinseq v0.20.4 (http://prinseq.sourceforge.net).

Comparison of genome assemblers

To produce a high confidence de-novo assembly genome, several pipelines based on different strategies were tested: 1) Assembly of short reads previously produced for this monosporous isolate (Demené et al. 2019), followed by the mapping of long reads to close gaps of the assembly graph (HybridSPAdes using the De-Bruijn graph (DBG) algorythm; Antipov et al., 2016), 2) Assembly of long reads which have been corrected by short reads (Ra using the Overlap Layout Consensus (OLC) algorythm; https://github.com/lbcb-sci/ra), or 3) Assembly of raw long reads followed by a polishing of the assembly using the short reads (Miniasm using the OLC algorythm; Li, 2016). For HybriSPAdes, an optimized k-mer size has to be determined to close gaps, depending on the read length and depth. We tested six different K-mer values (33, 55, 77, 99, 111 and 127) and used Bandage (https://github.com/rrwick/Bandage/wiki/Effect-of-kmer-size) to identify the best k-mer value (Marijon et al., 2019). HybridSPAdes was ran on R1 and R2 paired-end reads corrected with the short read error correction step (BayesHammer; Nikolenko et al., 2013), the accurate mode on, and the Mismatch correction step. The Ra assembler was run on the complete ONT raw data, with the corrected unpaired R1 Illumina reads (having a higher quality than R2), and with basic parameters and option -x ont. For Miniasm, highly sensitive to sequencing errors, an hybrid correction step of the raw Nanopore long-reads with CoLoRMap (Haghshenas et al., 2016) has been added prior to runs. Miniasm was run on the complete set of corrected ONT reads with the parameters -ax ava-ont.

For each method, the following metrics were extracted to assess the assemblies quality: N50, L50, genome size, total number of contigs , length of the largest contig, GC content. Completeness of genome assemblies was assessed by three methods: 1- searching for the 1,315 genes from the Ascomycota database using BUSCO (Simão et al., 2015), 2- searching for the 11,609 genes annotated on the EP155 assembly version 2 (Crouch et al., 2020) using Megablast (Chen et al., 2015) and Geneious (https://www.geneious.com), and 3- mapping on each assembly the corrected paired-end reads Illumina libraries using Bowtie2 (Langmead and Salzberg, 2012) with basics parameters

Manual curation of the new reference genome

A manual curation step was done on the assembly yielding the best assembly metrics. First, a scaffolding of contigs was performed using npScarf (Cao et al., 2017), and small contigs (i.e. < 1000bp) were removed. Second, long reads were then mapped on the scaffolds using minimap2 (Li, 2018), as well as short reads using bowtie2 (Langmead and Salzberg, 2012). Reads with a map quality of zero (i.e. mapped with an equal quality on at least two locations) were removed. Read depth (Deeptools, Ramirez et al., 2016) and read quality (Samtools, Li et al., 2009) were then estimated to

detect regions with less than two mapped long reads, long reads coverage higher than twice the mean coverage of the genome, and more than five mis-paired short reads. All these regions were manually checked using the Integrative Genomics Viewer (IGV, Thorvaldsdóttir et al., 2013), and manually cut when misassemblies were detected (i.e. regions with non overlapping long reads, mis-assemblies, or with outliers for assembly metrics). When these putative chimeric regions were associated with mis-paired short-reads, the pairing information was used to reassemble the cut parts and to construct new scaffolds. Finally, we looked at each end of the scaffolds for mis-paired reads to perform an additional manual scaffolding using these informations. Three cycles of scaffolding with this manual curation were performed to obtain the final reference genome assembly. Finally, we used BUSCO v3 (Simão et al., 2015) with the Ascomycota odb9 single-copy orthologs set to re-assess genome assembly completeness. Telomeric regions were identified on the basis of -TTAGGG-repeated sequences described for fungi (Casas-Vila, 2015), and of -TTAGGGCTAGGG- and -CTAGGG- known to be specifically associated to such regions in *C. parasitica* genome (Qi, 2013). Synteny between this assembly and the EP155 reference genome was assessed using nucmer (from MUMmer4, Marçais et al., 2018). Visualisation of the synteny was done using Circa (http://omgenomics.com/). Filtering of syntenic links > 10kb or with an identity < 95% has been made using the delta-filter program from MUMmer4.

Prediction, annotation and curation of transposable elements

For the TEs detection, the REPET pipeline [https://urgi.versailles.inra.fr/Tools/REPET] was used on the curated assembly, including TEdenovo for the consensus prediction (Flutre et al., 2011, Hoede et al., 2014) and TEannot for their annotation (Quesneville et al., 2005). A manual curation step was performed on the TEs consensus library following the instructions of the REPET pipeline. Genome coverage (% of the genome covered by TEs) obtained were compared for the two TEs libraries before and after curation in order to check if no information has been lost. Transposable elements sequences without at least one full length copy (FLC) found in the genome are doubtfull because sequences used to generate its consensus has probably be catched by an other consensus during annotation. These TE consensuses were removed. Part of the TE sequences which have been inferred from only one high-scoring segment pair (HSP) were cut. Each TE identification was validated according to its repeated extremities and genes content using the Wicker's classification (Wicker et al., 2007). Two TE databases were created: TEs_db1 for ESM015, the curated one, and TEs_db2 for EP155. A final TEs data base (TEs_db3) was then created gathering the two first data bases. This data base consist of the complete Tes_db1 plus the TEs of Tes_db3 covering at least 0,05% of one of the two genomes (i.e. 22kb). TEs_db3 was then used to re-annotate both the genomes. Details of the curation of the TE annotation are given in Sup. Mat. 2. Divergence among pairs of TEs sequences annotated in the ESM015 genome was estimated by aligning them to each consensus using nucmer (Marçais et al., 2018).

In order to test whether a signal of repeat induced point mutation (RIP), an active defense mechanism against the TE replication in fungi (Selker, 1990) was present in the genome of *C. parasitica*, we first looked for the presence of AT-rich isochores in the ESM015 isolate genome, a typical feature of RIP-containing genomes (Gout et al., 2006). Second, we calculated two ratios of dinucleotides measuring the ratios of pre-RIP target and post-RIP residuals dinucleotides (i.e. (CpA+TpG)/(ApC+GpT) and TpA/ApT respectively). Transposable element sequences with a pre-RIP index lower than the baseline (estimated from the genomic sequences masked for TEs), and a post-RIP index higher than this baseline, indicate a bias in AT frequencies in agreement with a RIP mutation activity (Margolin et al., 1998, Selker 1990). We also estimated a third index we specifically designed for *C. parasitica*: CpG/GpC, measuring the depletion of the RIP on the basis of the preferential target in this species (Clutterbuck, 2011). Confidence intervals at 99.9% of the three baseline RIP indexes was estimated using a sliding window of 10kb over both masked genomes.

Genes, effectors, small-secreted proteins (SSPs) and secondary metabolites (SM) annotation, and comparison of the two genomes

Gene prediction was performed on the curated genome using BRAKER v2.1.2 pipeline (Hoff et al., 2015). This pipeline first trained AUGUSTUS software (Stanke et al., 2008) using the gene Catalog 20091217 of the reference genome EP155 (Crouch et al., 2020). Three steps with default parameters were performed: 1) EP155 proteins aligned on the ESM015 genome assembly using GenomeThreader (Gremme 2013), 2) Augustus training from the alignment file using NCBI BLAST (Altschul et al., 1990) and 3) Augustus gene prediction on the curated genome. Gene function were predicted by i) searching for protein signatures on the different InterPro databases using Interproscan V5.29-68.0 (Jones et al., 2014) in cluster mode with standard parameters and ii) by comparing protein sequences with proteins described in the manually annotated SwissProt database (assessed the 18th of November 2020) using blastp (ncbi-blast-2.10.0+). Blastp results were mapped against the Gene Ontology Annotation Database using Blast2GO V5 (Götz et al. 2008). Annotations from InterproScan and BlastP were merged and annotated using Blast2Go V5. In addition, genes encoding secreted proteins were predicted using EffectorP version 2.0 (Sperschneider et al., 2018) taking into account only predictions with a likelihood of 0.6 or higher, and using SignalP version 5.0 (Armenteros et al., 2019), keeping only predictions with a likelihood of 0.5 or higher. In order to limit the number of putative false negative, only genes predicted by the two methods were finally considered as candidate secreted effector proteins (CSEP). Secondary metabolite biosynthesis gene clusters were identified and annotated using antiSMASH fungal version web tool (antiSMASH 5.0, Blin et al., 2019).
The predicted proteins content between the previously annotated reference genome (Crouch et al. 2020) and this new reference genome have been compared using OrthoFinder v2.4.0 (Emms and Kelly 2019) using default parameters. Differences in gene content were corrected for technical biases, mainly due to predictions using different tools in Crouch et al. (2020) and this study.
The nuclear sequence of the predicted proteins showing no homologue in the other genome were searched on the other genome sequence using blastn (v2.9.0+). Using a conservative filter on these blast results, gene sequence alignments of the request starting after the start codon, aligning less than 80% in size with the target sequences, or showing alignments with nucleotide similarities < 80 % were considered as non functional.

Results

Identification of the best assembly for the ESM015 genome

Two pooled DNA extractions yield a total of 66.0 µg of double-stranded DNA (estimated in 110 µL with the Qbit) of good quality (1.87 and 1.45 for 260/280 and 260/230 ratio estimated with the ND8000 nanodrop, respectively). Nanopore sequencing (one run) produced 453,365 reads having a mean length of 9.40kb and median length of 8,72kb, N50 of 15.46kb, a mean quality of 8.0 (median 8.9), and a cumulative length of 4.26Gb (details on https://github.com/Ademene/CParasiticaGenome_scripts_and_data). Based on a 45Mb genome (Eusebio-cope *et al.* 2009, Crouch *et al.* 2020), the estimated coverage of the genome is 94.7X. The Miniasm assembler using Nanopore reads only led to an assembly size of 46.6Mb (N50 = 5.3Mb; L50 = 4), but the recovery rate for the 1,315 genes using BUSCO was only 0.5%, and only half (53.15%) of Illumina reads properly mapped on this assembly (Table 1). Adding a preliminary correction step of long reads using paired-end Illumina reads with CoLoRMap, significantly improved the results with a genome size (43.6Mb) close to the EP155 genome (43.8Mb) and a better completeness for gene contents (BUSCO genes recovery rate of 69.2%, Table 1). Using Ra, we obtained the shortest genome assembly (42.4Mb; N50 = 2.8Mb; L50 = 6), with a higher GC rate than in EP155 (51.3% and 50.8%, respectively). The completeness of this genome was high (98.6% of the BUSCO genes recovered and 94.61% Illumina reads mapped), but the de-novo assembly was more fragmented than with the Miniasm assembly (Table 1). For HybriSPAdes, we finally selected 127 as the optimized kmer size (see Table S1 for details).

Although this assembly was the most fragmented of all those produced in this study (i.e. 235 contigs, maximum length 3.2Mb and minimum length 129bp), it yielded the best result considering both the basic genome statistics (genome size of 43.4Mb close to the EP155 assembly, N50 = 1.9Mb, L50 = 9, and GC rate similar to EP155, Table 1), BUSCO analysis (recovering 98.7% of the genes of the Ascomycota database), and the alignment rate of Illumina reads (96.68%) (Table 1). This last genome assembly was chosen for the following analyses.

Detection and correction of several chimeric scaffolds through a manual curation

The scaffolding step using npScarf with long reads on the hybridSPAdes assembly allowed to obtain a new assembly with 113 scaffolds for a total length of 43.46Mb (L50=4, N50=3.66Mb). Ninety-three small scaffolds (< 10,000bp) were removed (~ 150kb total length, 47.7 % GC). Twenty chimeric regions were cut, and 15 of which have been anchored to the corresponding part using paired-end reads information. Eight new bonds were also determined between ends of the scaffolds using the paired-ends information. We identified the 148kb mitochondrial genome on the basis of a high coverage of ~ 1000X with Nanopore reads, and ~4000X with Illumina paired-end reads. In addition, one putative mitochondrial gene (680bp) was predicted on this region, and corresponds to a putative homing endonuclease usually involved in genomic DNA hydrolysis (Chevalier and Stoddard, 2001).

The final assembly after two others similar steps of scaffolding and manual curation yielded 17 scaffolds (plus the mitochondrial genome) for a total length of 43.31Mb (L50=5, N50=4,1Mb, Figure 1, Table 1). The assembled scaffolds range from 39kb (ESM_16) to 5.38Mb (ESM_2). Fourteen telomeric regions were found at the end of ten scaffolds, with four scaffolds (ESM_2, ESM_3, ESM_4 and ESM_6) having telomeric motives on both ends, suggesting entire chromosomes (Figure 1). The 18S ribosomal coding DNA sequence (rDNA ITS) has been identified on the scaffold ESM_6 between 2,312kb and 2,322kb, in a locally enriched transposable elements (TEs) region of 100kb (20 TE copies, see TE section below, Figure 1). This region was covered at 2,292X due to the tandem duplication of the element that has been assembled in a single copy. The mating-type locus (MAT1-2-1 allele, GenBank accession: AF380364.1, McGuire et al., 2001) was located at the end of the scaffold ESM_7 (Figure 1).

Compartmentalization and gene landscape of the two reference genomes

Gene prediction and annotation of the ESM015 genome assembly identified 12,015 gene models (Table S2). From these 12,015 models, 95% (n=11,461) were predicted to contain at least one protein domain on the different Interpro databases tested (Table S2), and 63% (n=7,564) show homology with a protein registered in the manually curated SwissProt database (Table S2). Gene ontology (GO) assignment based on these Interpro and SwissProt databases was successful for 64% of the total gene number (n=7,745). EffectorP identified 1,117 models with a putative signal peptide, while SignalP resulted in 1,081 genes. The intersect of both predictions yielded 88 high confidence candidate secreted effector proteins-coding genes (CSEP, Table S3). A total of 47 predicted secondary metabolite (SM) clusters, containing between 5 to 53 genes, were annotated using antiSMASH. Near half (n = 23) of these clusters were categorized in the Type 1 polyketide synthase group. Finally, 4.4% of genes (n=532) failed to be assigned to any known protein domain or to any homologous proteins of known function (Table S2).

Genes were separated by an average inter-genic distance of 1.9kb (SE = 0.034). Only few genes (n = 318) were separated by large inter-genic distances indicating a low genomic compartmentalization (Figure 2). The 88 putative CSEP had a similar inter-genic distance than the other genes (1.87 kb, SE=0.15, t-test pvalue = 0.44). Identical results were observed for both SignalP and EffectorP complete predictions (Fig. S1A and S1B). The SM clusters were located on all scaffolds, except for five small ones (ESM_11, ESM_12, ESM_15 and ESM_16), and were not preferentially located in gene sparse regions (Fig. S1C).

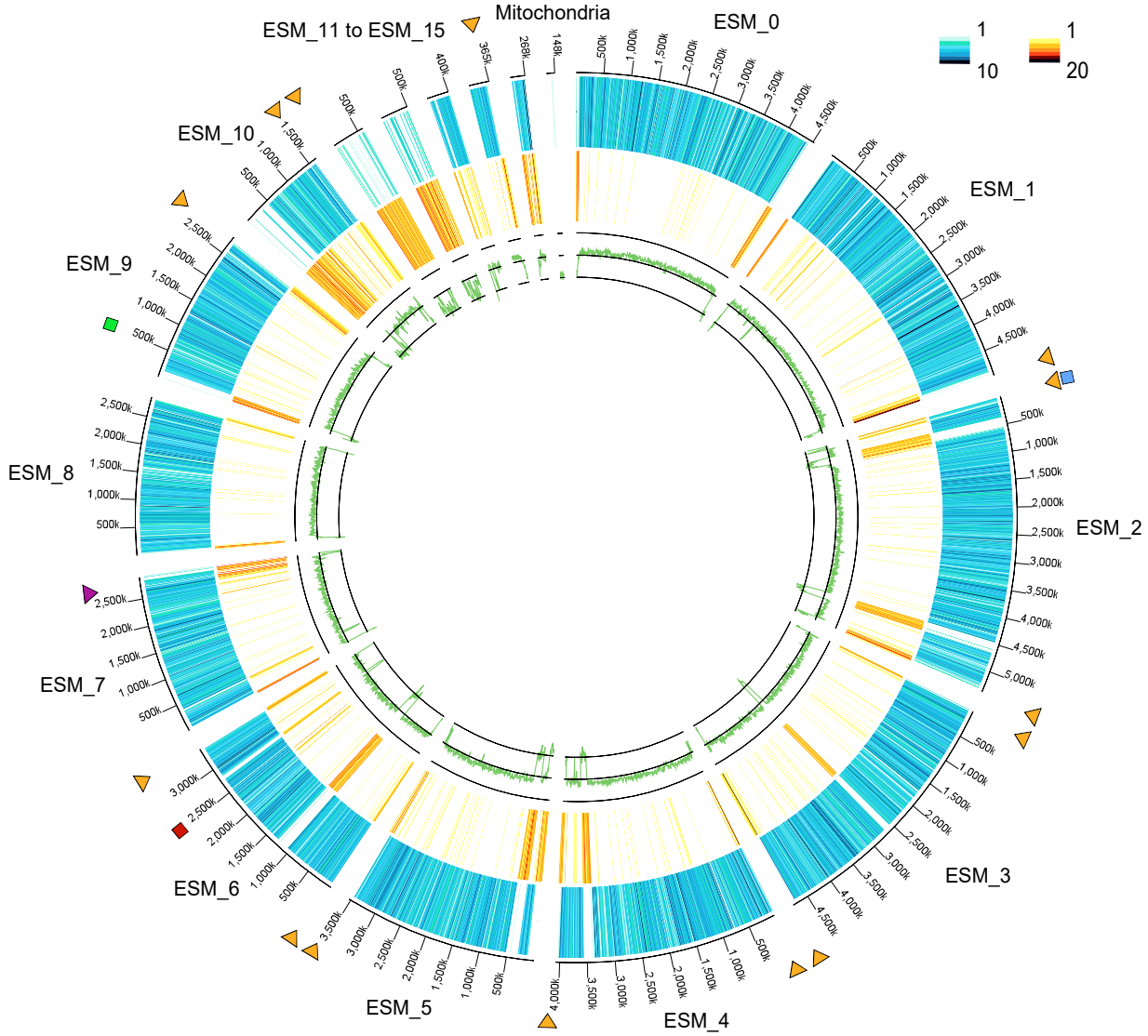

Figure 1. Circular representation of the final genome assembly of the *Cryphonectria parasitica* isolate ESM015.

First circle: ID scaffolds (M is the mitochondria scaffold), telomeric motifs (orange triangle), mating type locus (dark purple triangle), genes mapped in Eseubio-Cope et al. (2006) are nam-1 (blue square), rDNA ITS (red square) and β-tubulin (green square). Second circle: Number of predicted genes using BRAKER (Hoff et al. 2019) per 10kb. Color scale is shown in the top-right. Third circle: Number of transposables elements per 10kb. Color scale is shown in the top-right. Fourth circle: GC rate per 10kb, black lines represent 60%, 50%, and 40%.

Out of the 12,015 predicted genes, 92% (11,056) had at least one orthologous predicted in the EP155 reference genome (Crouch et al. 2020; Table S4). After querying the missing gene models of ESM015 against the EP155 genome assembly with blastn, 611 (5.1% of all genes) of them were found with 100% of identity on their full length, and 308 (2.6%) had minimum 80% of identity on at least 80% of the alignment length. Only 40 predicted genes of the ESM015 genome were considered lost in EP155, due to a high divergence (sequence similarity smaller than 80%), an alignment overlap < 80%, an absence of the start codon, or complete absence of the coding sequence (i.e. no hit: 3 genes). Considering the 348 lost or partial genes, most of them (269; 77.3 %) had not known function (i.e. no annotated GO function; Table S2). Eleven of these lost or partial genes were found in different

Table 1. Assembly statistics for the genomes of the *Cryphonectria parasitica* isolates EP155, YVO003 and ESM015.

Reference	EP155 Crouch *et al.* 2020	YVO003 Demené *et al.* 2019	ESM015 This study	ESM015 This study	ESM015 This study	ESM015 This study
Assemblers	**Arachne**	**PbcR**	**Miniasm**	**Colormap + Miniasm**	**Ra**	**HybridSPAdes**
Data type	Sanger	PacBio and IonTorrent	ONT	ONT and Illumina	ONT and Illumina	ONT and Illumina
Coverage (x)	8.54X	> 100X				
GC-count (%)	50.8	52.9	49.3	50.8	51.3	50.8
Contigs	26	35	152	21	56	235
Assembly length (bp)	43,870,411	39,261,148	46,611,147	43,615,442	42,421,489	43,409,456
N50 (bp)	5,118,729	2,722,809	5,271,534	4,798,365	2,855,323	1,873,635
L50 (#)	4	6	4	4	6	9
N90 (bp)	1,008,593	170,449	2281627	2279830	355752	364893
L90 (#)	11	26	9	9	19	33
Max length (bp)	7,437,273	4,766,472	8,751,242	7,311,149	4,428,309	3,213,437
Min length (bp)	2,579	19,618	17,429	32,202	30,899	129
Complete BUSCO (%)	98.6	98.7	0.5	69.2	98.6	98.7
Overall illumina reads Alignment rate (%)	NA	NA	53.15	87.01	94.61	96.68

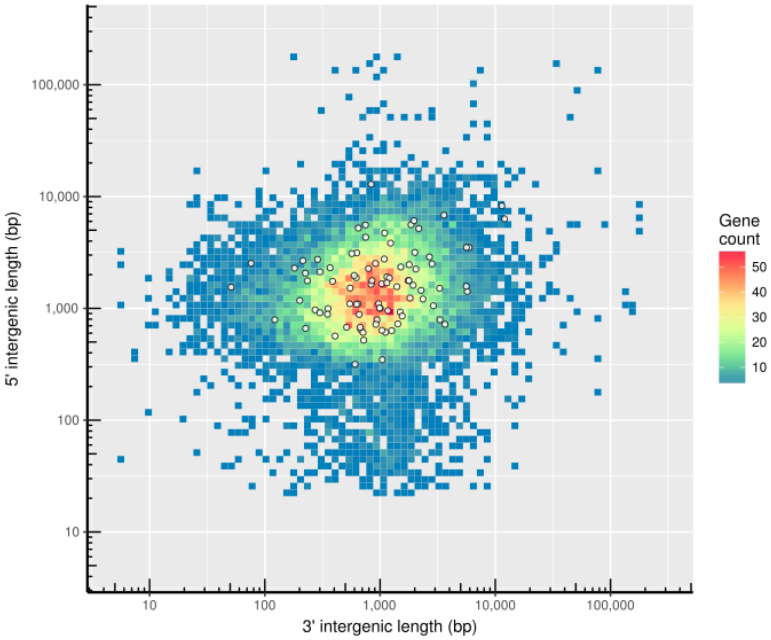

Figure 2. Estimated intergenic distances between predicted genes of the ESM15 genome. Density of genes for each pair of distances (3' and 5' intergenic distances) is given according the legend on the right. White circles are the candidate secreted effector-proteins predicted using the intersection of the predictions of EffectorP (Sperschneider et al., 2018) and SignalP (Armenteros et al. 2019).

secondary metabolites clusters, and two were predicted as CSEP. Conversely, out of the 11,609 genes predicted in EP155 (Crouch et al. 2020), 94.2 % (10,932) had at least one orthologous, 1.1 % (133) were found in the ESM015 sequence but not predicted as a gene model, and 1.0 % (123) were divergent (between 80 and less than 100% of sequence similarity), or with an incomplete overlap (between 80 and less than 100%) (Table S4). Finally, 321 (2.7%) predicted genes in EP155 were considered lost in ESM15 generally because of a missing start codon. Only 11 were considered totally absent (no hit after searching in the ESM015 genome sequence with blastn). Out of the 321 genes considered lost in ESM015, 279 (86.9%) had no annotated GO function, and nine were found in a SM cluster in EP155. Most of these lost genes were located within or close to a TE cluster (Fig. S2).

Comparison of the TE repertoire between the two genomes and identification of RIP signatures

The transposable element database, curated and representative of both ESM015 and EP155 genomes, contained 18 TEs sequences (9 RNA TEs, 7 DNA TEs, one potential host gene and one unclear RNA/DNA TE). Annotation of the ESM015 and EP155 genomes led respectively to 1,915 complete and incomplete TE copies (total length of

Table 2. Distribution of the different categories of transposable elements in the ESM015 genome assembly

	ESM015			EP155		
	N copies	Load in kb	% genome	N copies	Load in kb	% genome
Total	1915	4375	9.97	2116	4991	11.37
LTR (class I) Gypsy invader	982	2708	6.17	1099	3140	7.15
LTR (class I) COPYA	161	186	0.42	173	218	0.50
LARD (class I)	463	1269	2.89	505	1379	3.14
TIR (class II) Mariner	162	146	0.33	170	171	0.39
Crypton (class II) Crypt1	34	27	0.06	46	43	0.10
Helitron (class II)	49	13	0.03	53	12	0.03
Chimeric LTR TIR (class I / class II)	18	7	0.02	20	9	0.02
PotentialHostGene	46	18	0.04	50	19	0.04

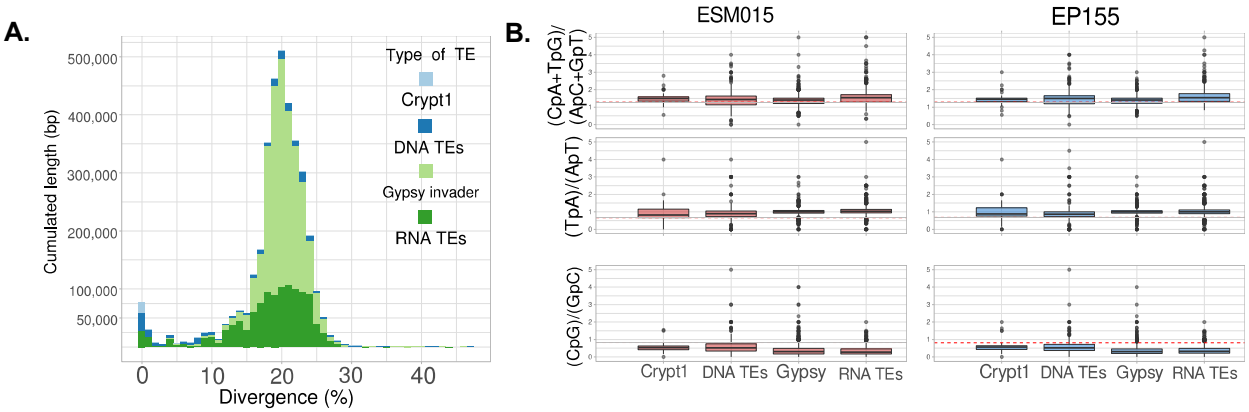

Figure 3. Transposable elements (TEs) landscape of the ESM015 and EP155 genome.

A. Nucleotidic divergence of TEs copies to their consensus, grouped by type of TEs. **B.** Inference of the signature of the repeat induced point (RIP) mutation. Three estimated indices are presented (CpA+TpG)/(ApC+GpT), TpA/ApT and CpG/GpC (see text for details). The dashed red line indicates the threshold values obtained from the non-TE-containing genomic sequences for the corresponding genome (ESM015 or EP155). Confidence intervals at 99.9% for the threshold values are indicated in grey.

715 4.37Mb, 9.97% of the genome), and 2,116 copies (total length of 4.99 Mb, 11.37%; Table 2). Class I retrotransposons were the most abundant TEs, counting respectively for 9.48% and 10.79% of each genome. Class II transposons represented 720 only 0.38% and 0.44% (Table 2). The ESM015 assembly contains an average of 4.6 TEs per 100kb (CI95%=0.82), that are not randomly distributed along the genome (number of TE per 100kb, $\chi2$=259.46, df=5, *p-value* < *2.2e-16*). Those 725 TEs were usually found clustered at the end and sometimes in central position of the scaffolds (Figure 1, Fig. S3). The most widely represented TE is a Gypsy like element (Class I), described as Metaviridae (Gypsy/Ty3 elements) in EP155 730 (Crouch et al., 2020), which contains the five protein coding domains and the long terminal repeats (LTR) sequences needed for its duplication (Wicker et al., 2007). Its cumulative genome coverage represented more than 2.7Mb (982 735 copies, 6.17% of the genome) in the ESM015 genome and 3.1Mb in the EP155 genome (1,099 copies, 7.15% of the genome, Table S5). The mating type locus, located on the scaffold ESM_7, is close to one of these regions rich in Gypsy 740 elements (Figure 1), including fifty Gypsy copies out of the 95 incomplete or complete copies (270 kb total length). The difference in copies of TEs (mainly the Gypsy element) between the two genomes was likely due to the variability found in 745 the mating-type region, sub-telomeric and telomeric regions that were all less well assembled (i.e. shorter) in the ESM015 than in the EP155 assembly. One identified Crypton DNA transposon

correspond to Crypt1, the only *C. parasitica* element that has been shown experimentally to be active (Linder-Basso et al. 2001). Five full length copies (FLC) of Crypt1 have been detected within the ESM015 genome and eight in the EP155 genome with a nucleotidic identity ranging from 95.5% to 99.8%.

Relationships between CSEP genes and TEs has been investigated in ESM015 genome. The average minimal distance between TEs and genes predicted to be effectors by EffectorP (63.16kb, SE = 2.07kb) was slightly significantly different from the mean distance of all the other predicted genes (67.36 kb, SE = 0.76kb; Wilcoxon rank test, W = 5425810, *p-value* =0.034), but not for SignalP (66.27 kb, SE = 2.23kb; Wilcoxon rank test, W = 5115078, *p-value = 0.49*) (Fig. S4). By contrast, secondary metabolites (SM) clusters were found highly significantly closer to TEs than the other predicted *C. parasitica* genes (average minimal distance 46.03kb, SE = 1.96kb; Wilcoxon rank test, W = 3657390, *p-value = 4.009e-15*, Fig. S4). Out of the 47 SM clusters predicted, ten were located inside a TE-rich region.

Most of the nucleotide sequence divergence between TE copies and their consensus sequence was estimated between 15 and 25% in the ESM015 genome (Figure 3A). We did not detect any differences between the proportions of TE families identified between the two genomes (Table 2, Table S6). The presence of several AT-rich isochores (i.e. with a GC content <50%; Fig. S5) was also identified in some regions of the ESM015 genome. For both the two genomes and the four tested groups of TEs (Crypt1; all DNA TEs, the Gypsy family and the remaining RNA TEs), the mean value of Pre-RIP index was significantly higher than the estimated baseline frequency (1.28 in both the genomes, Figure 3B), suggesting the absence of a RIP signature. By contrast, estimates of the two post-RIP indexes for the four classes of TEs were either significantly higher or lower than the two estimated baseline frequencies (0.67 and 0.82 for TpA/ApT and CpG/GpC respectively, Figure 3B), suggesting a RIP activity for both the two genomes.

Major structural variations between the two genome assemblies.

Alignment length between the two genomes was 43.34Mb, with a mean nucleotide identity of 95.1%. This pairwise alignment revealed nine major synteny breaks (i.e. genomic translocation or inversion > 100 kb; Figure 4). Out of these nine synteny breaks, six were inter-scaffold translocations involving seven scaffolds of EP155 (scaffolds 1, 2, 5, 6, 7, 10 and 11) and five for ESM015 (ESM_2, 4, 5, 7, 10) (Figure 4, details in Table S6). The three remaining intra-scaffold translocations involved one extremity of the scaffold 2 of EP155 and ESM_11 and ESM_12 of ESM015, and the scaffold 6 of EP155 versus the scaffold ESM_6 of ESM015. The two detected major translocations on the scaffold 2 of EP155 are located in a region rich in TEs of about 1.7Mb between the MAT locus and a telomeric region (Fig. S6). All the detected translocations were associated with one break per scaffold, except for the scaffolds 2 and 5 of EP155, and the scaffold ESM_2 of ESM015 with two breaks. All these rearrangements were confirmed by the visual inspection of reads mapped on the assemblies, suggesting they were not chimeric assemblies for the two genomes (Fig. S7). However, at the exception of the rearrangement between the scaffold 6 of EP155 and ESM_10 of ESM15, and associated with the two class of TEs, Crypt1 and Crypt2 (Figure 4), other chromosomal translocations were linked to regions poor in TEs and rich in predicted genes (Figure 4 and 5A). We observed that breaks are not included within homologous regions between the involved scaffolds (Figure 5A), and suggested that these chromosomal rearrangements were associated with non-homologous end-joining events. Focusing on the four synteny breaks involving ESM_2, ESM_5 and ESM_7, three events would have led to gene disruptions, for which functional prediction were a transcription factor (g3531.t1 on scaffold ESM_2), and two MFS transporter (g7138.t1 scaffold ESM_5 and g9176.t1 on scaffold ESM_7) (Figure 5B). Finally, the synteny break between the ESM_7 of ESM015 genome and the scaffolds 5 and 2 of the EP155 genome occurred in a predicted SM cluster (T1PKS) (Figure 5B), a class of polyketide synthase putatively involved in mycotoxin and phytotoxin productions (Bills and Gloer 2016).

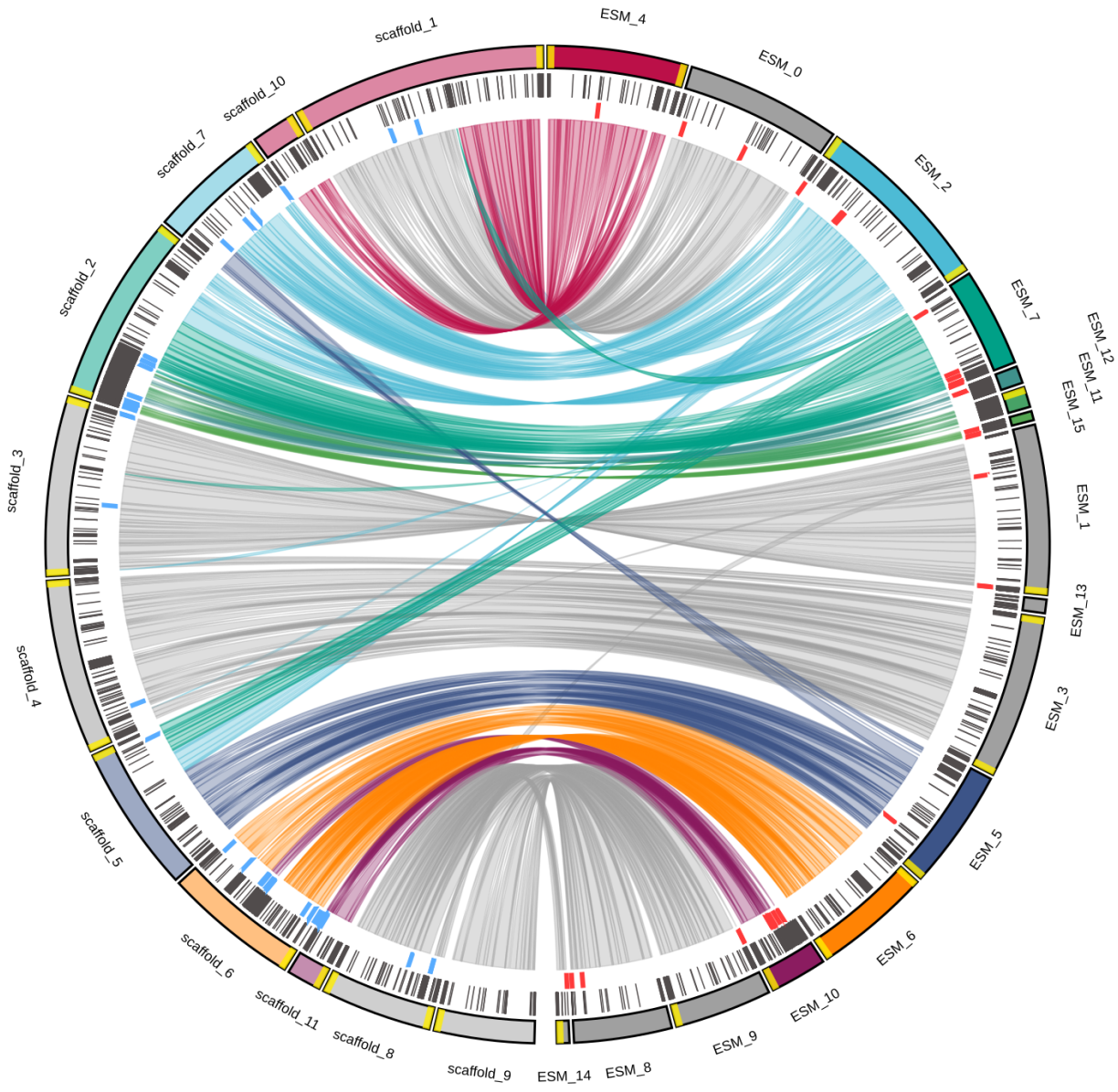

Figure 4. Syntenic relationships and genomic rearrangements between the two genomes of the Cryphonectria parasitica isolates ESM015 and EP155.

Circular representation of the syntenic relationships between the two genomes. Links are the syntenic regions higher than 10kb and with a similarity higher than (95%). Coloured scaffolds are scaffolds presenting chromosomal rearrangement between the two genomes. Yellow marks at the extremities of scaffolds are the identified telomeric motifs. Black marks on the second circle represents the density of TEs. Blue and red marks represent the location of the Crypt1 copies for EP155 and ESM015 genomes respectively.

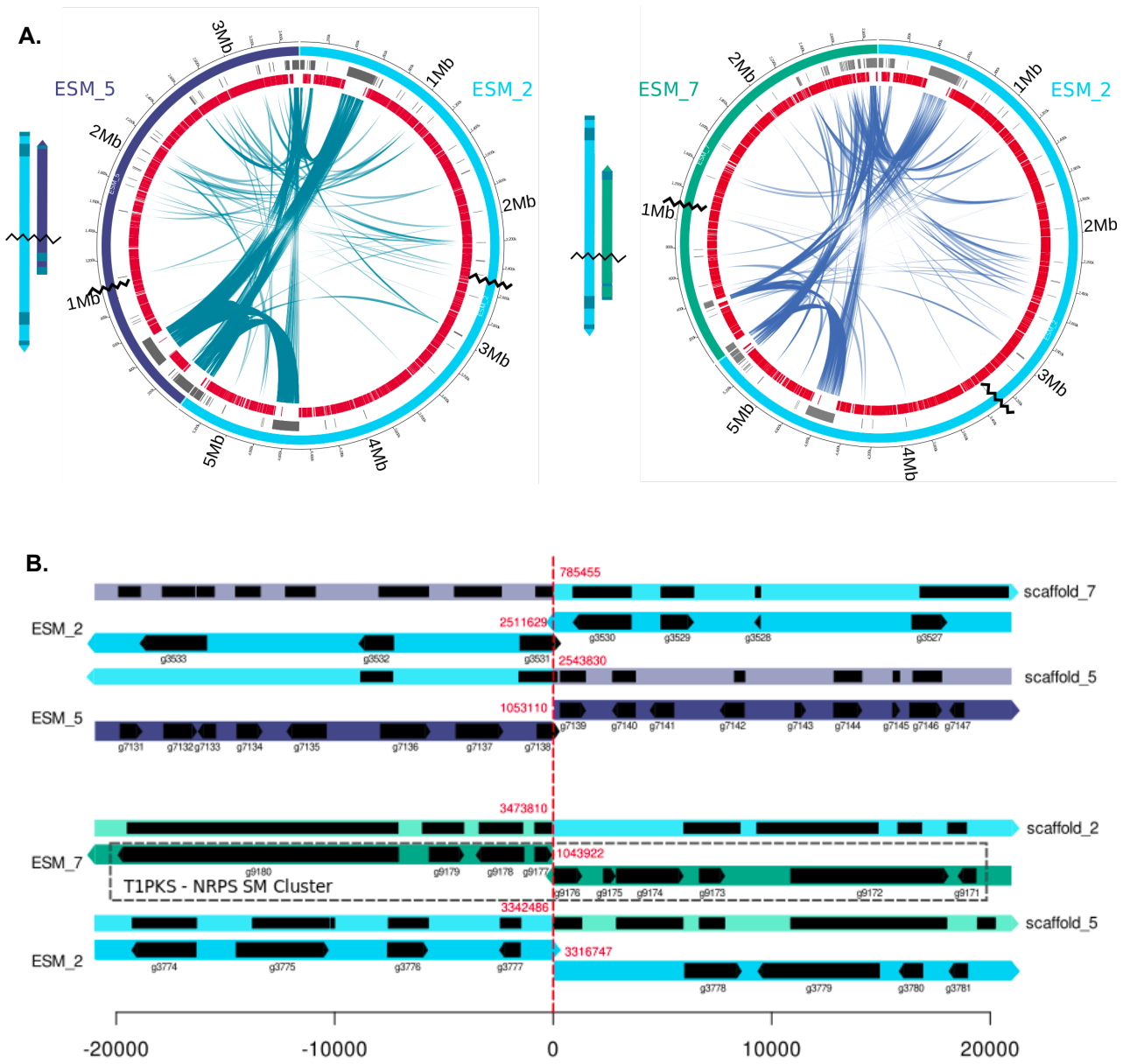

Figure 5. Zoom on the Syntenic relationships between the three scaffolds of ESM015 involved in two major inter-chromosomal translocations detected between the two genomes EP155 and ESM015.

A. Transposable elements are shown in grey and genes in red. Synteny breaks are represented by the black broken lines. All syntenic links obtained with Nucmer are shown. **B.** Schematic representation of the 40kb genomic regions around the synthenic breaks for these three syntenic breaks. Positions of the break for each scaffold are given in red, and ID of genes and their position on the scaffolds are in black. The secondary metabolite cluster T1PKS is indicated by the rectangle in dotted line on the scaffold ESM_7 of the ESM015 isolate.

Discussion

Long-reads Nanopore sequencing technology: an efficient method to obtain a near-chromosome level genome assembly in fungal species

This study confirmed that long-reads sequencing produced with Nanopore technology is well adapted to assembly small genomes such as found in fungal species, and for regions with low complexity (Rajarammohan et al. 2019). Our final assembly was close to a near-chromosome level assembly. Its total length was 43.3Mb, close to the 43.8Mb of the EP155 genome assembly (Crouch et al., 2020), and contained four putative chromosomes with both telomeric regions and six scaffolds with one telomeric region. This result is consistent with the number of chromosome and genome size estimated in a previous cytological and electrophoretic karyotyping study (i.e. 9 chromosomes and 50 Mb estimated in Eusebio-cope *et al.* 2009). The large quantity (66.0 µg) DNA obtained using the new DNA extraction protocol for fungal species was a key of this success. This protocol resulted in a DNA sample highly concentrated in double-stranded DNA, which allowed to perform several steps of purifications and size selection. Another significant advantage of this protocol is the avoidance of using heavy and time-costly methods such as centrifugation on a caesium gradient and numerous purification steps (Cheeseman et al. 2014, Demené 2019). The use of this new DNA extraction method should greatly help the assembly of new genomes at the chromosome level in other filamentous fungi.

In addition, the comparison of few methods of assembly was very useful in identifying the best strategy to obtain a near-chromosome assembly without generating chimeric scaffolds. The comparison of three methods, and the estimate of various metrics, beyond the classic L50 and N50, greatly helped to identify the less fragmented and chimeric assemblies. HybridSPAdes (Antipov et al., 2016) is a hybrid method based on de Bruijn graph algorithm (the two others used in this study were based on overlap-layout-consensus, OLC, method). Associated with the npScarf scaffolding tool, it was the most satisfactory method for assembling this genome. In addition, our study confirmed the importance of performing several steps of manual curation, and identifying possible chimeric scaffolds (Courtine et al. 2020). However, several repeated regions along the genome could still be imperfectly assembled (estimated to 0.5 Mb, little more than 1% of the genome). This result called for additional studies to better identify advantages and drawbacks of each method, according to the size, the genome content, and the sequencing technology used (Lu et al., 2016; Bayat et al., 2020).

No significant change of transposable elements and CSEP repertoire between the native and the introduced *C. parasitica* genomes

The proportion of TEs in the ESM15 genome was estimated to 10%, similar to the estimates performed on the EP155 reference genome (Crouch et al. 2020). More than two-third of TEs belong to the Gypsy family, the most abundant TE in the fungal kingdom (Muszewska et al., 2011). A high genetic divergence among most TEs sequences was estimated, suggesting ancient genomic duplications and subsequent accumulation of mutations. This high divergence could be due to an ancient burst of the main TE families which was stopped by a molecular mechanism such as RIP mutations, described in fungal species (Selker et al., 1987). Contrary to Crouch et al. (2020), we identified a signature of RIP mutation in the two *C. parasitica* genomes by comparing different dinucleotide ratio between TEs and other gene sequences. It was identified by estimating a higher TpA/ApT ratio in TEs, which is one of the products of RIP (Margolin et al., 1998). By contrast, the more classical target considered in RIP analysis (CpA + TpG / ApC + GpT; Selker, 1990) produced no robust proof of RIP signature for most TE families, as reported in Crouch et al (2020). However, the targets of RIP may differ significantly between fungal species (Ikeda et al., 2002). For example, the analysis of the Gypsy elements showed that CpG was the preferred target of the RIP mutation in *C. parasitica* (Clutterbuck, 2011). By estimating a new index (CpG/GpC), depletion of this RIP target was identified in the two reference genomes for all TE families. This supports that the RIP is active and

repressed the TEs expansion in the genomes of *C. parasitica*. In addition, regular sexual reproduction that is necessary for the occurrence of RIP mutations (Selker 1990), has been described, or inferred, several times, although at different frequencies, in native and introduced areas in *C. parasitica* (e.g. Milgroom et al. 1996, Dutech et al. 2012, Demené et al. 2019).

We also detected a slight gene compartmentalization in the *C. parasitica* genome, and, at the exception of secondary metabolites, and no clear association between genes and TEs. Transposable elements were often found clustered in telomeric and sub-telomeric regions in *C. parasitica,* as well as the secondary metabolite (SM) clusters. The coding sequences predicted to produce effectors were slightly located closer to TEs than other genes, and no particular proximity with TEs has been found for putative secreted protein coding sequences. The concept of "two-speed genome", assuming that genes involved in host-pathogen interaction like CSEPS, would be clustered together in regions having a rapid evolution due to the presence of active TEs in their neighborhood, is indeed widely debated in fungi (Frantzeskakis, 2019; Torres et al., 2020). Our analysis, more consistent with a low gene compartmentalization and no significant change in CSEP and SM repertoires, is like what has been described in another plant fungal pathogen of natural ecosystems (Hartmann et al. 2018), but also for other fungal species infecting crops (Stam et al., 2018; Schwessinger et al., 2018).

Comparison of the gene landscape between the two genomes also showed no major variation. Most of the predicted genes in one genome were present in the other one. The small number of missing genes either had unknown functions or did not have a start codon which may be due to sequencing or annotation errors. More noteworthy, we did not detect any significant changes in the SM and CSEP gene repertoires between the two genomes. This small variation in gain and loss of genes confirmed the results obtained in Stauber et al. (2020), who compared the genomes of 90 *C. parasitica* isolates sampled in both the native and invasive areas, using Illumina sequencing technology. Similar results were also obtained in *Microbotryum* sp., the causal agents of anther-smut diseases, for which the low number of gene gains and losses observed between a ten of pairs of isolates have been considered neutral or lowly deleterious (Hartmann et al. 2018). Large variations in gene repertoires, especially associated with effector gene candidates have been regularly described within fungal pathogen species or within genera infecting different host species, and considered as a signature of host specialization (e.g. Yoshida et al. 2016, Wang et al. 2020). Such a signature was not detected between the EP155 genome infecting the American chestnut (*C. dentata*), and ESM015 infecting Asian chestnuts (such as *C. mollisima* and *C. crenata*). However, molecular interactions between *C. parasitica* and the Chestnut species may be more quantitative, and/or plastic, than qualitative, involving other metabolic pathways and regulations (Lovat and Donnelly, 2019). Furthermore, the none significant variation in host-virulence observed between native and introduced strains of *C. parasitica* against the European Chestnut also suggested that no or low selective pressure has affected the virulence traits of the fungus during the European introduction (Dennert et al. 2019).

Numerous inter-chromosomal translocations with putative important consequences on sexual reproduction of *C. parasitica*

We detected six major inter-chromosomal translocations between the two genome assemblies, involving four scaffolds, and in some cases, comprising two events on the same chromosome. By contrast, a small number of large intra-chromosomal inversions and duplications were detected from this genomic comparison, except close to the mating-type region. These differences in extend between the intra- and inter-chromosomal variations were less often described in the genomic studies at the species level; chromosomal inversions, duplication or a limited translocation of genes being more abundantly described in fungi (e.g. Chuma et al. 2011, Hane et al. 2011, Raffaele and Kamoun 2012, Plissoneau et al. 2018). Inter-chromosomal translocation were however several times identified between species of the same genus (e.g. Wang et al. 2020), between isolates of mainly asexual species (De Jonge et al.

2013, Olarte et al. 2019, Tsushima et al. 2019), but also in few cases, in partially sexual species, such as *Saccharomyces cerevisiae* (Hou et al. 2014, Chang et al. 2013). This low number of reports on inter-chromosomal rearrangements may be explained by still a limited number of comparisons of genome assemblies at the near-chromosome level. We assume that the new sequencing technologies, such as those used in this study, will allow to obtain rapid and robust assemblies at the chromosome level for numerous genotypes within species, and would lead to more frequent report of such events in fungal species in a next future.

The synteny breaks were not associated with homologous regions between the involved scaffolds, especially with no cluster of repeated sequences, such as TEs, in the proximity of the breakpoints. These results suggest that these inter-chromosomal translocations were associated with random double-break strands (DBS) of the chromosomes, and led to the repair of these DNA breaks by non-homologous end-joining events. This process has been described in several Eukaryotes, and especially in fungi (e.g. Hou et al. 2014, Yadav et al. 2020). Double break strands may occur during episodic stresses, for example during some specific recombination events (Yadav et al. 2020), and have been described under laboratory conditions (e.g. Dunham et al. 2002), and also under natural conditions (e.g. Chang et al. 2013). For *C. parasitica*, we cannot identify which conditions may have led to this extensive chromosome shuffling between the native ESM015 and the introduced EP155 genome. Additional comparisons of *C. parasitica* genomes sampled in the native and the introduced areas must be performed to reconstruct the origin of these chromosomal rearrangements. Our two genome assemblies (Demené et al. 2019, this study), suggested that the North-American EP155 strain would not be the standard karyotype of *C. parasitica,* as argued in Eusebio-Cope et al. (2009). Furthermore, the identification of another karyotype in this later study (i.e. the GH2 strain sampled in Michigan) also suggested that chromosomal rearrangements would have occurred several times during the world *C. parasitica* invasion.

One of the consequences of these chromosomal rearrangements may be dramatic phenotypic changes among genotypes (e.g. Chang et al. 2013, Olarte et al. 2019). As discussed above, chromosomal rearrangements did not lead to major changes in the repertoire of genes between the two genomes. Nevertheless, the detected synteny breaks showed the disruption of three genes (one being included in a secondary metabolite cluster), and for which the phenotypic expression would be interesting to investigate. Chromosomal translocation may also change gene expression via, for example, change in DNA methylation or in proximity with some TEs (Castanera et al. 2016). The recent identification of changes in epigenetic marks between *C. parasitica* strains along the European gradient of colonization (Vukovic et al. 2019) provide more rationale for investigating the role of these mechanisms in the putative adaptation of the species to these new environments. Another important consequence of these chromosomal rearrangements is the impact on the success of sexual reproduction between these genomes, and the raise of putative pre-zygotic barriers, leading to incipient speciation (Hou et al. 2014, Yadav et al. 2020). Inter-chromosomal translocations lead to abnormal segregation of homologous chromosomes during meiosis (Kistler and Miao 1992), and possible acquisition of an incomplete repertoire of genes in the progenies of parents with different karyotypes (Yadav et al. 2020). Pre-zygotic barriers involving these rearrangements may actually explain the limited number of intermediate genotypes among the predominant genetic lineages observed in south-western Europe, and despite the regular presence of the two mating types within populations (e.g. Dutech et al. 2010). Usually, chromosomal rearrangements are strongly reduced in sexual species (Plissonneau et al. 2018). However, the specific context of introductions, associated with genetic bottleneck and new environmental conditions, and the occurrence of clonal reproduction in *C. parasitica* in introduced areas (Milgroom et al. 1992, Dutech et al. 2010) may have favoured the fixation of new genetic lineages in this invasive fungal species. With the emergence of long-reads sequencing technology, this hypothesis can be now more easily investigated in the *C. parasitica* populations, and allows us to understand the role of large structural

genomic variations in the adaptation of this invasive species.

Data availability

All bash, python and R scripts used for filtering, generating assemblies, performing the analyses and figures may be downloaded at https://github.com/Ademene/CParasiticaGenome_scripts_and_data. All supplementary figures, tables and data are available at https://github.com/Ademene/CParasiticaGenome_scripts_and_data/tree/main/Sup_Figures_and_Tables. Genes and TEs databases are available here https://github.com/Ademene/CParasiticaGenome_scripts_and_data/tree/main/Data_to_share. Raw sequence data and the ESM015 genome assembly are available on the bioproject PRJNA700518.

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Author contributions

A. D. extracted DNA, sequenced and assembled the genome, performed the data analyses and interpretation and wrote the manuscript. B. L. performed the gene content analysis and helped in data interpretation and writing the manuscript. C. D. conceived and supervised the study and wrote the manuscript. S C-A conceived the protocol of DNA extraction for long-reads, and C. B. did the DNA purifications after extraction and sequenced the genome.

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