



DATA NOTE

REVISIED Progression of the canonical reference malaria parasite genome from 2002–2019 [version 2; peer review: 3 approved]

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Abstract

Here we describe the ways in which the sequence and annotation of the *Plasmodium falciparum* reference genome has changed since its publication in 2002. As the malaria species responsible for the most deaths worldwide, the richness of annotation and accuracy of the sequence are important resources for the *P. falciparum* research community as well as the basis for interpreting the genomes of subsequently sequenced species. At the time of publication in 2002 over 60% of predicted genes had unknown functions. As of March 2019, this number has been significantly decreased to 33%. The reduction is due to the inclusion of genes that were subsequently characterised experimentally and genes with significant similarity to others with known functions. In addition, the structural annotation of genes has been significantly refined; 27% of gene structures have been changed since 2002, comprising changes in exon-intron boundaries, addition or deletion of exons and the addition or deletion of genes. The sequence has also undergone significant improvements. In addition to the correction of a large number of single-base and insertion or deletion errors, a major miss-assembly between the subtelomeres of chromosome 7 and 8 has been corrected. As the number of sequenced isolates continues to grow rapidly, a single reference genome will not be an adequate basis for interpreting intra-species sequence diversity. We therefore describe in this publication a population reference genome of *P. falciparum*, called Pfref1. This reference will enable the community to map to regions that are not present in the current assembly. *P. falciparum* 3D7 will continue to be maintained, with ongoing curation ensuring continual improvements in annotation quality.

Keywords

Plasmodium, falciparum, genome, reference, annotation, curation

Open Peer Review

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REVISED Amendments from Version 1

We would like to thank the reviewers for their helpful feedback. We have responded to the three reviewers' comments. We have made minor changes to the manuscript and improved [Figure 2](#). Gene IDs have been added on the panels. The TBLASTX matches are now shown in grey and the height of the TBLASTX matches has been shortened. All genes are shown in red.

In [Figure 3](#) the description of 2007-2010 has been corrected to "69 new".

See referee reports

Introduction

The genome of *Plasmodium falciparum* 3D7 (a clone from the NF54 ([Walliker et al., 1987](#)) isolate), the species responsible for the most severe form of malaria, was the first reference genome published to support *Plasmodium* research. Its publication more than almost two decades ago ([Gardner et al., 2002](#)) was a milestone, the impact of which is reflected in several thousand citations that mention the *P. falciparum* 3D7 genome. The sequencing of *P. falciparum* was initially accompanied by the draft genome of a rodent malaria species, *P. yoelii* ([Carlton et al., 2002](#)). These genomes were followed by those of several other *Plasmodium* spp, sequenced using Sanger sequencing technology, including human-infective species *P. vivax* ([Carlton et al., 2008](#)), the monkey and human malaria parasite *P. knowlesi* ([Pain et al., 2008](#)) and further rodent *Plasmodium* spp ([Hall et al., 2005](#)). With the advent of much cheaper short-read technology, many more genomes have been sequenced, including the chimpanzee parasite *P. reichenowi* ([Otto et al., 2014](#)), the monkey malaria parasites *P. cynomolgi* ([Tachibana et al., 2012](#)), *P. coatneyi* ([Chien et al., 2016](#)), *P. inui* and *P. fragile*, the murine parasite *P. vinkei*, the human parasites *P. malariae*, *P. ovale* ([Rutledge et al., 2017](#)) and the avian malaria parasites *P. gallinaceum* and *P. relictum* ([Böhme et al., 2018](#)). Although, many of these genomes are highly fragmented draft assemblies, algorithms that use high coverage of aligned short reads have enabled a variety of cost-effective genome-assembly improvements for several species ([Swain et al., 2012](#)).

P. falciparum 3D7 is a major focus of malaria research and the accuracy of its reference genome and annotation are vital for accelerating hypothesis-driven research. Moreover, the availability of a reference genome has additional importance: it underpins genome comparisons, across the suite of genome sequences that are now available for multiple *Plasmodium* species, and the global efforts to analyse genome variation amongst thousands of clinical and lab isolates. The need for a commitment to maintain and improve this genome has long been recognized by the Wellcome Sanger Institute. Through careful manual curation, highly accurate predictions of coding and non-coding genes have been added. Functional descriptions of genes have also been kept up to date, to reflect the growing volume of *P. falciparum* related scientific literature. In many ways the depth of annotation is similar to that more commonly associated with model organisms. For instance, Gene Ontology terms have been manually selected that capture from the

scientific literature the richness of gene roles in a format that can be easily queried or used for inference in genome-wide analyses. Recent examples include the genome-wide analysis of transcriptional dynamics ([Painter et al., 2018](#)) and the uncovering of common functions in essential genes ([Zhang et al., 2018](#)).

Genome improvement and curation has resulted in thousands of individual changes over more than 15 years. In particular, the resolution of subtelomeric regions has been transformed along with the ability to annotate important multigene families that are often found in those regions.

This is the first paper to describe the changes since the *P. falciparum* 3D7 genome was first published. Originally 5,268 protein-coding genes were annotated and of those, over 60% (3,465 genes) of predicted genes had unknown functions ([Table 1](#)). Despite the fact that there still seems to be a common perception that over 50% of genes remain functionally unannotated ([Briquet et al., 2018](#); [Tang et al., 2019](#)) the number of predicted genes has risen to 5,438 and the proportion without ascribed functions has now shrunk to 33% (1,776 genes) ([Table 1](#)). Since 2002, 27% of genes have undergone structural changes or have been added based on RNAseq data and other data from publications. New ncRNAs have also been added and complete apicoplast and mitochondrial genomes have been assembled. One of the many purposes of a reference genome is to interpret natural variation data. In the latest version, we have therefore included alternative contigs representing major haplotypic differences. This reference dataset has been named Pfref1 to reflect the fact that it does not simply comprise *P. falciparum* 3D7 data but has been supplemented with other reference data to better represent the pan-genome for this species. The aim of Pfref1 is to enable robust mapping to analyse genome variation in regions of *Plasmodium* genomes where the current Pf3D7 genome (v3.2) is an unsuitable reference.

Methods

Curation and annotation

Changes to the genome annotation reflect ongoing work at the Wellcome Sanger Institute. The software [Artemis](#) (version 10 to version 18) was adapted to use a [CHADO](#) database schema ([Carver et al., 2008](#)) and has been used continuously for manual curation and annotation. This database system is directly connected to [GeneDB](#). Every 4 to 6 months data is transferred to [PlasmoDB](#). To update functional annotation, Pubmed was searched (search terms *Plasmodium* and apicomplexa) on a regular basis for publications related to *Plasmodium*. Relevant information, i.e. gene product descriptions, EC numbers, gene names and functional descriptions to be captured by Gene Ontology terms, was extracted and changes manually added in Artemis. RNA-Seq data and TBLASTX comparisons were the primary supporting evidence for manual improvements to gene models. Information from user comments that were submitted to gene record pages in PlasmoDB were assessed and where relevant used to update annotation. Evidence codes that support product descriptions are available as GFF format genome annotation files from the following FTP site: <ftp://ftp.sanger.ac.uk/pub/gedb/releases/latest/Pfalciparum/>. To find annotation differences

Table 1. Table showing the main differences between *P. falciparum* 3D7 version 1 (2002), version 2 (2005), version 2.1.4 (2007) and version 3.2 (March 2019). *Numbers includes partial genes, pseudogenes are not included. ** Nucleotide ambiguities present in genome v1 and v2 have been changed to gaps. ***Pseudogenes defined here are based on gene predictions that contain at least one frame shift or premature stop codon.

	2002 (version 1)	2005 (version 2)	2007 (version 2.1.4)	2019 (version 3.2)
Nuclear genome				
Genome size (bp)	22,853,764	23,289,065	23,264,337	23,292,622
Gaps	93	10	160**	0
Genes*	5268	5414	5387	5280
Pseudogenes***	NA	70	73	158
ncRNAs	0	0	606	103
Hypothetical proteins	3465	3545	3099	1776
tRNAs	43	27	44	45
Apicoplast genome				
Assembly size (kb)	Absent	Absent	Absent	34250
genes	Absent	Absent	Absent	30
Mitochondrial genome				
Assembly size	Absent	Absent	Absent	5967
genes	Absent	Absent	Absent	3

between genome versions we've performed pair-wise TBLASTX comparisons using the [Artemis Comparison Tool \(ACT\)](#) (version 13) ([Carver et al., 2005](#)).

DNA sequencing and correction of the *P. falciparum* 3D7 genome

After publication of the genome in 2002, manual finishing continued. Sequence changes and gap closure between genome versions 1 and 2 have been described ([Berry et al., 2004](#)). Using a combination of capillary sequencing, Illumina sequencing, Pacific Biosciences sequencing and automated sequence correction, we have continued to improve the reference genome. Sequence errors on all chromosomes were corrected using the [iCORN algorithm](#) (version 1) ([Otto et al., 2010a](#)). Two ambiguous regions towards the telomeres of chromosomes 7 and chromosome 8 were resolved using a PCR tiling path. The tiling path spanned the region between genes PF3D7_0805400 (MAL8P1.200) to PF3D7_0831200 (MAL8P1.204) on chromosome 8 and from PF3D7_0833500 (MAL7P1.212) to PF3D7_0701900 (PF07_0004) on chromosome 7. From the results of these the assembly of the left hand side of chromosome 8 was confirmed. There was a gap in chromosome 7 over a highly repetitive region of ~20kb. Read pair information from a 3kb insert Illumina library was used to identify unassembled contigs that could close the gap and PCR was used to confirm the assembly. Unassembled contigs were also searched for any unique coding sequence. One contig was found and this was linked to a region on the right hand side of chromosome 8 by Illumina read pairs. This was also confirmed by PCR. For genome version 3.1, the complete apicoplast was included. Resolving this sequence has been described ([Hunt et al., 2015](#)). For genome version 3.2, the *P. falciparum* 3D7 mitochondrion was also included. This mitochondrion was part of a recently described PacBio assembly of *P. falciparum* 3D7 ([Otto et al., 2018](#)).

The mitochondrion was corrected using the [iCORN algorithm](#) ([Otto et al., 2010a](#)) followed by [circlator](#) ([Hunt et al., 2015](#)).

PfRef1 reference genome

The *P. falciparum* 3D7 version 3.2 assembly was compared with PacBio assemblies that we have recently described for several other isolates ([Otto et al., 2018](#)) to create a population reference that we have termed PfRef1. BLASTN comparisons of 3 lab isolates (*P. falciparum* IT, *P. falciparum* DD2, *P. falciparum* HB3) were inspected together using ACT software ([Carver et al., 2005](#)). Excluding single nucleotide polymorphisms and small insertions and deletions, major sequence differences were identified, manually extracted and are provided as small EMBL files. Each file contains a sequence variant with a 500 bp anchor sequence on either side to enable unambiguous placement along the 3D7 reference. The files are available on the following FTP site: <ftp://ftp.sanger.ac.uk/pub/project/pathogens/Plasmodium/falciparum/PfRef1>

Results

Improvement of the *P. falciparum* 3D7 assembly

An update to the published version of the *P. falciparum* 3D7 genome was released in 2005 (version 2), this included gap closure and completion of many chromosomes from telomere to telomere ([Table 1](#)) ([Berry et al., 2004](#)). In September 2011, version 3 of the genome was released that included the correction of two major miss-assemblies on chromosome 7 and 8, the replacement of all "N"s in the genome with corrected sequence and the correction of hundreds of sequencing errors. These improvements were brought about largely due to the availability of Illumina technology and the development of a genome correction algorithm ([Otto et al., 2010a](#)). In addition, gene locus identifiers were changed to bring them into line with guidelines published by the European Nucleotide Archive

(ENA): systematic identifiers were changed to start with the prefix PF3D7 followed by an underscore and the chromosome number. All previous identifiers were retained as searchable synonyms.

Version 3.1 included a complete apicoplast genome with a length of 34 kb. In the original genome project that was published in 2002 the *P. falciparum* 3D7 apicoplast was not sequenced. For the re-annotation process the apicoplast from *P. falciparum* isolate C10 was temporarily used (Genbank X95275.2, X95276.2) (Wilson *et al.*, 1996) and included in genome version 2.1.4. The published apicoplast from isolate C10 consisted of two large contigs that could not be assembled due to a large deletion caused by an almost identical inverted repeat. As previously reported (Hunt *et al.*, 2015), version 3.1 of the genome includes a complete apicoplast genome that includes the resolved 5kb repeat.

For the reannotation process the mitochondrial genome with Genbank ID M76611 was included. This Genbank entry only reports the source as *P. falciparum*. Our recently described *P. falciparum* 3D7 PacBio assembly (Otto *et al.*, 2018) contained a mitochondrial genome. Comparing this PacBio genome with M76611 revealed a difference of two bases: a SNP at base 772 (T to C) and at base 4952 (C to T). The SNP at base 772 is non-synonymous and results in an isoleucine to valine substitution in COX3 (PF3D7_MIT01400) at amino acid 250. The genome version with the correct mitochondrial genome has been named version 3.2.

Manual annotation of *P. falciparum* 3D7

At the start of the *P. falciparum* 3D7 genome project manual gene finding was heavily reliant on sequence composition, especially GC content differences, due to an absence of alignable evidence. Over time additional *Plasmodium* genomes became available, in 2005 the rodent malaria genomes (Hall *et al.*, 2005) and in 2008 *P. knowlesi* (Pain *et al.*, 2008) and *P. vivax* (Carlton *et al.*, 2008). Having these additional *Plasmodium* genomes enabled gene structures to be revisited. A comprehensive reannotation process began with a workshop in 2007, involving approximately 40 members of the *Plasmodium* research community (see Box 1). One of the goals of the workshop was to ascribe updated functions to predicted proteins, check gene structures and systematically revisit the nomenclature for large gene families. A major new addition to the evidence was genome wide TBLASTX comparisons between species that were used to highlight conserved regions at the protein level and therefore identify positionally conserved orthologues and refine their exon-intron boundaries. In 2010, we published the first RNA-Seq data for this species (Otto *et al.*, 2010b). These data were used to further evaluate gene models and improve the accuracy of gene structures. As a result, 27% of genes have been added or had their structure changed since 2002 (Figure 1). 1255 genes had changes to exon-intron boundaries or exons added or removed (Figure 2A); this number include genes that were merged (Figure 2B) or split (Figure 2C). Since 2002, 244 genes have been added (Figure 2D, Extended data: Table 1 (Böhme, 2019)) and 36 predicted genes have been deleted

Box 1. *Plasmodium falciparum* community reannotation workshop

A *Plasmodium falciparum* community reannotation workshop, co-organised by EuPathDB (David Roos) and GeneDB (Matthew Berriman) took place at the Wellcome Genome Campus Conference Center in Hinxton in October 2007. During this week-long workshop several hundred gene products were changed, including the annotation of ApiAP2 proteins.

Workshop participants:

Oliver Billker, Serge Bonnefoy, Pete Bull, Jane Carlton, Brendan Crabb, Hernando Del Portillo, Christian Doerig, Malcolm Gardner, Hagai Ginsburg, George Githinji, Aravind Iyer, Taco Kooij, Dominic Kwiatkowski, Sue Kyes, Thomas Lavstsen, Manuel Llinás, Eric Marechal, Dan Milner, Fingani Mphande, Dan Neafsey, Stuart Ralph, Gowthaman Ramasamy, Dhanasekaran Shanmugam, Robert Sinden, Worachart Sirawaraporn, Dominique Soldati, Tim Stedman, Xin-zhuan Su, Tom Templeton, Akhil Vaidya, Scott Westenberger and Jennifer Wortman.

Facilitators during the workshop included:

Andrew Berry, Céline Carret, Al Ivens, Arnab Pain, Adrian Tivey, Brian Brunk, Zhongqiang Chen, Mark Heiges and Lucia Peixoto.

Maintenance and setup of the Artemis Chado instance:

Tim Carver, Adrian Tivey, Chinmay Patel and Robin Houston.

due to a lack of evidence supporting their earlier prediction in regions of repetitive or unusual sequence, or because later RNAseq evidence (including strand-specific information) suggested that they were ncRNAs rather than protein-coding (Figure 2E, Extended data: Table 2 (Böhme, 2019)). In addition, a number of genes were created after 2002 based on algorithmic predictions but subsequently deleted due to a lack of supporting evidence (Extended data: Table 3 (Böhme, 2019)). Figure 3 shows the number of changes to predicted gene structures, as well as the addition and deletion of new genes at four different time points.

New non-coding RNAs have been annotated based on transcriptome data, examples published in the scientific literature (Chakrabarti *et al.*, 2007; Guizetti *et al.*, 2016; Raabe *et al.*, 2010) and new predictive models in Rfam (Kalvari *et al.*, 2018). In 2007, 603 automatically predicted ncRNAs were included in the annotation (Table 1) (Mourier *et al.*, 2008). Since 2002 the amount of aligned functional genomics data has increased enormously for this species providing deeper evidence support for most genuine transcripts. However, due to a lack of supporting evidence, the majority of previously predicted ncRNAs were subsequently removed from the reference annotation. Currently there are 103 ncRNAs annotated (Extended data: Table 2 (Böhme, 2019)), including a recently described spliced antisense ncRNA that acts as a negative regulator (PF3D7_0935390), (Filarsky *et al.*, 2018).

Using a combination of manual and automated methods, functional annotation has been radically improved since the initial publication in 2002. Revised annotation is based on a combination of literature searching, comments received from the research community, InterPro (Jones *et al.*, 2014) and



Figure 1. Distribution of genes with structural changes and new genes on chromosomes 1 to 14 of *P. falciparum* 3D7. The positions of new genes (shown in red), genes that have undergone structural changes (shown in blue) and genes that stayed the same since 2002 (shown in grey) are shown on the 14 chromosomes. The values along the right of each chromosome indicate the total sequence length in base pairs. Genes above the chromosome lines are located on the forward strand, genes below the chromosome lines are on the reverse strand.

sequence-similarity searches. Using these approaches the number of proteins with unknown function has almost halved, from 60% in 2002 to 33% in March 2019 (Figure 4). The number of experimentally verified genes has changed from 597 genes in 2002 to 1296 in 2019 and the number of genes with putative functions has risen from 1215 to 2206. The richness of the annotation is reflected in the number of Gene Ontology (GO) terms (Ashburner *et al.*, 2000; The Gene Ontology Consortium, 2017) that have been manually assigned to genes based on published experiments, reflected in the following evidence codes: Inferred from direct assay (IDA), physical interaction (IPI), mutant phenotype (IMP) and genetic interaction (IGI). Altogether there are 1302 genes annotated using GO and supported by experimental evidence: 1095 genes captured by the

“component” aspect of GO; 609 captured by “molecular function” and 369 genes captured by “biological process”. Because individual genes have been annotated with multiple terms, the number of individually curated and experimentally verified GO terms is much higher. There are 1867 GO components annotated, 979 GO functions and 857 GO processes. The manual GO annotation also includes 342 protein binding interactions (Table 2). Annotation is updated continuously as new literature is published.

Throughout the annotation improvement process, engagement of the malaria research community has played an important role. The process started with the workshop in 2007 (Box 1) but has continued through the activities of a dedicated full time

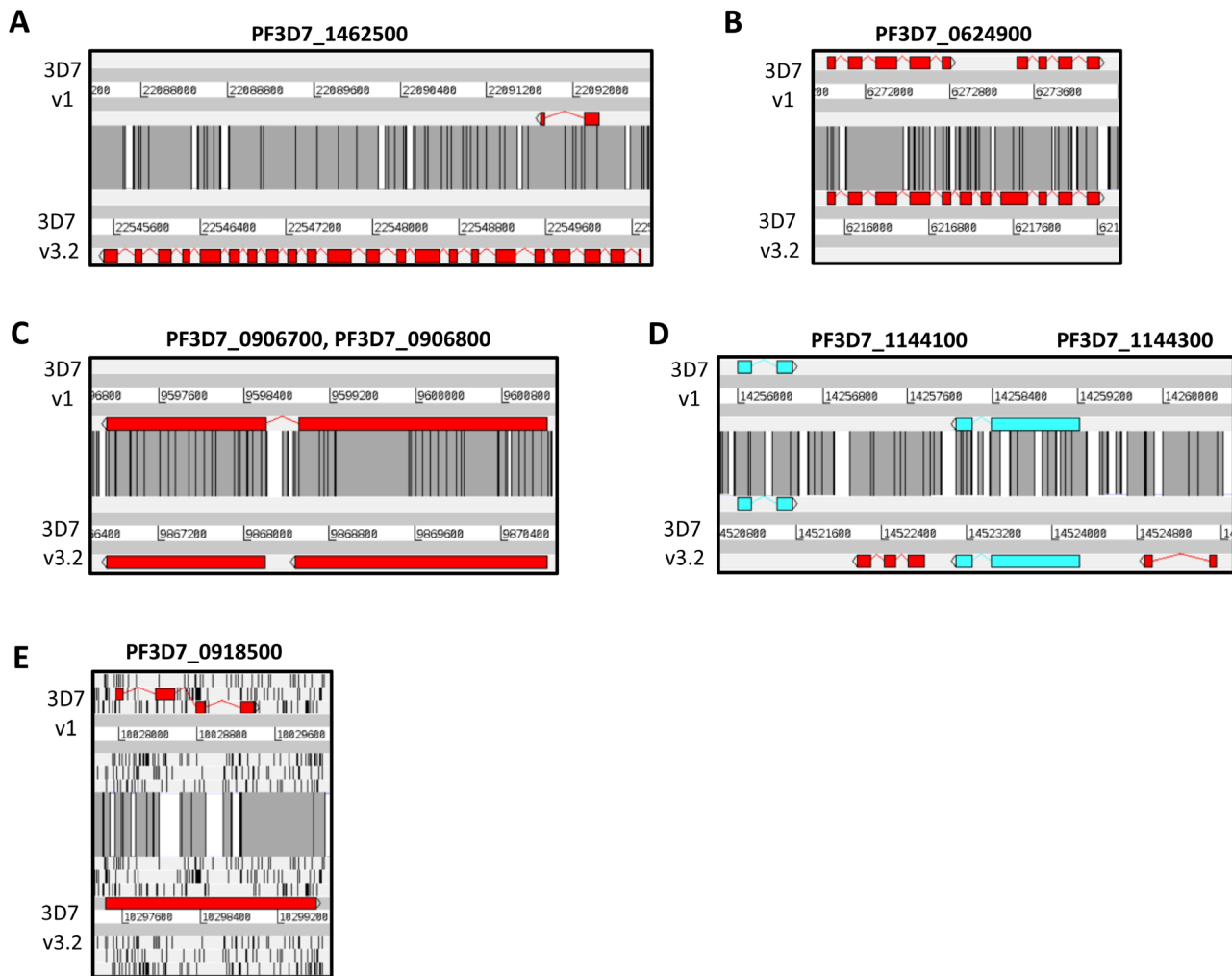


Figure 2. Gene structure changes. Artemis Comparison Tool (ACT) screenshot showing a comparison between 2002 and 2019. Coloured boxes represent genes. The grey blocks between sequences represent sequence similarity (TBLASTX). **(A)** A 2-exon gene has been changed into a 22-exon gene (PF3D7_1462500) **(B)** Two genes that have been merged (PF3D7_0624900) **(C)** A gene that has been split into two genes (PF3D7_0906800, PF3D7_0906700) **(D)** Two genes shown in red have been added (PF3D7_1144100, mitochondrial large subunit ribosomal protein; PF3D7_1144300, 60S ribosomal protein L41) **(E)** A hypothetical gene (PFI0905w) has been deleted and a ncRNA (PF3D7_0918500, telomerase RNA) has been added. In (E), the six reading frames are shown with tick marks indicating stop codons.

curator aided by direct feedback and through comments that can be added by the community to gene record pages at [PlasmoDB](#). These comments are constantly being evaluated and incorporated where relevant. The ongoing annotation is physically housed at the Sanger Institute, with updates regularly passed on to PlasmoDB (every 4 to 6 months).

Population reference genome Pfref1

One of the many purposes of a reference is to interpret natural variation data, the aim being to enable robust mapping of re-sequencing reads from subsequent isolates. In the latest version we have incorporated sequence differences derived from 3 lab isolates assembled *de novo* as part of a collection of 15 PacBio reference genomes (Otto *et al.*, 2018). The differences have been

incorporated into the reference as three classes (Figure 5). The first (type-1) are “patches” to correct errors in Pf3D7 (version 3.2), for example a missing centromere on chromosome 10 and a missing gene on chromosome 13 (Figure 5, Figure 6A), the second (type-2) are core genes that are present in other sequenced isolates, i.e. *P. falciparum* IT or *P. falciparum* DD2 but are missing in Pf3D7 (Figure 5, Figure 6B) and the third (type-3) are dimorphic genes where alternative alleles cannot be mapped to the one currently present in Pf3D7 (Figure 5, Figure 6C, Figure 6D). In total, there are now 17 type-1, four type-2 and 17 type-3 patches. The type-2 patches include genes encoding gamete associated protein (GAP), CLAG and hypothetical proteins. Type-3 include dimorphic genes encoding DBL-containing protein (PF3D7_0113800), Surfin 1.2, Surfin 8.3, Surfin 13.1, Surfin 14.1, MSP1,

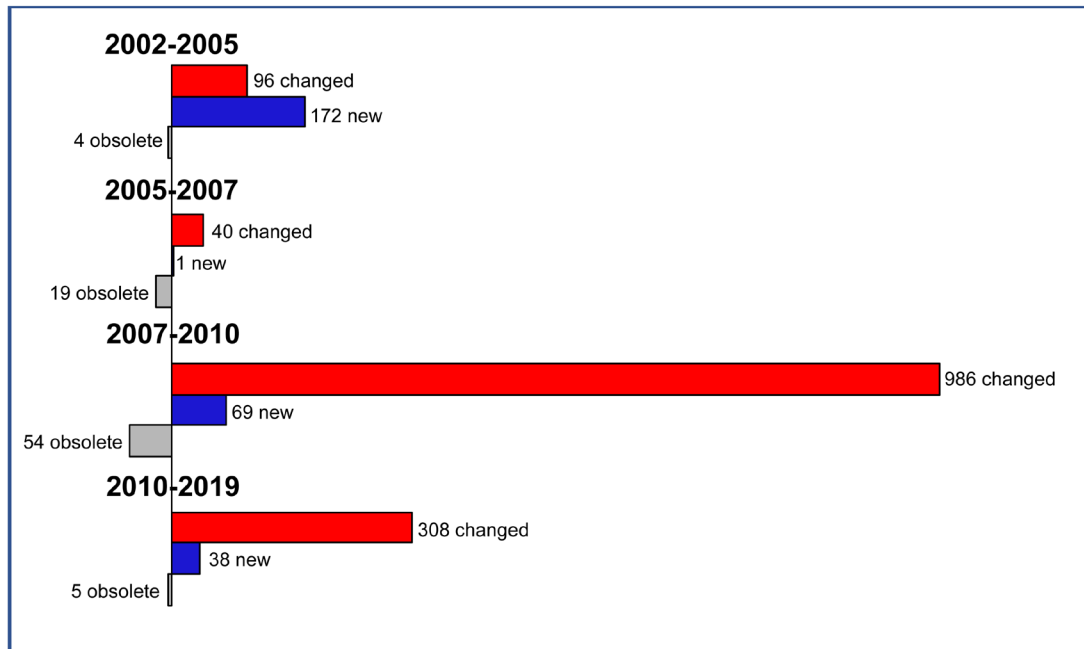


Figure 3. Diagram showing gene structure changes. Number of genes that have been added, deleted or changed are shown over four different time frames: October 2002 (genome version 1) and 2005 (genome version 2), between 2005 (version 2) and September 2007 (version 2.1.4), between September 2007 (genome version 2.1.4) and February 2010 (version 2.1.4) and between February 2010 and March 2019 (version 3.2). The number of changed genes includes gene models that have been merged, split or had a deletion/addition of exons or change of exon boundaries.

	Unknown function	Experimental evidence	Putative function	No. of genes
2002 (version 1)	3458	597	1215	5268
2005 (version 2)	3545	581	1258	5484
2007 (version 2.1.4)	3099	672	1552	5460
2009 (version 2.1.4)	2581	764	1939	5432
2010 (version 2.1.4)	2514	899	1885	5426
2011 (version 2.1.4)	2491	920	1887	5429
2012 (version 3)	2414	963	1887	5419
2013 (version 3)	2304	1013	1942	5418
2014 (version 3)	2222	1084	1956	5417
2015 (version 3)	2172	1164	1958	5421
2019 (version 3.2)	1776	1296	2209	5438

Figure 4. *P. falciparum* 3D7 annotation changes between October 2002 and March 2019. The number of genes between October 2002 and March 2019 are compared. The total number of genes includes pseudogenes. The number of genes with unknown function is shown (blue), genes with experimental evidence (red), genes with putative function (yellow) and the complete number of genes (light blue). Genes with unknown function have the following product description: conserved Plasmodium protein, unknown function; conserved protein, unknown function; conserved Plasmodium membrane protein, unknown function; Plasmodium exported protein, unknown function; probable protein, unknown function; hypothetical protein.

Table 2. Gene Ontology (GO) annotation of *P. falciparum* 3D7 (version 3.1, 14.02.2019).

The number of manually curated experimentally verified GO terms, manually curated terms that are based on sequence similarity and GO terms based on automated searches are listed (Ashburner *et al.*, 2000; The Gene Ontology Consortium, 2017). IDA, inferred from direct assay; IPI, inferred from physical interaction; IMP, inferred from mutant phenotype; IGI, inferred from genetic interaction; HAD, inferred from high throughput direct assay; ISS, inferred from sequence or structural similarity; ISO, inferred from sequence orthology; ISM, inferred from sequence model; RCA, Reviewed computation analysis; IEA, inferred from electronic annotation. The IEA evidence code is either based on InterPro (Jones *et al.*, 2014) or based on Chitale *et al.*, 2009 (Chitale *et al.*, 2009). The GO annotation for 2002 was taken from (Gardner *et al.*, 2002).

Gene Ontology	Number of GO annotations (2019)	Number of GO annotations (2002)
Cellular Component	6437	2,412
Experimental evidence code: IDA, IPI, IMP, IGI	1,867	
Evidence code based on sequence similarity: ISS, ISO, ISM	1,187	
Evidence code: RCA	175	
Evidence code: HDA	962	
Evidence code: IEA (InterPro)	719	
Evidence code: IEA (PMID:19435743)	1527	
Molecular Function	4,921	1,244
Experimental evidence code: IDA, IPI, IMP, IGI	979	
Evidence code based on sequence similarity: ISS, ISO, ISM	1,111	
Evidence code: IEA (InterPro)	1,732	
Evidence code: IEA (PMID:19435743)	1,099	
Biological Process	3,803	1,301
Experimental evidence code: IDA, IMP, IGI	857	
Evidence code based on sequence similarity: ISS, ISO, ISM	1,270	
Evidence code: IEA (InterPro)	1,117	
Evidence code: IEA (PMID:19435743)	559	

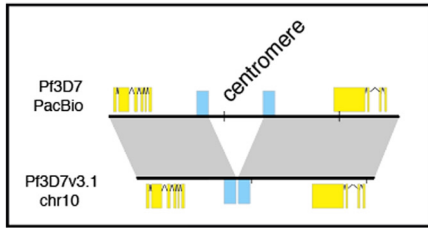
MSP2, MSP3, MSP6, S-antigen, EBA175, CLAG3.1, CLAG3.2, DBLMSP, DBLMSP2, CSP and VAR1CSA. For the new population reference, EMBL files containing the different types of patches including a 500 bp alignment on each side of the patch are provided. To reflect the fact that changes to 3D7 as well as data from other isolates have been included, we have termed the new reference sequence Pfref1.

Discussion

In this paper we have provided an overview of the sequence and annotation changes the *P. falciparum* 3D7 genome has undergone since the initial publication in 2002. The inclusion of long-read sequencing has been critically important for spanning gaps that persisted for years in the reference assembly due to their extreme AT-richness and length. A previous attempt to produce an improved *P. falciparum* 3D7 reference assembly used Pacific Biosciences sequencing data assembled *de novo*

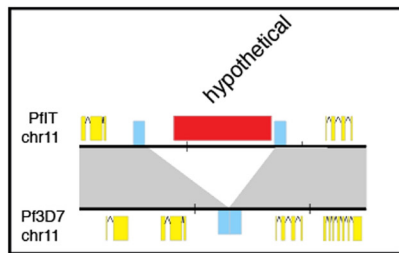
(Vembar *et al.*, 2016). Although the assembly contiguity metrics were impressive, the authors did not attempt error-correction. As a consequence, a high proportion of gene sequences contained frameshifts and there were many unresolved repetitive sequences. In the present study, we have used automated error-correction assisted by a high coverage of aligned short reads, plus extensive manual review of individual read alignments. This has enabled us to drive the accuracy of underlying reference sequence, bringing a range of benefits. First, end users interested in individual genes have access to the most up to date information. Second, users interested in high throughput functional genomics or genome variation need the most up to date and complete sequence for mapping purposes to be available and used by all labs. Third, detailed curation in *P. falciparum* has a knock on effect across other important species of the genus because functional insights from one species can be projected to others based on homology. It is

Type 1 (sequence differences in Pf3D7 PacBio)

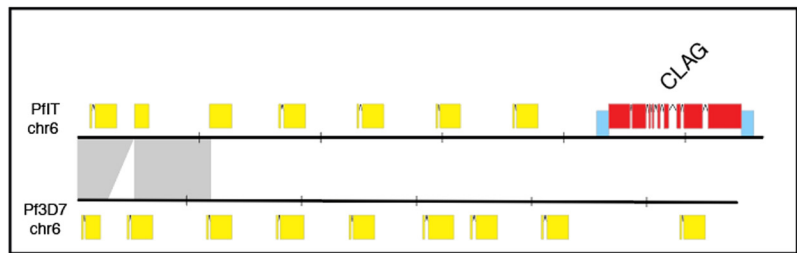


Type 2 (new gene)

Type 2.1 (anchored on both sides)

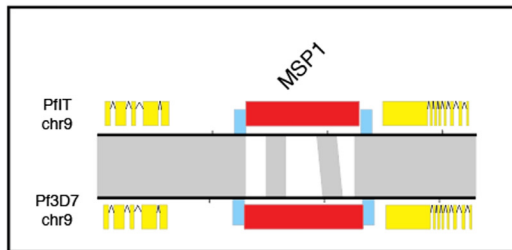


Type 2.2 (not anchored)



Type 3 (dimorphic gene)

Type 3.1 (anchored on both sides)



Type 3.2 (anchored on one side)

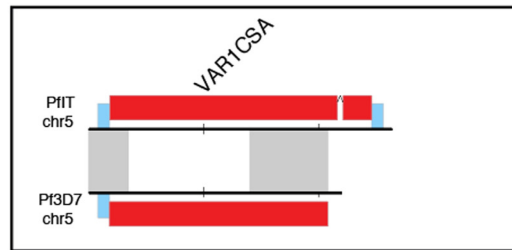


Figure 5. Diagram showing different types of patches created for the *P. falciparum* 3D7 population reference (PfRef1). Type-1 are sequence differences between the current *P. falciparum* 3D7 assembly version 3.2 and a new Pf3D7 PacBio assembly. 500 bp are provided on each side as anchor (shown in blue). Type-2 are new genes, that are either anchored on both sides (type 2.1), or not anchored (type 2.2). Type-3 are dimorphic genes that are either anchored on both sides (type 3.1) or anchored on one side (type 3.2).

inevitable that there is a law of diminishing returns. However, with 33% of genes still of unknown function it is essential that ongoing maintenance, annotation and curation are continued. In particular, our future plans include the annotation of untranslated regions (UTRs) and the annotation of additional common alternative splice-forms for genes. We also plan to provide better visibility for evidence codes that support protein descriptions but are currently only available as GFF format genome annotation files. New possibilities are now being explored for the community to get involved with annotation. GeneDB will soon provide an opportunity for the community to contribute directly to structural annotation. Equivalent to that of an annotator's view, the user will be able to view the curated *Plasmodium*

genomes in Apollo (Lee *et al.*, 2013), a collaborative genomic annotation editor which allows multiple users to access the data.

The genetic structure of *P. falciparum* populations is currently studied by aligning whole genome sequencing reads to the Pf3D7 reference (Manske *et al.*, 2012; Neafsey *et al.*, 2012). However, the approach has limitations: genomic regions that are absent or extremely diverged from 3D7 can not be analysed by alignment. This applies to genes that are completely missing as well as alleles of genes that are extremely different (either due to high sequence diversity or dimorphism). By supplementing *P. falciparum* 3D7 v3.2 with alternative loci we have created a combined new reference called Pfref1. Utilising such alternative

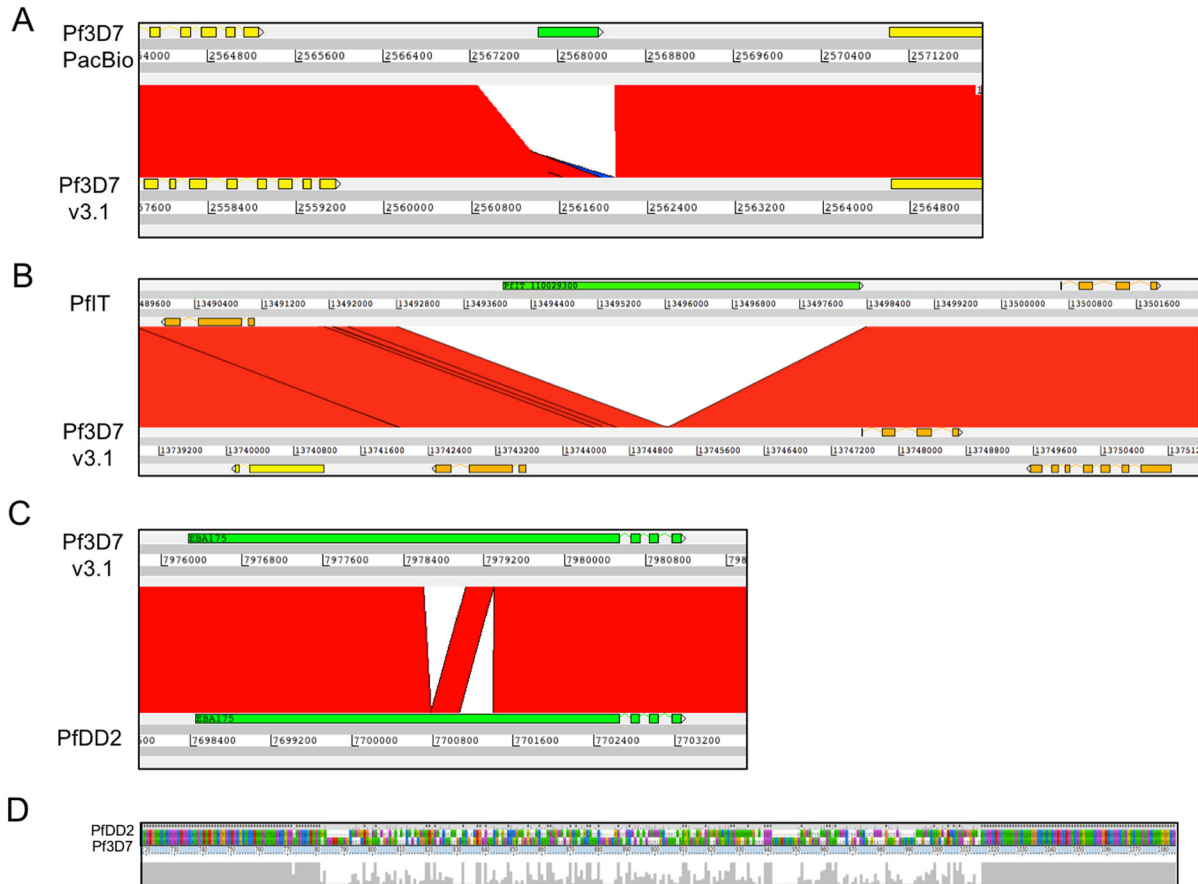


Figure 6. Differences between *P. falciparum* 3D7 genome version 3.2, a PacBio assembly of *P. falciparum* 3D7 and two lab strains *P. falciparum* IT and DD2. ACT comparisons between regions of the above genomes. Coloured boxes represent genes. The red blocks between sequences represent sequence similarity (BLASTn). **(A)** In the current *P. falciparum* 3D7 genome assembly v3.2, a hypothetical protein on chromosome 13 is missing. This gene is present in a Pf3D7 PacBio assembly (shown in green). **(B)** Comparison between *P. falciparum* IT chromosome 11 and *P. falciparum* v3.2 chromosome 11. *P. falciparum* 3D7 is missing a hypothetical gene on chr11. This gene is present in *P. falciparum* IT (PfIT_110029300) (shown in green). **(C)** Comparison between Pf3D7 v3.2 chromosome 7 and *P. falciparum* DD2 chromosome 7. The comparison shows the dimorphic gene EBA175 erythrocyte binding antigen-175 (PF3D7_0731500). **(D)** Clustalx alignment of EBA175 from PfDD2 and Pf3D7. The area shown is the dimorphic part of the two genes.

loci, rather than simply excluding them from population analyses, remains a challenge and will require the further development of variant-calling methods. However, as a first step, the popular short-read alignment tool BWA-MEM (Li, 2013), used in the GATK variant call pipeline, has been able to perform alignments in an alternative-aware mode for several years.

Data availability

Underlying data

P. falciparum 3D7 is maintained in GeneDB (<http://www.genedb.org>) and updates are passed on at regular intervals to PlasmoDB (<http://www.plasmodb.org>).

The annotation (GFF) files are being extracted from the annotation database on a monthly basis. They are available on the following FTP site:

<ftp://ftp.sanger.ac.uk/pub/genedb/releases/latest/Pfalciparum/>

The latest version of the database at time of publication is available here:

<ftp://ftp.sanger.ac.uk/pub/genedb/releases/2019-03/Pfalciparum/>

The patches for the population reference are on the following FTP site.

<ftp://ftp.sanger.ac.uk/pub/project/pathogens/Plasmodium/falciparum/PfRef1>

This page also includes an explanation of the naming of the short EMBL files and instructions on how to map them to the reference genome.

Extended data

Open Science Framework: Progression of the canonical reference malaria parasite genome from 2002–2019, <https://doi.org/10.17605/OSF.IO/5K9VJ> (Böhme, 2019)

This project contains the following extended data:

- Table_1.xlsx (*P. falciparum* 3D7 genes present in 2019 that were missing in 2002)
- Table_2.xlsx (List of ncRNAs present in *P. falciparum* 3D7 version 3.2)
- Table_3.xlsx (*P. falciparum* 3D7 genes that were deleted anytime between 2002 and 2019)

Data are available under the terms of the [Creative Commons Zero “No rights reserved” data waiver](#) (CC0 1.0 Public domain dedication).

Software availability

The Artemis software used for annotation is available on GitHub: <http://sanger-pathogens.github.io/Artemis/Artemis/>

Grant information

This work was supported by the Wellcome Trust through a core grant to the Wellcome Trust Sanger Institute [206194] and a Wellcome Investigator Award to CIN [104792].

The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Acknowledgments

We would like to thank Bart Barrell for contributing to the structural annotation. We would also like to thank Daniel Depledge for his contribution to the GO annotation, Blessing Adamu for her work on ncRNAs and Andrew Berry for *Plasmodium* curation between 2004 and 2007. We would like to thank Sue Kyes and Zoe Christodolou for resolving the chromosome 7/ chromosome 8 misassembly. We would like to thank PlasmoDB for providing the main portal to access *Plasmodium* genome data and for setting up an option to add user comments to gene record pages.

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Manuel Llinas 

Department of Biochemistry and Molecular Biology, Penn State University, University Park, PA, USA

I have read through the manuscript and comments and am fine with the modifications that have been made. In my opinion, this important manuscript can be approved for indexing.

Competing Interests: No competing interests were disclosed.

I have read this submission. I believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

Version 1

Reviewer Report 26 April 2019

<https://doi.org/10.21956/wellcomeopenres.16577.r35172>

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Manuel Llinas 

Department of Biochemistry and Molecular Biology, Penn State University, University Park, PA, USA

This work by Böhme *et al.* provides a unique summary of a number of iterative improvements that have been made to the *Plasmodium falciparum* reference genome since 2002. In some regards it is a historical review detailing the evolution of this critical genome, highlighting a significant number of gene modifications, losses as well as additions. As described, the current status of the *P. falciparum* genome should be the envy of any field focused on a single model species. The examples of modifications to the genome are adequately depicted throughout and easy to follow. Overall, the exceptional curation of this

genome is largely due to the diligent and consistent attention to the quality and completeness that it has received over the years from this team at the Wellcome Sanger Institute.

One new feature for the malaria parasitology community is the creation of a “population” reference genome, Pfref1, that accounts for sequence differences between strains. While I applaud this effort since there is a need to encompass the diversity of parasites strains, it is not clear to me whether 3 isolates is sufficient to capture the known major *P. falciparum* haplotypes, as claimed. Perhaps this is true, but do IT, DD2 and Pf3D7 provide sufficient haplotype diversity? If so, can you demonstrate this? And what type of genes account for the greatest haplotype diversity?

Also, with Pfref1, how many genes are now included (and nucleotide increase) to map against?

I think the manuscript could also be somewhat enhanced by describing which sequencing and/or annotation algorithms/approaches have contributed the most significantly to the changes and improvements to the current *P. falciparum* genome overall.

Although the manuscript describes a large gain in pseudogenes, given recent reports that some pseudogenes may actually express functional proteins¹ this should be mentioned as a possible outcome for genes predicted to be non-functional.

On page 5, it is stated that the number of verified genes has changed from 597 to 1296 genes. It is unclear what “experimentally verified” implies. What verification was applied to these genes?

Minor comment:

Please change reference to “AP2 proteins” to ApiAP2 proteins. AP2 refers solely to the DNA binding domain region of these proteins.

On page 7, three “types” of genes are described (type-1, type-2, and type-3). For the non-experts, please describe what these types refer to?

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Is the rationale for creating the dataset(s) clearly described?

Yes

Are the protocols appropriate and is the work technically sound?

Partly

Are sufficient details of methods and materials provided to allow replication by others?

Yes

Are the datasets clearly presented in a useable and accessible format?

Yes

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Molecular Plasmodium parasitology, genomics, transcriptomics, metabolomics.

I have read this submission. I believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard, however I have significant reservations, as outlined above.

Author Response 24 May 2019

Ulrike Böhme, Wellcome Sanger Institute, Hinxton, Cambridge, UK

Thank you for your constructive feedback.

1. One new feature for the malaria parasitology community is the creation of a “population” reference genome, Pfref1, that accounts for sequence differences between strains. While I applaud this effort since there is a need to encompass the diversity of parasites strains, it is not clear to me whether 3 isolates is sufficient to capture the known major *P. falciparum* haplotypes, as claimed. Perhaps this is true, but do IT, DD2 and Pf3D7 provide sufficient haplotype diversity? If so, can you demonstrate this? And what type of genes account for the greatest haplotype diversity?

Our intention is to provide a reference that will be sufficient to capture the major haplotypes by sequence-mapping approaches. IT, DD2 and Pf3D7 do not represent the full of universe of haplotype diversity. In the paper we state that this supplemented sequence “better represents the pan genome for this species”. Additional sequences can be easily added as they are identified, using this consistent format.

2. Also, with Pfref1, how many genes are now included (and nucleotide increase) to map against?

We found 4 core genes that are present in other isolates.

3. I think the manuscript could also be somewhat enhanced by describing which sequencing and/or annotation algorithms/approaches have contributed the most significantly to the changes and improvements to the current *P. falciparum* genome overall.

As shown in Figure 3, the biggest number of changes were done between 2007 and 2010. This is due to RNA-Seq data and TBLASTX comparison which is described in the methods section: “RNA-Seq data and TBLASTX comparisons were the primary supporting evidence for manual improvements to gene models.”

4. Although the manuscript describes a large gain in pseudogenes, given recent reports that some pseudogenes may actually express functional proteins this should be mentioned as a possible outcome for genes predicted to be non-functional.

We’ve added a sentence to the Table 1 legend to state that pseudogenes have simply been defined operationally as genes with premature stop codons or at least one frameshift.

5. On page 5, it is stated that the number of verified genes has changed from 597 to 1296 genes. It is unclear what “experimentally verified” implies. What verification was applied to these genes?

These are genes that have been mentioned by others in a peer-reviewed paper containing some level of experimental evidence.

Minor comment:

1. Please change reference to “AP2 proteins” to ApiAP2 proteins. AP2 refers solely to the DNA binding domain region of these proteins.

AP2 has now been changed to ApiAP2.

2. On page 7, three “types” of genes are described (type-1, type-2, and type-3). For the non-experts, please describe what these types refer to?

This has now been clarified in the text.

“The differences have been incorporated into the reference as three classes (Figure 5). The first (**type-1**) are “patches” to correct errors in Pf3D7 (version 3.2), for example a missing centromere on chromosome 10 and a missing gene on chromosome 13 (Figure 5, Figure 6A), the second (**type-2**) are core genes that are present in other sequenced isolates, i.e. *P. falciparum* IT or *P. falciparum* DD2 but are missing in Pf3D7 (Figure 5, Figure 6B) and the third (**type-3**) are dimorphic genes where alternative alleles cannot be mapped to the one currently present in Pf3D7.”

Competing Interests: No competing interests were disclosed.

Reviewer Report 25 April 2019

<https://doi.org/10.21956/wellcomeopenres.16577.r35170>

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Anthony A. Holder 

Francis Crick Institute, London, UK

In the almost 20 years since the publication of the *Plasmodium falciparum* 3D7 genome sequence there have been tremendous improvements in the completeness and accuracy of the sequence and genome structure, as well as an impressive improvement in the annotation. These advances have been achieved by a combination of further sequence analysis of both genome and transcripts, as well as automatic and literature and community-based manual annotation. This paper spells out the patient and often painstaking strategies that have been used since the first publication to ensure that there is as far as possible a complete and fully annotated genome sequence available to the scientific community. Such information is not only essential for much hypothesis-driven research into parasite biology and parasite-host interactions, or for studies of parasite evolution and epidemiology, but also underpins other global approaches, such as proteomics analysis. The work highlights some of the problems that needed to be addressed and provides some examples of the solutions that were found and applied. The ongoing improvements in annotation will facilitate research into specific areas of cell biology and metabolism, and contribute to efforts to translate this knowledge into products useful for interventions to control malaria.

In addition to the work on the reference cloned 3D7 parasite line, the authors also describe the establishment of an extended data set comprised of a population reference genome of *P. falciparum*, called Pfref1. This will facilitate mapping and comparative studies of isolates and lines that cannot be achieved using the 3D7 reference alone. Such a reference is likely to be very useful for studies of parasite evolution and spread, for example in response to selective pressures.

The data are updated regularly and readily available, for example through GeneDB or PlasmoDB and through the documented web sites for further specific details.

Minor textual corrections:

1. The last sentence of the abstract needs improvement.
2. In the Methods section, subsection 'PfRef1 reference genome', the second to last sentence requires attention.
3. On page 5, second paragraph, the amino acid names isoleucine and valine are not normally capitalized.
4. In Figure 3, during the period 2007-2010, presumably the blue bar should represent 69 new rather than 69 changed.

Is the rationale for creating the dataset(s) clearly described?

Yes

Are the protocols appropriate and is the work technically sound?

Yes

Are sufficient details of methods and materials provided to allow replication by others?

Yes

Are the datasets clearly presented in a useable and accessible format?

Yes

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: I have worked for many years on malarial parasite-host interactions including host cell invasion and cell and molecular biological aspects of parasite growth and proliferation in red blood cells.

I have read this submission. I believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

Author Response 24 May 2019

Ulrike Böhme, Wellcome Sanger Institute, Hinxton, Cambridge, UK

Thank you for your constructive feedback.

Minor textual corrections:

1. The last sentence of the abstract needs improvement.

This sentence has been corrected to:

“P. falciparum 3D7 will continue to be maintained, with ongoing curation ensuring continual improvements in annotation quality.”

2. In the Methods section, subsection ‘PfRef1 reference genome’, the second to last sentence requires attention.

This sentence has been corrected: *“Each file contains a sequence variant with a 500 bp anchor sequence on either side to enable unambiguous placement along the 3D7 reference.”*

3. On page 5, second paragraph, the amino acid names isoleucine and valine are not normally capitalized.

This has now been changed.

4. In Figure 3, during the period 2007-2010, presumably the blue bar should represent 69 new rather than 69 changed.

Thank you for noticing this. Figure 3 has now been corrected.

Competing Interests: No competing interests were disclosed.

Reviewer Report 17 April 2019

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Thomas E. Wellems 

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The availability and accuracy of *Plasmodium falciparum* genome information is crucial to molecular and genetic studies of malaria parasites. This manuscript describes valuable updates and improvements to the sequences and annotations of the 14 nuclear chromosomes, apicoplast and mitochondrial sequences of the *P. falciparum* 3D7 clone, including summaries of the progressive assemblies, gap closures, gene structure refinements, and functional annotations. In addition, a *P. falciparum* population database (Pfref1) of parasite variant types is provided for the first time; Pfref1 and its future expansion will facilitate studies of genome regions that are missing or greatly diverged from those of the 3D7 reference.

Specific comments:

1. In Figure 1, state whether or not coding directions of the gene sequences (orientations) are indicated by positions of the marks above or below the chromosome lines.
2. The numbers of genes in several versions listed in Table 1 appear to differ from the numbers in the corresponding versions of Figure 4. For example, Table 1 lists 5280 genes in Version 3.2 but Figure 4 notes 5438 genes. Check and correct/explain the differences.

3. Figure 2 can be improved and made easier to read by providing the gene IDs directly on the panels. The red blocks between v1 and v3.2 can be much less tall and the coding regions heightened to draw better attention to the gene information.
4. In Figure 4, the 2007, 2009, 2010, 2011 versions are all labeled the same: 2.1.4. However, the 2010 version in Figure 3 is labeled as 2.1.5. Correct/clarify the labels of the different versions.
5. In Table 2, should the “Number of GO annotations (2018)” be corrected to read “Number of GO annotations (2019)”?
6. For the Pfref1 population reference, major sequence variations are included from the three different lab isolates. Please clarify how copy number variations are treated.
7. Introduction, page 3. *P. falciparum* 3D7 is from the NF54 isolate (Walliker *et al.* 1987, *Science*, footnote 11¹). NF54 has served along with 3D7 as a major focus of malaria research. Inclusion of this information would be helpful to readers, especially as the close relationship of 3D7 to NF54 is often unrecognized or forgotten.

References

1. Walliker D, Quakyi I, Wellems T, McCutchan T, Szarfman A, London W, Corcoran L, Burkot T, Carter R: Genetic analysis of the human malaria parasite *Plasmodium falciparum*. *Science*. 1987; **236** (4809): 1661-1666 [Publisher Full Text](#)

Is the rationale for creating the dataset(s) clearly described?

Yes

Are the protocols appropriate and is the work technically sound?

Yes

Are sufficient details of methods and materials provided to allow replication by others?

Yes

Are the datasets clearly presented in a useable and accessible format?

Yes

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Malaria biology, pathogenesis, and genetics.

I have read this submission. I believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

Author Response 24 May 2019

Ulrike Böhme, Wellcome Sanger Institute, Hinxton, Cambridge, UK

Thank you for your constructive feedback.

Specific comments:

1. In Figure 1, state whether or not coding directions of the gene sequences (orientations) are indicated by positions of the marks above or below the chromosome lines.

Thank you for this suggestion. This information has now been added in the figure legend.

“Genes above the chromosome lines are located on the forward strand, genes below the chromosome lines are on the reverse strand.”

2. The numbers of genes in several versions listed in Table 1 appear to differ from the numbers in the corresponding versions of Figure 4. For example, Table 1 lists 5280 genes in Version 3.2 but Figure 4 notes 5438 genes. Check and correct/explain the differences.

As stated in the figure legend, Table 1 lists the gene numbers without pseudogenes. Pseudogenes are separately listed in Table 1. Version 3.2 has 5280 protein-coding genes and 158 pseudogenes. Adding both numbers will give you a total of 5438 genes. We've now added the following sentence to the legend of Figure 4 to make this clearer.

“The number of genes between October 2002 and March 2019 are compared. The total number of genes includes pseudogenes.”

3. Figure 2 can be improved and made easier to read by providing the gene IDs directly on the panels. The red blocks between v1 and v3.2 can be much less tall and the coding regions heightened to draw better attention to the gene information.

Thank you for the suggestion to improve this figure. Gene IDs have been added on the panels. The TBLASTX matches are now shown in grey and the height of the TBLASTX matches has been shortened. All genes are shown in red. This is an ACT screenshot which means that coding regions cannot be heightened. But we hope that the other changes will draw more attention to the gene information.

4. In Figure 4, the 2007, 2009, 2010, 2011 versions are all labeled the same: 2.1.4. However, the 2010 version in Figure 3 is labeled as 2.1.5. Correct/clarify the labels of the different versions.

Thank you for noticing this. The number in the legend of Figure 3 has now been changed from 2.1.5 to 2.1.4.

5. In Table 2, should the “Number of GO annotations (2018)” be corrected to read “Number of GO annotations (2019)”?

This has now been corrected.

6. For the Pfref1 population reference, major sequence variations are included from the three different lab isolates. Please clarify how copy number variations are treated.

Most CNVs can be detected and quantified using the strictly 3D7 sequence as a reference (based on mapped coverage of reads). The Pfref1 simply extends the ref to those areas that are missing or highly diverged from 3D7.

7. Introduction, page 3. *P. falciparum*3D7 is from the NF54 isolate (Walliker *et al.* 1987, *Science*). NF54 has served along with 3D7 as a major focus of malaria research. Inclusion of this information would be helpful to readers, especially as the close relationship of 3D7 to NF54 is often unrecognized or forgotten.

We have addressed this with the following text “the genome of *Plasmodium falciparum* 3D7 (a clone from the NF54 isolate) ...”. We’ve also added the reference.

Competing Interests: No competing interests were disclosed.
