

Genetic Diversity of the Flavohemoprotein Gene of *Giardia lamblia*: Evidence for High Allelic Heterozygosity and Copy Number Variation

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Purpose: The flavohemoprotein (gFIHb) in *Giardia* plays an important role in managing nitrosative and oxidative stress, and potentially also in virulence and nitroimidazole drug tolerance. The aim of this study was to analyze the genetic diversity of *gFIHb* in *Giardia* assemblages A and B clinical isolates.

Methods: *gFIHb* genes from 20 cultured clinical *Giardia* isolates were subjected to PCR amplification and cloning, followed by Sanger sequencing. Sequences of all cloned PCR fragments from each isolate were analyzed for single nucleotide variants (SNVs) and compared to genomic Illumina sequence data. Identical clone sequences were sorted into alleles, and diversity was further analyzed. The number of *gFIHb* gene copies was assessed by mining PacBio de novo assembled genomes in eight isolates. Homology models for assessment of SNV's potential impact on protein function were created using Phyre2.

Results: A variable copy number of the *gFIHb* gene, between two and six copies, depending on isolate, was found. A total of 37 distinct sequences, representing different alleles of the *gFIHb* gene, were identified in AII isolates, and 41 were identified in B isolates. In some isolates, up to 12 different alleles were found. The total allelic diversity was high for both assemblages (>0.9) and was coupled with a nucleotide diversity of <0.01. The genetic variation (SNVs per CDS length) was 4.8% in sub-assemblage AII and 5.4% in assemblage B. The number of non-synonymous (ns) SNVs was high in *gFIHb* of both assemblages, 1.6% in A and 3.0% in B, respectively. Some of the identified nsSNV are predicted to alter protein structure and possibly function.

Conclusion: In this study, we present evidence that gFIHb, a putative protective enzyme against oxidative and nitrosative stress in *Giardia*, is a variable copy number gene with high allelic diversity. The genetic variability of *gFIHb* may contribute metabolic adaptability against metronidazole toxicity.

Keywords: *Giardia*, genetic diversity, copy number variation, flavohemoprotein, oxidative stress, nitrosative stress, allele

Introduction

Giardia lamblia is a microaerophilic protozoan parasite that infects up to 280 million humans annually by causing giardiasis.¹ This gastrointestinal infection is more common in developing countries, and may negatively affect growth properties and cognitive functions in children.^{2,3} In developed countries giardiasis is usually related to sporadic waterborne outbreaks, or seen in travelers returning from endemic areas.^{4,5} To treat giardiasis, the prodrug nitroimidazole antibiotic known as metronidazole (MTZ)

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is often used as first-line treatment.⁶ Over the past few years, treatment failures with MTZ have been reported more frequently, and 10–40% of the cases will not be eradicated after a 5–7 day course of MTZ treatment.^{7–9} The currently understood mode of action of MTZ depends on partial reduction (activation) resulting in highly reactive intermediates that further initiate damage to DNA and proteins, or on the other side, regeneration of MTZ, where oxygen radicals are created ('futile cycling').^{10–12} The enzymes in the detoxification system in *Giardia* must then be able to handle oxidative stress resulting from metabolizing MTZ, as well as being able to neutralize substances such as molecular oxygen (O₂) and nitric oxide (NO) encountered in the gut habitat and released by the host.^{13,14} There are several known enzymes connected to free radical neutralization, including flavoprotein, desulfoferredoxin (SOR), NADH oxidase and flavohemoprotein (gFIHb).^{13,15} The gFIHb functions as a nitric oxide dioxygenase, responsible for catalyzing the formation of nitric oxide (NO) to nitrate (NO₃⁻) by using O₂ as a co-factor.^{16,17} The gFIHb enzyme may also possess NADH/NAD(P)H oxidase activities, similar to flavodiiron protein, by catalyzing O₂ to H₂O in low NO level conditions.¹⁸ The *gFIHb* gene was characterized a decade ago, and is likely to be an important detoxification enzyme in *Giardia*.^{15,18} It has been shown to be up-regulated during exposure to oxidative stresses caused by both O₂ and H₂O₂, in addition to being upregulated during nitrosative stress.^{14,15,19} It was also recently shown that gFIHb protein levels were increased during MTZ exposure in an MTZ and nitazoxanide (NTZ) resistant *Giardia* isolate.²⁰ In another anaerobic or microaerophilic pathogen, *Trichomonas vaginalis*, it has been observed that in vitro MTZ-resistant parasites can handle higher levels of oxygen than susceptible ones, probably linking resistance to increased tolerance or better mechanisms to handle oxidative stress.²¹ It has been proposed that refractory *Giardia* has a higher tolerance towards O₂, as O₂ will compromise the activation of MTZ through futile cycling, but also potentially through an O₂ induced resistance mechanism.²² Because gFIHb uses O₂ as a co-factor for converting NO to NO₃⁻, it could also be relevant for increased MTZ tolerance in this way.

Activities of enzymes having similar properties as the gFIHb have been shown to be inhibited by bulky imidazoles (such as azoles; miconazole, econazole and ketoconazole) by binding to the heme pocket of the protein and generating reactive oxygen species (ROS), which may well mean that MTZ could potentially affect the function of the gFIHb enzyme, and link it to *Giardia*'s ability to handle and tolerate

the toxic effects of MTZ.^{23,24} *Giardia* is a functionally tetraploid organism, with two diploid nuclei, each of them harboring two sets of its 5 chromosomes.^{25–27} However, aneuploidy with unequal distribution of chromosomes may also occur.^{25,28} Thus, even single-copy genes may occur in up to four versions, ie, alleles, per strain.^{25,28}

The degree of allelic sequence heterozygosity (ASH), has been shown to differ between assemblages of *G. lamblia*. Current genome data suggests a comparably low ASH in sub-assemblage AI (<0.01%), a little higher in sub-assemblage AII (based on reference strain DH with an ASH of 0.04%), and highest in assemblage B isolates (cf GS reference strain's ASH of 0.5%).^{25,29,30} Genetic diversity at the allele level, especially in assemblage B, has been analyzed mainly for typical genotyping genes or housekeeping genes (β -giardin (*bg*), glutamate dehydrogenase (*gdh*), elongation factor 1-alpha (*ef-1*), *mlh1* (*mlh*), the FLORF-C4 (*C4*) and triosephosphate isomerase (*tpi*).^{29,31–34} The allelic forms, however, have rarely been determined by cloning.^{35–41} In a recent study on the genetic diversity of genes involved in MTZ induced oxidative and nitrosative stress management, we found indications that *gFIHb* genes may not only present allelic variation, but also be present at variable copy numbers per haploid genome.⁴² The current study is a follow-up study of this recent published article.⁴² As gFIHb may play a role in the ability of *Giardia* to tolerate MTZ, we performed this study to further explore the copy number variability and the allelic diversity of *gFIHb* in *G. lamblia* strains representing recent sub-assemblage AII and assemblage B isolates.

Materials and Methods

Giardia Lamblia Isolates

Trophozoite cultures of a recently established *G. duodenalis* biobank at the Robert Koch-Institute in Berlin, containing twelve *Giardia* sub-assemblage AII and eight *Giardia* assemblage B isolates, were cultured according to the methods of Keister.⁴³ Collection, DNA extraction, concentration measurements and Illumina-based whole genome sequencing were carried out as previously stated.⁴² No clinical data have been collected from the clinical samples of *Giardia*.

Cloning of Flavohemoprotein

The coding regions and approximately 150 bp up/downstream of the gene flavohemoprotein, *gFIHb*, in sub-

assemblage AII (DHA2_154000) and B (GSB_151570) were amplified from genomic DNA by PCR. The reference genomes for *Giardia* sub-assemblage AII and assemblage B (v.26) were downloaded from *Giardia* DB January 2016 versions 2013–11–25.⁴⁴ Specific primers for the two orthologs of *gFIHb* of sub-assemblage AII and assemblage B were designed in Geneious Prime[®] 2019.0.3 (Biomatters Ltd., Auckland, New Zealand) (see Table 1) based on conserved pre- and post-CDS regions of the *gFIHb* gene represented in twelve assemblage A and eight assemblage B whole genome sequenced isolates previously presented in a former study.⁴² Each 25 µL PCR reaction contained 1X Q5 Reaction Buffer (cat. nr: B90276, New England BioLabs (NEB) Ipswich, MA, USA), 2 mM MgCl₂ (included in buffer), 0.2 mM dNTP's (catalog nr N0447L, NEB), 0.5 U Q5 High-Fidelity DNA Polymerase (catalog nr M0491L NEB) 0.2 µM each of forward and reverse primer, 1 µL template DNA and nuclease-free water up to 25 µL. Negative controls using master mix reactions with nuclease-free water were included in all PCR experiments. All PCR reactions included an initial denaturation at 98°C for 30s, followed by 35 cycles of denaturation at 98°C for 10 s, annealing for 30 s (55°C for sub-assemblage AII and 60°C for assemblage B), extension at 72°C for 45–60 s and final extension at 72°C for 3 minutes. Amplified PCR products were run on 1% Agarose gels stained with GelGreen[®] Nucleic Acid Stain (catalog nr: 41,005, Biotium, San Francisco, CA, USA) and positive bands were cut from the gel using blue light illuminator (Serva, Heidelberg, Germany) and extracted using Wizard SV gel and PCR Clean-Up System (catalog nr: A9282, Promega, Madison, WI, USA) according to manufacturer's descriptions, the only exception was using 70°C nuclease-free water in the last elution step. Concentrations of the PCR products were measured using Quantus[™] Fluorometer (catalog Nr: E6150, Promega). DNA was available from 19 of the original Illumina sequenced samples, and two of the

isolates were not included in the *gFIHb* gene cloning experiments due to unsuccessful amplification of the gene target.

The pJET 1.2/blunt cloning vectors (catalog nr: K1232, CloneJET PCR Cloning kit, Thermo Fisher Scientific, Waltham, MA, USA) were used in all of the cloning experiments. The blunt end protocol for ligation of PCR-product to vector was followed according to the manufacturer's instructions. The ligation mixtures were used immediately or kept at –20°C until usage. The ligation mixtures were introduced into *Escherichia coli* DH5a competent cells by heat-shock transformation using standard protocols.⁴⁵ The *E. coli* was plated on lysogeny broth (LB) agar plates containing ampicillin (100 µg/mL) (catalog nr: 10,835,269,001 (Sigma-Aldrich), Merck KGaA, Darmstadt, Germany) and cultured overnight at 37°C in a CO₂ incubator. Approximately 20 clones from each *Giardia* isolate were picked for colony PCR. 14–20 positive clones were cultured overnight in a shaking incubator at 37°C in Falcon[®] 17x100 mm, 14 mL high-clarity polypropylene (PP) round bottom test tubes (Item nr: T7597-14F, Corning Life Sciences, NY, USA). The plasmids were purified from the overnight cultures using Zyppy plasmid miniprep kit (catalog nr: D4037, Zymo Research Corp., CA, USA) as advised by the manufacturer and DNA was eluted using nuclease-free water. The plasmid concentrations were measured using Quantus and sequenced using pJET1.2 F and R sequencing primers provided in the cloning kit together with the BigDye[™] Terminator v3.1 Cycle Sequencing kit (catalog nr: 4,337,455, Thermo Fisher Scientific). The PCR products were Sanger sequenced at the Sequencing Laboratory of the Robert-Koch Institute, Berlin, Germany.

Data Analysis of Sequences and Single Nucleotide Variation

SNV-called Illumina sequences of *gFIHb* presented in a former study, accession numbers MK043521.1–MK0435

Table 1 Primers Designed for Gene-PCR of the *gFIHb* of *Giardia lamblia* Sub-Assemblage AII and Assemblage B All Primers Were Ordered from Eurofins Genomics (Ebersberg, Germany)

Primer Set	Type ^a	Sequence, 5'-3'	Amplicon Size	Melting Temperature [°C]
DHA2_154000	F	CGCCACCACAAGCGATCATT	1433	59.4
DHA2_154000	R	GTGTGTAGAGCGATTACAT		52.4
GSB_151570	F	CGGCCTTCAGTACTTCCCC	1807*	63.5
GSB_151570	R	GAGACCAAAAGTCCATATGAACT		57.1

Notes: *The GSB *gFIHb* gene exists in a longer version which is not likely to be the true length, however, the whole annotated gene obtained from the reference genome was covered by the primers. Only the CDS length of 1377 bp (same as in sub-assemblage AII) was analyzed in the present study.

Abbreviations: *F, forward; R, reverse.

40.1 from Genbank (NCBI), were used in the present study to investigate SNVs.⁴² A SNV in the Illumina sequencing data was defined by a read coverage of minimum 10 and variant frequency above 0.1 (minimum 2 reads would need to have the SNV if the coverage was 10). The Illumina sequenced files with read data were used to compare and verify SNV positions in the cloned sequences in Geneious Prime[®] (Biomatters Ltd.). The forward and reverse sequences of one clone were aligned against the respective reference gene orthologs DHA2_154000 and GSB_151570 and trimmed at start and end of the sequences before further analysis. The chromatograms were inspected manually, and sequences with ambiguous base calling, or not covering the full CDS were not included. To manage potential random amplification or sequencing errors in the present study, we set criteria to exclude likely false SNVs by verifying SNVs found in clones with Illumina read data. SNVs found in the clones in the present project were termed high confidence (HC) and SNVs and included in the analysis if one or several of the following criteria were met:

- the SNV position was also found to be present in Illumina data for the same isolate.
- multiple clones would have the same SNV within one isolate.
- if the SNV was not found in Illumina data as a major nucleotide, the reads in the Illumina were checked for the presence of the SNV and the nucleotide had to be presented by two reads or more.

The SNVs that were not classified as HC were discarded from the analyses and termed low confidence (LC) SNVs. De novo assemblies were generated for eight of the 20 *Giardia* isolates at RKI using the software tools HGAP 2.0 (PacificBiosciences) as described elsewhere (Klotz et al 2020, manuscript in preparation). The gFIHb copy number was retrieved by mapping whole or partial sequences of the *gFIHb* AII and B reference sequences to de novo assemblies of PacBio consensus genomes of each isolate. To also identify partial genes or genes split between contigs, mapping of 20 bp parts of the start, middle and end of the reference genes were also performed. The identified *gFIHb* copies in PacBio consensus sequences were then extracted, and aligned together with the cloned allele sequences of the *gFIHb* gene separately for sub-assembly AII and B. Further phylogenetic trees (Tamura-Nei with method UPGMA) were made. All sequence analysis work was carried out in Geneious Prime[®]. All nonsynonymous (ns) substitutions were analyzed using Geneious and DNA Sequence Polymorphism

(DnaSP) v6.^{46,47} Nucleotide diversity (π) was calculated as the average number of nucleotide differences in gene sequences for pairwise comparisons. Haplotype diversity, defined as allelic diversity in the present study, gives a measure of the uniqueness of a specific allele in a population, or the probability that two alleles differ from one another.

Characterization of Amino Acid Changes

The bacterial genetic code was used for translation of the nucleotide codons in the gene sequences of *gFIHb* (DHA2_154000 and GSB_151570) in sub-assembly AII and assembly B. The abbreviations and characterization of the amino acid (aa) changes are based on the International Union of Pure and Applied Chemistry (IUPAC). As the crystal structure of the protein is not known, the estimation as to whether the aa change would affect the protein structure and function was based on homology models. Homology modeling was carried out using Protein Homology/analogy Recognition Engine V2.0 (Phyre2).⁴⁸ Protein sequences Uniprot ID: E2RTZ4 and A0A482ESB4 were selected to create models for gFIHb assembly A and B, respectively. The model was created using the single highest scoring template, a crystal structure of *E. coli* flavohemoglobin (PDB-ID 1GVH) sharing a 40% sequence identity with the gFIHb.⁴⁹ Illustrations for the homology models were created using PyMol. A conservative replacement was identified as an aa substitution between two aa with rather small physicochemical distance, whilst a radical aa change would be considered as aa having large physicochemical characteristics, or potential rearrangement of the secondary structure.⁵⁰

Results

gFIHb Copy Number Variation and Allele Diversity

Re-analysis of the mapping of Illumina sequencing data from the AII isolates onto the AII reference strain DH, showed that higher coverage for the *gFIHb* gene was present along the whole coding regions (CDS) of the gene and adjacent 0–230 bp upstream and 461–1271 bp downstream of the reference CDS.⁴² For the B isolates the coverage was found to be higher starting from 600 to 816 bp upstream of the GS reference CDS and extending to 90–913 bp downstream of it. PacBio consensus sequences derived from de novo assembly were available for eight isolates, five assembly B isolates and three sub-assembly AII isolates. More than one copy of the *gFIHb*

gene was found in the PacBio sequences-derived assemblies of all three AII and five B isolates. In general, higher Illumina coverage fold difference corresponded to higher copy numbers in PacBio sequence assemblies. Isolate P344 had the same estimated copy number of *gFIHb* based on both analyses. Isolate P424 showed the highest relative coverage in Illumina sequence data with 5.1 fold the average and six copies were detected in the respective PacBio sequence derived assembly. The respective values for P392 were 3.6 and four (see Table 2 for more information). The *gFIHb* gene was successfully amplified by PCR from 17 of the 20 isolates (11 AII isolates and 6 B isolates). Between five and seventeen clones per isolate were obtained (Table 2). The cloned *gFIHb* genes were categorized into different alleles depending on their sequences whereby 37 alleles were identified in eleven sub-assembly AII isolates, and 41 alleles were identified in six assembly B isolates. In the AII isolates, the number of *gFIHb* alleles identified by cloning varied from two to eight, while in the B isolates two to twelve alleles per isolate were found (Table 2). The allelic diversity, the probability that two alleles are different from one another, for sub-assembly AII was calculated to be 0.94 ± 0.01 and 0.95 ± 0.01 for

assembly B. To evaluate how alleles determined by cloning were represented in the *gFIHb* genes identified by de-novo assembled consensus genomes from PacBio sequenced isolates, we aligned all the CDS sequences and analyzed correspondence by creating phylogenetic trees (Figures 1 and 2). The phylogenetic tree of sub-assembly AII in Figure 1 represents the relations between the alleles and PacBio copies found in the different isolates. Several allelic forms of *gFIHb* were found in different isolates, for example one allele was found to be present in four isolates represented by allele AA16 found in P033, P506, P034 and P064. A total of six alleles were found to be present in more than one isolate (table S4). A total of nine PacBio consensus sequences of *gFIHb* were available from three AII isolates, representing the five, three and two copies found in isolates P392, P407 and P064, respectively. These sequences were aligned to the cloned sub-assembly AII alleles in order to check whether cloned alleles would match these consensus sequence copies. Three PacBio copies were found to be identical to alleles in their respective isolates (table S4), whereas the P407 AA37 allele and P407 PacBio copy 3 were identical with the exception of three, likely artefactual, indels in the PacBio consensus sequence.

Table 2 Estimates of *gFIHb* Copy Numbers in PacBio and Illumina Sequencing Data, Number of Clones, and Identified Alleles and SNVs in Cloned Sequences

Isolate	Average Coverage 5 Largest Contigs	Coverage <i>gFIHb</i> CDS	Estimated Number of Copies by Illumina	Copies Found in PacBio	Number of Clones Sanger Sequenced	Unique <i>gFIHb</i> Alleles per Isolate	Number of HC SNVs in all Clones	HC nsSNVs in all Clones
P033	30.6	64.9	2.1	Nd	11	3	18	6
P034	29.7	64.9	2.2	Nd	12	2	6	2
P064	94.2	97.9	1	2	11	2	6	2
P316	26.0	106.3	4.1	Nd	11	5	13	4
P324	30.1	97.9	3	Nd	NA	NA	NA	NA
P361	31.0	84.5	2	Nd	14	4	13	4
P368	42.4	139.9	3	Nd	5	2	23	9
P392	51.0	183.3	3.6	4	12	8	32	12
P403	27.8	86.9	3	Nd	8	2	26	5
P407	43.5	235.9	5.4	3	12	8	48	16
P478	11.5	106.3	3.4	Nd	9	7	34	10
P506	29.8	64.9	2	Nd	12	2	7	3
P344	23.7	45.4	2	2	15	9	22	7
P387	36	126.3	3.5	2	11	9	24	13
P413	23	110.6	4.8	Nd	13	12	28	21
P424	22.4	114.6	5.1	6	17	9	20	12
P427	17.2	24.9	1.5	2	14	3	21	10
P428	14	20.5	1	Nd	NA	NA	NA	NA
P433	13.4	13.1	1.5	Nd	NA	NA	NA	NA
P458	26.1	44.2	1.7	3	7	2	14	7

Abbreviations: Nd, not done; HC, high confidence; CDS, coding regions.

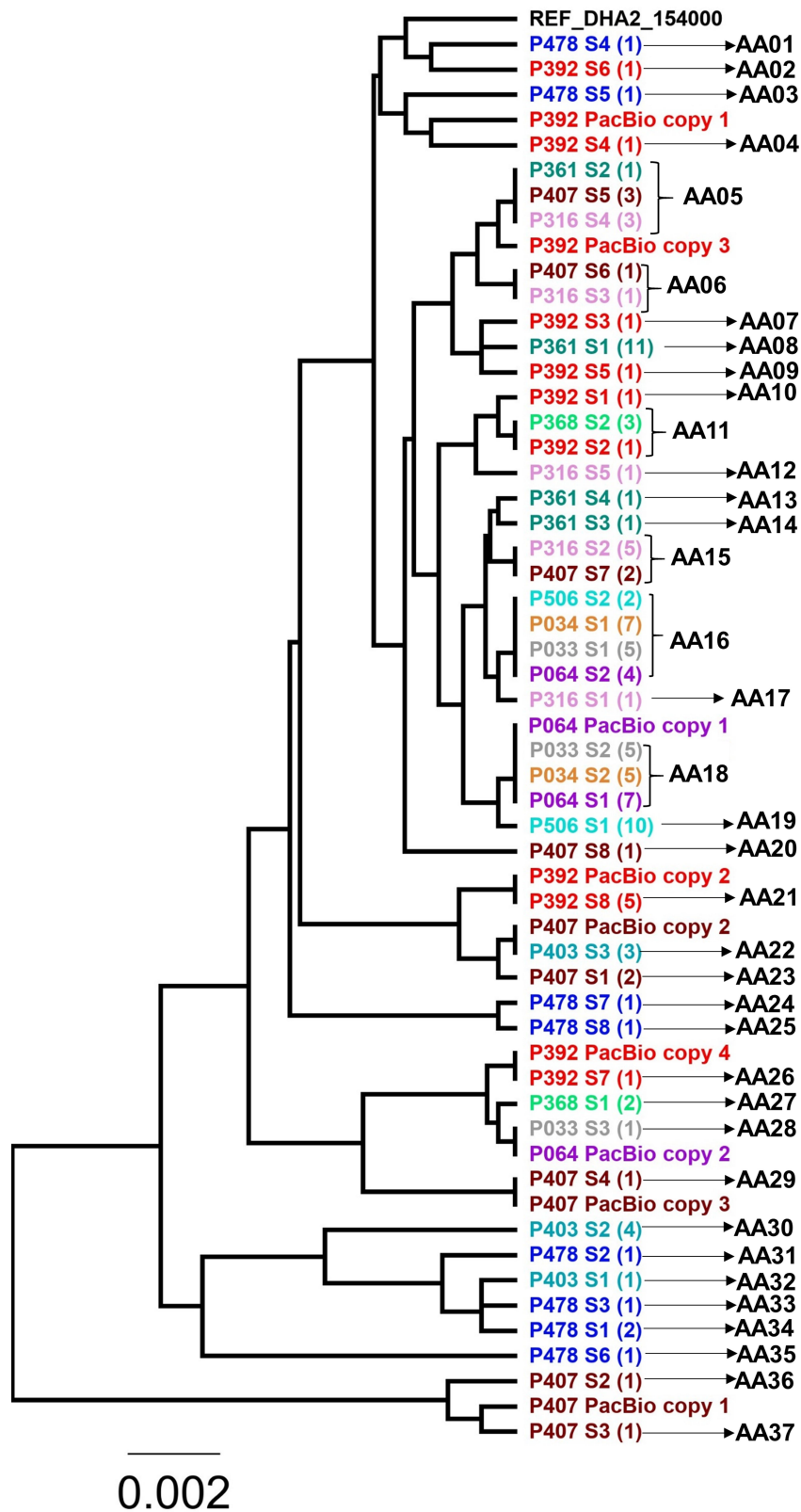


Figure 1 Phylogenetic tree of all the alleles of *gFIHb* found in the sub-assembly All isolates and *gFIHb* copies found in the PacBio sequencing data. A is abbreviated for allele, and the number of clones representing each allele is listed in the parenthesis.

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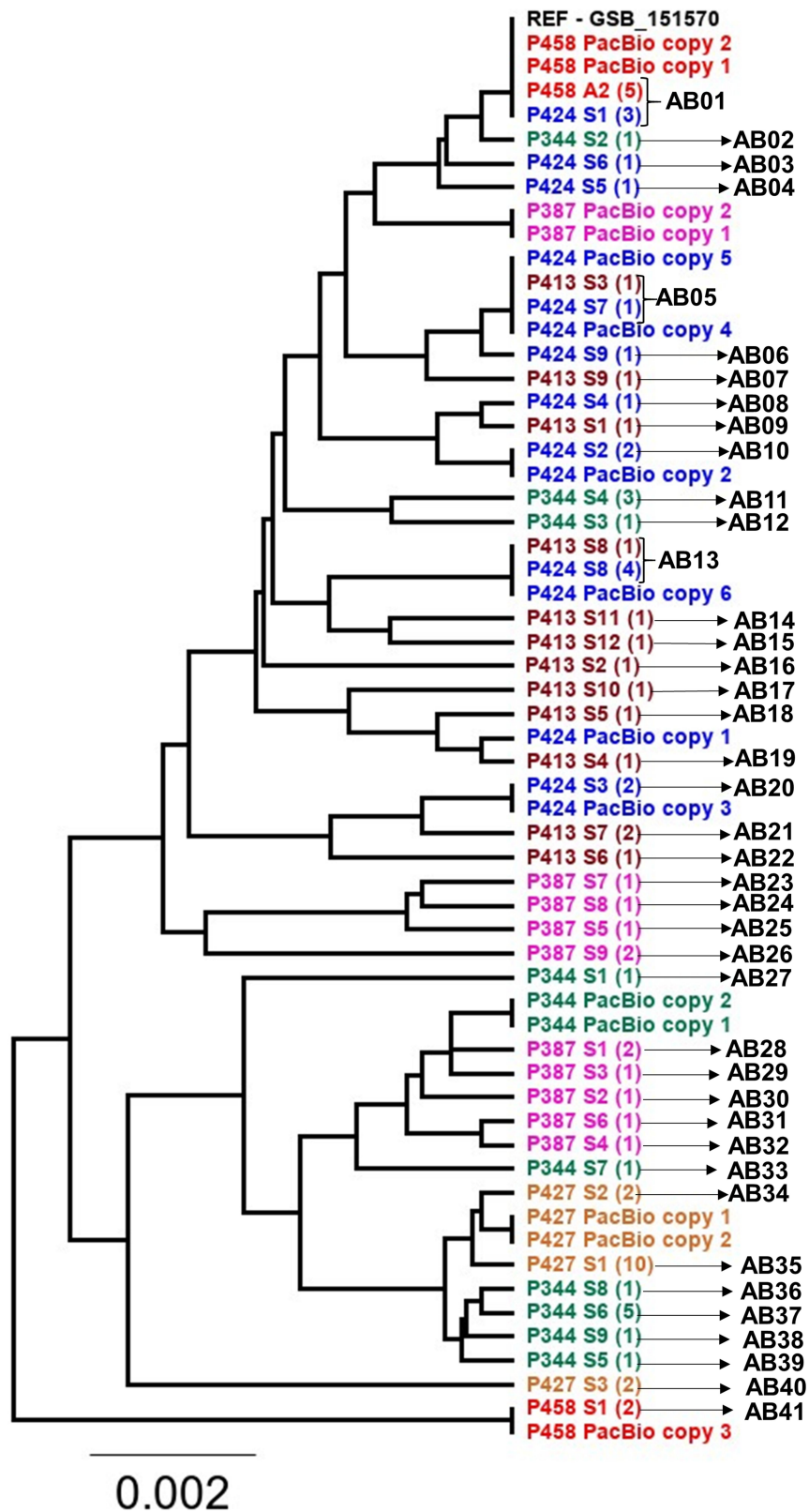


Figure 2 Phylogenetic tree of all the alleles found in the assemblage B isolates and *gII-Hb* copies found by PacBio sequencing. A is an abbreviation of allele, and the number of clones representing each allele is listed in the parenthesis.

P392 PacBio copy 1 and 3 and P407 PacBio copy 1 and 2, were not identical to alleles from the same isolate, but closely related (2–6 SNVs difference), and were likely to be part of the alleles resulting in the consensus PacBio copy. Intriguingly, two PacBio copies, P064 copy 2 and P407 copy 2 were identical to alleles found in other isolates, suggesting that sequencing of more clones would be necessary to pick up all possible alleles of each isolate. The relations between the 41 alleles and PacBio copies that were discovered in assemblage B are presented in phylogenetic tree in [Figure 2](#). Fewer alleles were shared between the assemblage B isolates than in the sub-assemblage AII isolates, where only three alleles were found in more than one isolate, such as AB01 in isolates P424, P458 and reference sequence GSB_151570, and alleles AB05 and AB13 in isolates P424 and P413 (see [table S5](#)).

Fifteen PacBio consensus sequences of *gFIHb* were obtained from five assemblage B isolates, and the copies were checked for similarity to the cloned alleles. Eight of the copies, all in P458 and P424, were found to match cloned alleles in the same isolates. For the isolates P344, P387 the PacBio copies were not identified in the clones, however the alleles from isolate P427 were highly similar to the two identical PacBio copies found in the isolate (1 SNV difference). The PacBio copies found in isolate P387 had 14 bp shorter sequences, probably due to assembly artefacts. Isolate P344 had two identical PacBio copies and the closest allele, P344 AB33, had a total of four SNVs different from the PacBio sequences. Some of the *gFIHb* PacBio copies in assemblage B were also found to be identical, such as P458 copy 1 and 2, P387 copy 1 and 2, P424 copy 4 and 5 ([table S5](#)). See [supplementary box 1](#) for more information about the PacBio copies.

The copy number found in the PacBio data was compared to the number of cloned alleles. For the three sub-assemblage AII isolates with available PacBio data, more alleles were identified in isolates with a higher copy number (P064 two copies and two alleles, P392 four copies and eight alleles and P407 three copies and eight alleles). Among the assemblage B isolates, two isolates with two identified PacBio copies (P344 and P387) both had a total of nine identified alleles, thus higher than the theoretical maximum for a tetraploid organism with two gene copies. Isolates P427 and P458, both with two identified PacBio copies, had three and two alleles, respectively. In the isolate with the highest number of identified copies, P424, with six copies, nine alleles were identified.

Sequence Variation of the *gFIHb* Gene in *Giardia* Assemblages A and B

The identified SNVs in the cloned sequences were compared against Illumina sequencing data and categorized into high confidence (HC) and low confidence (LC) SNVs using the algorithm described in methods. LC SNVs were discarded and not used in the analysis, see [Supplementary Table S1](#) for full overview of HC and LC SNVs. Sequence analysis showed a higher proportion of nsSNVs/SNVs in assemblage B isolates (53%) than sub-assemblage AII isolates (38%) ([Table S1](#)). The number of SNV positions found in the respective cloned *gFIHb* CDS for each isolate varied from 6 to 48 for sub-assemblage AII and 14–28 for assemblage B sequences ([Table 2](#)). One AII isolate, P407, had the most SNV positions of all isolates with 48 SNV positions found, while the numbers of SNVs were more congruent among the B isolates with approx. 20 SNVs per isolate. A total of 4.8% and 5.4% of all positions of the *gFIHb* CDS showed some variation in AII and B, respectively (see [Tables S2–S5](#) and [S6–S7](#)). The total number of nsSNV positions per CDS was lower for AII isolates (22 positions, 1.6%), than for B isolates (42 positions, 3.1%). The average nucleotide diversity, π , between cloned alleles was calculated to be 0.007 in sub-assemblage AII isolates' sequences and 0.009 in assemblage B isolates. Generally, there were more nsSNVs found in just one or a few isolates in assemblage B isolates, compared to sub-assemblage AII, where numerous nsSNV positions were common for several isolates (see [Tables S3–S4](#)).

Amino Acid Changes and Relation to Predicted *gFIHb* Protein Structure

Based on homology modelling *gFIHb* shares the same domain structures as the homologous FIHb from bacteria^{49,51} and yeast.⁵² It is a protein formed of 3 structural domains: (1) heme binding globin domain; (2) a FAD-binding domain; (3) a C-terminal NAD binding domain. Homology models for *gFIHb* for assemblages A and B were generated and are shown in [Figure 3](#), where the detected nsSNVs that induced aa mutations are visualized. As noted before, assemblage B has a considerably higher number of aa substitutions than sub-assemblage AII. Most of the mutations are predicted to concern residues at the protein surface and, more accurately, those located in loop regions. Also, the majority is considered to only moderately affect the physicochemical

properties, eg, simply altering the size of a hydrophobic side chain. Some mutations, however, will cause a reversal of charge, hence affect local electrostatic properties of the protein surface. Some of the changes are predicted to be in near vicinity of the heme or FAD-binding sites and could have an effect for accommodating these co-factors. These changes are marked in red on Figure 3. The most drastic change amongst sub-assembly AII alleles is a premature stop codon at position 49 in alleles AA24 and AA25 in isolate P478 that likely results in early truncation within the first domain. In addition, there was a change of aromatic Y at position 211 to basic and positively charged H in several alleles (AA07, AA10, AA11, AA12, AA13 and AA15) observed in isolates P316, P361, P368, P392 and P407. This mutation is located in a putative FAD-binding region of domain 2. For assembly B, the most different allelic forms are obviously those with the deletion Del-75HEL77 that is located to the helix above the heme binding site, and the E80G variant is located on the same helix. Both the deletion and the E80G mutation are potential helix breakers that could disturb the secondary structure and affect heme binding.

Discussion

In this study, the allelic diversity of *gFIHb* was investigated through combined analyses of cloned sequences, genomic Illumina sequencing data, and de-novo assembled genomes derived from PacBio sequencing.

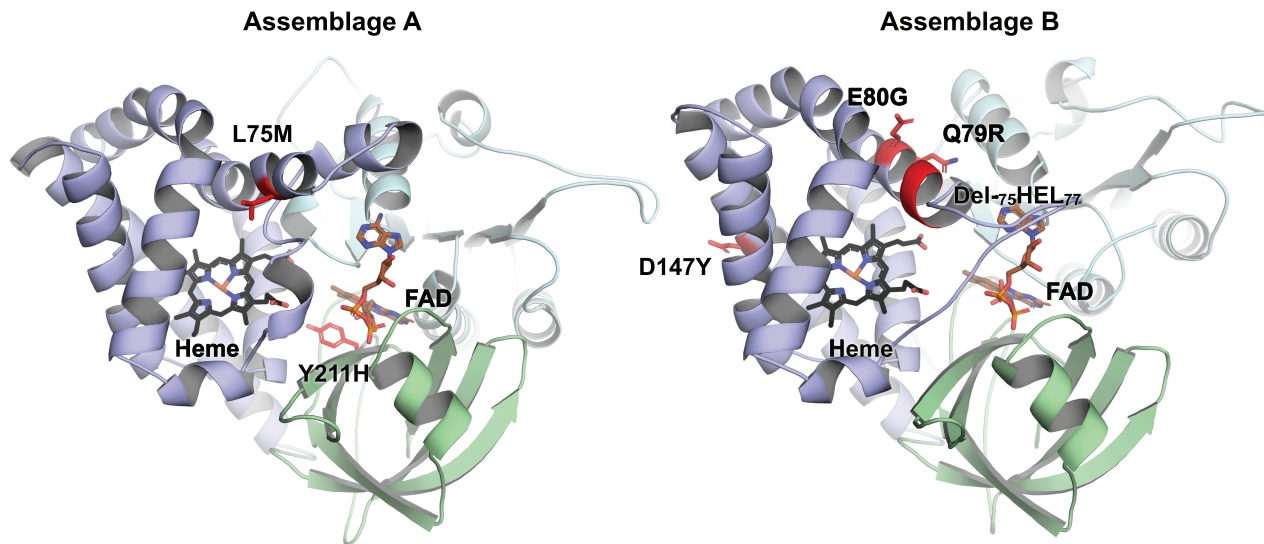
Sequencing Methods, PCR, Cloning and SNVs

Studies using a clone-based approach to identify SNPs in *Giardia* genes have been conducted earlier.^{37,38,41} In some of these studies a Taq-based polymerase was used for the PCR-amplification, and may have caused an inflated high diversity as the error rate of standard Taq is around 1 in every 3500 bp.⁵³ However, some of the studies have used Q5 or other high-fidelity polymerases that have a lower error rate.^{36,39,40,54} When identifying allele sequences it is important to utilize high-fidelity polymerases to minimize the chance of introducing errors during amplification.⁴⁰ The error rate of the Q5 polymerase used in this study has earlier been reported to be 1 per million bp.⁵³ Still, some SNVs identified in the clones could potentially be caused by amplification or sequencing errors, specifically within reads in the beginning or end of the Sanger sequences. The 35 cycles used in the initial gene-PCR

reactions could introduce amplification errors leading to false-positive SNVs in the clones. Validation of SNVs therefore becomes important. Indeed, identification of HC SNVs, and excluding LC SNVs from the analysis reduced the number of SNVs from an average of 23 to 21 in eleven sub-assembly AII isolates and from 37 to 22 for six assembly B isolates (table S1). We, therefore, consider the reported number of alleles and diversity as a conservative interpretation of the data. We could see that the majority of the SNVs identified in the clones were also identified in Illumina data for the same isolate. The clones had generally more unique SNVs than the number identified in Illumina data. However, for one isolate (P344), two different batches of DNA (trophozoites cultured an additional time to obtain enough DNA) were used for the Illumina sequencing data and the cloning experiments. Although derived by limiting dilution, P344 may represent a mixed isolate with variable contribution to, and dominance of, co-existing lineages between batches, and possibly introduction of new mutations. These could all be reasons why this isolate had the highest number of LC SNVs, and *gFIHb* alleles matching other alleles in the B assembly isolates.

General Features of *gFIHb* Genetic Diversity

Our analysis of SNVs in the CDS and copy number variation of the two ortholog *gFIHb* genes, DHA2_154000 and GSB_151570 in *Giardia* sub-assembly AII and assembly B reference strains DH and GS, respectively, show a high degree of genetic variation (number of variable SNV positions per CDS length) for both assemblies compared to the set of 29 MTZ-metabolizing and other metabolism genes analyzed in a previous study.⁴² One interesting finding in the present study is that sub-assembly AII isolates, shown to generally have less genetic variation than assembly B, possessed a higher number of SNVs than assembly B isolates in *gFIHb*.^{30,38,55,56} In addition, a relatively high allelic heterozygosity of the *gFIHb* gene coupled with nucleotide diversity values <0.01 was found in both assemblies. Other studies looking at nucleotide diversity in single copy genes glutamate dehydrogenase gene (*gdh*), beta-giardin (*bg*) and triosephosphate isomerase (*tpi*), that are often used for genotyping, have found similar nucleotide diversity ranging from 0.003 to 0.02.^{36,39} It is challenging to culture clinical isolates of *Giardia*, especially for assembly B parasites.^{57,58} *Giardia* strains that are able to grow in



Isolate number	Amino acid change	
Domain 1		
Assemblage A		
P033	N42D	D137N I138V E158D
P034	N42D	D137N I138V
P064	N42D	D137N I138V
P316	N42D	L75M D137N I138V
P361	N42D	D137N I138V
P368	N42D	L75M D137N I138V
P392	N42D	L75M D137N I138V
P403	N42D	L75M I138V
P407	N42D	L75M D137N I138V
P478	N42D	STOP-49Q* A66V D137N I138V
P506	N42D	D137N I138V
Assemblage B		
P344		V43I Q79R
P387		V43I Q79R E80G E88G L93P I119V
P413	E5G D6A	I72V Del-75HEL77 Q79R D135N
P424		Del-75HEL77 Q79R D135N
P427		V43I Q79R D147Y
P458		V43I Q79R
Domain 2		
Assemblage A		
P033		G264D
P034		G264D
P064		G264D
P316		G264D
P361		Y211H G264D
P368		Y211H G264D
P392		Y211H G264D
P403		Y211H G264D
P407		G202D G264D
P478	V195I	Y211H G264D
P506		G202D G264D
Assemblage B		
P344		I185V T233I K268E
P387	A183V	T233I K249R K268E
P413	E180K	I185V T239M K268E
P424	E180K	I185V T239M K268E
P427		I185V F190S A197T T233I K268E
P458		I185V T239M K268E A270V
Domain 3		
Assemblage A		
P033	P288A	A289V Q295P N354D A366T A413V N443D S444N
P034	P288A	A289V Q295P N354D A366T
P064	P288A	A289V Q295P N354D A366T
P316	P288A	A289V Q295P N354D A366T
P361	P288A	A289V Q295P A366T
P368	P288A	A289V Q295P N354D A366T A413V N443D S444N
P392	P288A	A289V Q295P N354D A366T I405V A413V A416V N443D S444N
P403	A283V P288A	A289V Q295P N354D R376H I405V
P407	P288A	A289V Q295P M313T N354D A366T R376H I405V A413V S444N R445S
P478	A283V P288A	A289V Q295P M313T N354D R376H
P506	P288A	A289V Q295P A366T
Assemblage B		
P344		D384N K437Q
P387	G285E	G290R L316P S318P M329L E335G K336R V363I R399H S401G D403N E412G Q434K K437Q P442S R445H
P413		G290R L316P S318P M329L E335G K336R V363I R399H S401G D403N E412G Q434K K437Q P442S R445H
P424		G290R
P427	R281S	W347R D384N
P458		M329L A365I K437Q

Figure 3 Cartoon representation of homology models created for gFIH from assemblage A and B. Heme binding globing domain is presented in purple, FAD-binding domain in green and C-terminal FAD-binding domain in cyan. Heme and FAD were fitted to the homology model and are presented by stick representation. Detected nsSNV-induced mutations to the amino acid sequences for individual isolates are presented in the table. Mutations possibly affecting directly to protein function by disturbing the heme or FAD binding are indicated with red in both cartoon models and in the table. The mutation marked as STOP-49Q introduces a stop codon into the sequence interrupting the protein synthesis.

culture could have an adapted metabolism of MTZ and detoxification processes of free radicals and O₂ and may represent a selected version of the isolates causing disease in humans. The isolates in the present study could therefore be biased with regard to gFIHb copy numbers or be the reason for the low nucleotide diversity and many different, but similar, alleles of *gFIHb*. With this caveat in mind, the alleles and copy number variation identified in the present study will nevertheless enable future studies and analysis of *gFIHb* in non-culturable isolates, as it provides a start of a respective database of gene variants.

Alleles of the gFIHb Gene

In the present study, several alleles of the *gFIHb* gene were identified and PacBio sequencing confirmed that the number of copies of *gFIHb* in each isolate is variable. As several copies of *gFIHb* are sometimes found on the same contig, we use the term allele rather than the term haplotype which has been used in previous studies of *Giardia* single-copy gene variants.^{39,40,54} The phylogenetic trees in Figures 1 and 2 represent all the identified alleles in each isolate from sub-assemblages AII and assemblage B. Assemblage B isolates had less available samples and clones than AII, but had more unique alleles (41 vs 37). No sub-assemblage AII derived allele was found in assemblage B isolates, or vice versa, thus indicating no inter-assemblage recombination. However, it is difficult to define full tetraploid *gFIHb* genotypes with the number of clones available for each isolate, further complicated by the presence of copy number variation (CNV) which allows for more possible combinations of *gFIHb* alleles. Phylogenetic trees for each assemblage, on the other hand, are consistent with the occurrence of intra-assemblage recombination and genetic exchange although mixed isolate infections cannot completely be ruled out. Some alleles were common and found to be present in more than one isolate, while the same isolates also harbor several other, and different, alleles only occurring in one isolate (see tables S4 and S5). The high allelic diversity indicates that the overall diversity in the population may be much larger. As *gFIHb* is a variable-copy gene, the maximum number of alleles one tetraploid *Giardia* strain may harbor is four times the number of copies. In sub-assemblage AII isolates, higher copy numbers correlated with higher numbers of identified alleles but no breach to said rule was observed. In previous studies investigating haplotypes of single copy genes such as (*bg*, *gdh* and *mlh*, *tpi*), more than

the expected maximum four haplotypes per paralog were encountered.^{36–39} At present, we cannot rule out that this could be due to unidentified additional copies of the gene hidden in the current versions of de novo assembled genomes. Also, mixed infections consisting of multiple *Giardia* strains as demonstrated by previous studies, cannot be discounted completely (see above).^{29,33,37–39,59} However, we favor the idea that supernumerary alleles reflect genome variations that have occurred during culture causing co-existence of daughter lineages as described by Choy et al.³¹ Remarkable genetic variation due to selective pressure during axenization has been recently described also for other parasites such as *Leishmania donovani*.^{60–62} In both assemblages, some of the identified alleles were not matching the identified PacBio copies. Minor alleles, representing 1:4 of the possible alleles in a tetraploid organism, are likely to be missed in consensus sequences as nucleotides of the major allele would be decisive. This, in addition to potential sequencing errors in combination with correction routines or assembly errors in the PacBio genomes might be the reason why not all copies are represented by the identified alleles.

Copy Number Variation

gFIHb is an important enzyme in the detoxification processes in *Giardia*, to eliminate the harmful effects of NO. One study showed that this was the sole enzyme that was upregulated in several different stress-exposures such as O₂ and H₂O₂, although there was no correlation between transcription responses to H₂O₂ and MTZ.¹⁴ Our finding of a variable number of *gFIHb* gene copies may be important in relation to tackling the oxidative stress caused by MTZ treatment. A recent study by Müller et al, reported upregulated gFIHb protein levels in an MTZ and nitazoxanide resistant isolate.²⁰ One can hypothesize that it is beneficial for the parasite to have more *gFIHb* gene copies, as it may promote survival in an environment with higher O₂ levels, where activation of MTZ is lower, or in the oxidative stress condition induced by MTZ. Interestingly, a major antibiotic function of MTZ is to cause oxidative stress, and it is tempting to speculate whether gFIHb could be involved in neutralizing the harmful effects of the drug as *Giardia* lacks conventional antioxidant enzymes.⁶³ In a previous study, the nitro-drug resistant line C4 of *Giardia* was compared to its corresponding wild-type WBC6 isolate with respect to mRNA expression, O₂ consumption and functional assays.⁶⁶ It was found that the C4

line exhibited lower nitroreductase activity, while mRNA levels of *gFIHb* were not significantly different before and after drug exposure while reduction of nitro-drug activation was found to be lower.⁶⁶ In another study by Ansell et al 2017, strand-specific RNA analysis was carried out in three resistant laboratory lines.⁶⁷ *gFIHb* was found to be strongly induced in one of the lines (713-r), and the authors suggested that *gFIHb* could play the role of an alternative MTZ detoxification enzyme.⁶⁷ This may be assay dependent, but is more likely to be strain specific, especially as different *Giardia* isolates harbor a variable number of *gFIHb* copies. Taken together these findings indicate that different *Giardia* isolates could have different MTZ resistance formation strategies, ie, isolates with a higher *gFIHb* copy number may be more prone to use an active detoxifying MTZ resistance strategy, while other isolates may adopt a strategy of reduced MTZ activation.⁶⁶ For higher eukaryotes, such as the insects *Anopheles gambiae* and *Culex pipiens*, increased CNV has been linked to insecticide resistance.⁶⁴ Aneuploidy causing increased copy numbers of several genes in fungi has also been linked with drug resistance.⁶⁵ Although several copies of the *gFIHb* gene in some isolates were found, we must acknowledge that we do not know how the copies, and their various alleles would be expressed or regulated in an MTZ exposed *Giardia* isolate in need of more potent free radical neutralization. Further studies combining single-cell DNA and RNA sequencing are needed to elucidate the effect of having multiple *gFIHb* copies on the ability to overcome MTZ toxicity or improve tolerance of oxidative stress. In the current reference genome of sub-assembly AII there are two shorter paralogs of *gFIHb* (DHA2_152971 and DHA2_153995) that could potentially result in falsely higher coverage for the *gFIHb* gene. There is no reason to believe that these shorter fragments contribute to the higher coverage found in the Illumina sequence data, and this was shown in a previous study.⁴² Furthermore, the PacBio consensus sequences were used to determine the CNV in the *gFIHb* gene, and the shorter paralogs could not affect the results, as full-length genes were investigated.

Putative Effect of SNV-Induced Mutations on *gFIHb* Proteins

The *gFIHb* gene in both sub-assembly AII and assembly B was found to have a high number of nsSNVs that would alter the protein's amino acid sequence. Some previous

studies have also reported high numbers of nsSNVs in house-keeping genes, especially for assemblage B isolates, but these SNVs were commonly only causing conservative aa changes, unlikely to affect protein function or structure.^{37,40} The crystal structure of *gFIHb* protein is not yet known, and structural mapping of the location of the mutated amino acids was consequently based on homology models. The premature stop codon found in two alleles in sub-assembly AII clones will cause a truncated protein without its normal function. Interpretation of the mutations that seem to be located on the surface of the protein is more challenging in terms of predicting the effect. Altering the surface charge could potentially have an effect on inter-molecular interactions. It is clear that further research is needed to investigate whether the aa changes can potentially affect the function of the respective protein variants. Specifically locating the exact site for NAD binding would help us investigate the effect of the mutations in the domain 3, the NAD binding domain. However, some of the mutations described might indeed affect heme and FAD binding, therefore altering protein function.

Limitations

For some of the isolates, few clones were obtained, and rare alleles may have been missed in some isolates. For isolate P064, one of the two *gFIHb* copies found in the PacBio consensus sequence, was not found among the clones obtained in this study, showing that several more alleles may exist for this isolate. One other explanation for missing alleles, is that the PCR primers targeting *gFIHb* in the initial amplification may not have matched all alleles and did not bind to the template DNA and amplify these. However, PacBio consensus copies may not be identical to the clones due to sequencing errors, or due to PacBio sequence correction routines. The study population in this study is rather small and future studies of non-cultured isolates are likely to extend information about the number of copies and genetic variation of the gene. The SNVs analyzed in the present study were all limited to the CDS of the *gFIHb* of assembly A and B isolates. There have been previous studies linking SNPs in intergenic areas to MTZ resistance in *T. vaginalis*, specifically 12 SNPs, that potentially could be markers of resistance.⁶⁸ SNVs in the up- or downstream regions of the *gFIHb* CDS could affect the transcription and therefore be of potential interest for investigating MTZ susceptibility and oxidative stress responses markers in future studies.

Conclusion

In this study, we show evidence that the *gFIHb* gene in *Giardia* sub-assembly AII and assembly B, is a variable copy number gene with a high allelic diversity. The high genetic diversity seems to be due to both high copy number variation, many similar but unique, alleles per isolate, and a high number of SNV positions among both *Giardia* sub-assembly AII and assembly B isolates. Relatively high percentages of nonsynonymous SNVs were identified in both assemblies and some changes could potentially affect the protein function. The variable copy number nature of the *gFIHb* gene may allow some *Giardia* strains to better adapt to nitrosative and oxidative stress and could thereby potentially play a role in MTZ susceptibility.

Abbreviations

CDS, coding region; *gFIHb*, *Giardia lamblia* Flavohemoprotein; HC, High Confidence; LC, Low confidence; MTZ, Metronidazole; ns, nonsynonymous; SNV, single nucleotide polymorphism; s, synonymous.

Data Sharing Statement

The sequences for the identified *gFIHb* alleles are available in NCBI genbank with accession numbers: MT713149-MT713229, MT713231-MT713243, MT713245-MT713263, MT713267, MT713269.

Ethics Statement

No patient data was collected and used in the present study. Any link between individual parasite data and patient information had been removed before WGS of trophozoites and cloning experiments were carried out.

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Author Contributions

All authors made a significant contribution to the work reported, whether that is in the conception, study design, execution, acquisition of data, analysis and interpretation, or in all these areas; took part in drafting, revising or critically reviewing the article; gave final approval of the version to be published; have agreed on the journal to which the article has been submitted; and agree to be accountable for all aspects of the work.

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Disclosure

Some of the data in this paper has been published as an abstract and was presented at the VIIth International *Giardia* and *Cryptosporidium* Conference (IGCC), 2019, as a conference talk with interim findings. The abstract was published in the “Conference abstracts on USB Key” and is available from [<https://en.rouentourisme.com/wp-content/uploads/2019/06/Programme-d%C3%A9finitif-modif%C3%A9-200619.pdf>].

The authors report no conflicts of interest for this work.

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