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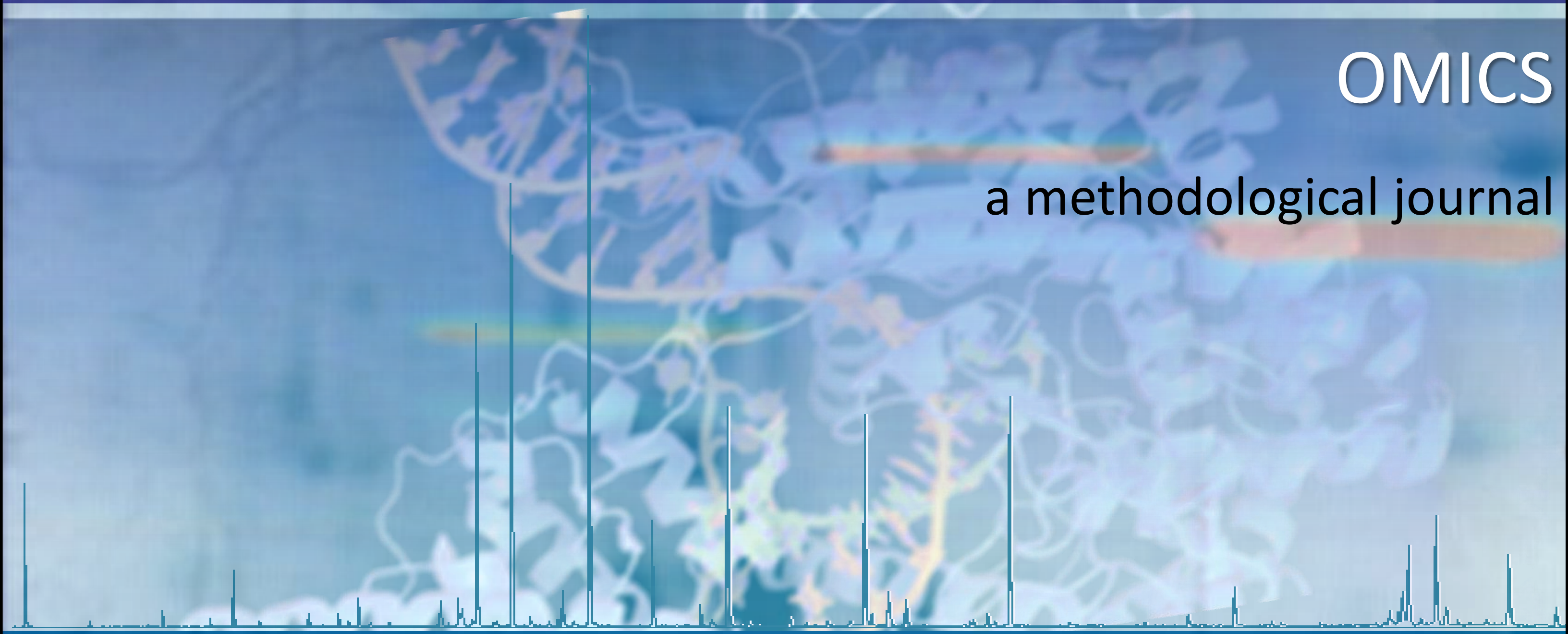

JIOMICS

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Journal of Integrated OMICS, JIOMICS, provides a forum for the publication of original research papers, preliminary communications, technical notes and critical reviews in all branches of pure and applied "-omics", such as genomics, proteomics, lipidomics, metabolomics or metallomics. The manuscripts must address methodological development. Contributions are evaluated based on established guidelines, including the fundamental nature of the study, scientific novelty, and substantial improvement or advantage over existing technology or method. Original research papers on fundamental studies, and novel sensor and instrumentation development, are especially encouraged. It is expected that improvements will also be demonstrated within the context of (or with regard to) a specific biological question; ability to promote the analysis of molecular mechanisms is of particular interest. Novel or improved applications in areas such as clinical, medicinal and biological chemistry, environmental analysis, pharmacology and materials science and engineering are welcome.

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Prescriptomics: the next frontier in medicine

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Analysis of proteins has been an integral part of clinical chemistry for decades. However, recent technological advances have opened new opportunities for the large-scale analysis of proteins for clinical diagnostic purposes and personalized medicine [1]. First, the development of mass spectrometers with significantly higher resolution and larger dynamic range has allowed generating high-quality quantitative data from complex sample matrices such as serum, plasma, urine, cerebrospinal fluid, and tissue biopsies without the need for isotopic labellings [2, 3]. Instruments like TOF, Orbitrap, FT -ICR and the most recent timsTOF [4, 5] were a stepping-stone towards proteomic-based personalized medicine by facilitating the detection of patient-specific protein signatures that reorganize over time due to genetic, environmental, and treatment constraints.

Second, the development of high-throughput robust sample preparation methods has allowed the processing of many clinical specimens in an efficient and reproducible manner [6]. Parallel to such achievements, the exciting advances experienced by bioinformatics have been a cornerstone in translating quantitative proteomics data into actionable clinical information [7]. Thus, the development of new and powerful algorithms, artificial intelligence, and information theoretics, combined with large datasets available in data repositories such as TCGA [8] or Proteome exchange [9] are moving biology and medicine where no other sciences have gone before [10]. Nowadays, the proteomics community is addressing a critical question: is it possible to obtain helpful information from these datasets to determine which combination of FDA or EMA-approved drugs is best suited to treat each patient? [11]. Exciting discoveries are expected from re-analyzing these already available datasets.

The concept of genomics soon evolved into the concept of phenome [12], the latter referring to the actual expression of an individual's genes. As phenomics evolves and matures, it is becoming clear that pre-defined categories where diseases were classified and grouped, contradict the vast heterogeneity of phenotypes. Thus, the treatment of phenotype-dependent complex diseases with extensive heterogeneity, like cancer, is likely to overlook unique patients that must be treated individually. We are what we express. And what we express can be now quantified with unprecedented precision and accuracy. By quantifying the proteome expressed by a patient, any disease can be diagnosed, prognosed and followed either using a tissue or in a liquid biopsy (urine, serum, plasma). However, a challenge remains. Can the information provided by proteomics and phenomics be translated to prescriptomics? This is, based on patient-specific alterations in protein-protein networks will prescription be personalized? Yes, proteomics will be a good bridge between diagnostics and therapeutics. This is our best answer based on our current knowledge on disease, genomics, proteomics, and phenomics [11–16].

So far, this is how we visualized the revolution in medicine ahead of our time. Within the next five to ten years, the ultrafast analysis of proteomes of liquid and solid biopsies via high-resolution mass spectrometry will be done in minutes. Currently, mass spectrometry technologies allow

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for the absolute quantification of hundreds of proteins in just 15 min. [16, 17]. Next, the bioinformatic analysis of the sampled proteome(s) will deliver information about the altered biological pathways in each patient, for instance, to uncover whether specific signalling pathways or the inflammatory and immune response pathways are dysregulated [18, 19]. Also, it will collect information about single and well-characterized biomarkers to complement the information taken from the interpretation of the proteome.

Altogether, each unique phenotype will lead to a personalized prescription based on a diagnosis done at a protein-pathway interaction level. This is what we call prescriptomics. Further, linking this technology with communication via electronic interface and drone delivery will make physician and patient interaction faster. Within the next ten years, technological tools will be implemented, allowing proteomic analysis to be done at home just using saliva or urine, not to mention blood. These tools are currently used in hospitals, but interfaces making them ready to use at home are soon expected. By accomplishing the tool to the computer or the mobile phone, the information will be delivered to the physician via a software interface addressing a potential prescription. In case of need, specific tools or sample collecting devices will be provided to the patient and picked up by drones, then transporting again the sample to the laboratory of analysis. Such an approach brings several advantages. For instance, a lower number of patients attending the hospital face to face, thus avoiding the risk of becoming infected or vectors spreading diseases. Also, a most effective medical decision making is expected. Furthermore, the following up of the patient's proteome during and after medical care will thus be made easier and will allow the implementation of dynamic therapy as the standard method to treat disease providing a unique system to alert for relapses.

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Comparative analyses of the complete mitochondrial genomes of the two filarial worms *Wuchereria bancrofti & Brugia malayi* with *Caenorhabditis elegans*

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ABSTRACT

Wuchereria bancrofti and *Brugia malayi* are filarial worms belonging to the phylum Nematoda and cause lymphatic filariasis (LF) disease in humans. *W. bancrofti* and *B. malayi* are *Wolbachia* dependent organisms while *C. elegans* is a free living *Wolbachia* independent nematode. To investigate the conserved regions present in the mitochondrial genome of these organisms, the complete mitochondrial (mt) genomes of *W. bancrofti* and *B. malayi* having sizes 13,636 bp and 13,657 bp in length, respectively are compared with *C. elegans* (13794 bp). These mt genomes were similar to each other in respect of their size, and AT content and encode the same 12 PCGs (nad1–6, nad4L, cytb, cox1–3, and atp6). Complete mt genome alignment identified 13 conserved regions in each of the organisms with some of these regions unique only to one organism. Phylogenetic analysis using the mt genome showed a close relationship between *W. bancrofti* and *B. malayi* but showed a common early ancestor with the *C. elegans* emphasizing an early evolutionary divergence.

Keywords: *Comparative genomics; Mitochondrial DNA; conserved regions; Phylogenetic analysis; ORFs .*

1. Introduction

Wuchereria bancrofti and *Brugia malayi* are parasitic filarial worms belonging to the phylum Nematoda and cause lymphatic filariasis (LF) in humans. Worldwide, LF is a neglected tropical disease [1] affecting thousands of individuals and has little research investment [2]. This disease is not lethal but its infection is chronic leading to lifetime deformity which is not curable and its treatment is also difficult [3]. The symptoms including lymphoedema, elephantiasis and scrotal swelling are painful and can lead to permanent physical impairment. Along with impairment, the patient suffers from economical losses and the psychological stigma related to it is also devastating in the sense of social as well as self-acceptance (WHO factsheet). The current focus is on controlling its transmission, but an in-depth exploration of its genomic sequences can provide the baseline molecular data on these parasites giving insight into their evolutionary path.

The genomic study of an individual is done either with its nuclear or mitochondrial (mt) genome or with both. This study deals with a comparative analysis of mitochondrial genomes which contains a minor but important component of a eukaryote's genome [4]. Even though animal mt sequences are known to evolve rapidly, their gene arrangements typically remained constant throughout their evolution [5]. That is why the mt genome has always been extensively used as a molecular marker for phylogenetic studies [1]. In all animals, the mt genomes, with a few exceptions, include the same 37 genes: 13 encoding for proteins, 2 for rRNAs, and 22 for tRNAs. The variation that exists in mitochondrial genome size is usually related to the length differences of non-coding regions, the repetitive nature of some sequences, and/or the presence of huge duplications in some species [6]. Parasitic nematodes

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have a compact, circular mt genome which varies in size from 13,000 to 26,000 bp [7]. The selected nematodes under this study have mt genome with 12 protein-coding genes (PCGs) namely nad1–6, cox1–3, nad4L, cytb, and atp6 (lacking atp8 gene), 2 rRNA genes, and 22 tRNA genes [6]. The comparative study of all these genes will help search for the resemblances and variations between them at the genomic level.

Comparative genomics is not only a tool but also a comprehensive approach in bioinformatics research for comparing species to find out similarities and differences at the sequence level. Its principle involves genes and genomes to be studied and compared in the phylogenetic context of the evolutionary process[8]. In this process, we exploit the fact that the genes encoding similar characters are part of conserved DNA between two species. The conserved DNA sequences, which encode functional proteins must remain preserved from the last common ancestor up to the current generation [9].

The purpose of this study is to perform comparative genomics of the mt genome of parasitic nematodes *Wuchereria bancrofti* and *Brugia malayi* with free-living nematode *Caenorhabditis elegans*. Since both the *W. bancrofti* and *B. malayi* are *Wolbachia*-dependent parasites [10], they are supposed to have some variations as compared to the free-living nematode *C. elegans* at the genomic level. Researchers previously compared the mt genomes of *Wolbachia* dependent and independent nematodes but could not find any major difference [11]. We hypothesized that the conserved regions in the mitochondrial genomes of these organisms may reveal the crucial differences or similarities that may help in understanding their nature, their genomic features, and their phylogenetic relationships with each other.

2. Material and Methods

2.1 Data retrieval

The mt genomes of the species *Wuchereria bancrofti* (GenBank accession number NC_016186), *Brugia malayi* (GenBank accession number AF538716.1), and *Caenorhabditis elegans* (GenBank accession number NC_001328) were retrieved from NCBI. The mt nucleotide content (ATGC) of all the three species was calculated using GC Content Calculator, online analysis, and plot tool provided by BiologicsCorp (https://www.biologicscorp.com/tools/GCContent/index).

2.2 Identification of conserved regions

The complete mt genomic sequences of the species *W. bancrofti*, *B. malayi* and *C. elegans* were aligned using an open-source MAUVE aligner, version 2.3.1, via progressive algorithm [12]. In Mauve software, the conserved sequences of genomes are aligned with rearrangements. First, the mt genomic sequence of *W. bancrofti* was aligned with *C. elegans*. It was followed by alignment of the mt genomic sequence of *B. malayi* with *C. elegans* and *W. bancrofti* respectively.

The sequences identified as conserved regions by mauve software were further analyzed against the NCBI database using BLASTP. In each conserved region identified, Open Reading Frames (ORFs) were predicted by using the ORFfinder tool of NCBI (https://www.ncbi.nlm.nih.gov/orffinder/) followed by smart BLAST analysis for functional identification.

2.3 Identification of conserved intergenic regions

The identification of conserved intergenic regions were performed by the alignment of complete mt genome sequence of *W. bancrofti* and *B. malayi* with *C. elegans* individually and at last *W. bancrofti* and *B. malayi* were aligned with each other. The species were aligned with the wgVISTA tool of the Vista server [13]. Similar alignment of the mitochondrial genomes of all these three species was also done by UCSC genome browser [14].

2.4 ORF prediction

The ORFs were predicted in the complete mt genome sequences of all the species using the ORFfinder tool of NCBI (https://www.ncbi.nlm.nih.gov/orffinder/). Each ORF predicted by the ORFfinder tool of NCBI was further subjected to BLASTP (protein-protein BLAST) to find out its probable function.

2.5 Multiple sequence alignment

Multiple Sequence alignment (MSA) of all three species was performed using the CLUSTALW server of EMBL-EBI [15]. For this, the slow and accurate pairwise alignment parameter was adopted.

2.6 Phylogenetic Analysis

Phylogenetic analysis of these species was done along with 59 other nematode species by using their complete mt genomic sequences in Mega X [16]. Neighbor-Join and BioNJ algorithms were applied to obtain the Initial tree(s) by using the Maximum Composite Likelihood (MCL) approach. The analysis involved 62 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. There was a total of 26194 positions in the final dataset.

2.7 Comparison of protein coding genes

All the 12 protein coding genes (PCGs) namely nad1–6, nad4L, cytb, cox1–3, and atp6 found in the mt genome of the three species, along with their amino acid sequence of proteins were retrieved from the NCBI database and aligned with each other using CLUSTALW [15] and their alignment score were recorded to determine the sequence identity in them. The amino acid sequence of proteins were cross referred with their sequence in PDB database. The amino acid sequence reterived from NCBI and PDB database were aligned by pBLAST to validate the sequence similarity.

3. Results

3.1 Genomic Details

The complete mt genomes of *W. bancrofti* (GenBank accession number: AP017705.1), *B. malayi* (GenBank accession number AF538716.1), and *C. elegans* (GenBank accession number NC_001328.1) are having size 13636 bp, 13657 bp, and 13794 bp respectively. *W. bancrofti* has the smallest genome among the three species. The nucleotide content of all three mt genomes is enlisted (Table 1). *W. bancrofti* and *B. malayi* has almost similar AT content while *C. elegans* has a slightly more percentage of A nucleotide.

3.2 Identification of conserved regions

With help of results generated by MAUVE software (Figure 1), the output backbone file was used for the quantitative identification of conserved genomic order. The information regarding the coordinates of the regions shared by two genomes and their localization in the genomes is present within it. The ORFs were located in each of the conserved regions.

In the case of alignment of mt genomes of *W. bancrofti* to *C. elegans*, a total of 13 conserved regions have been identified separately for each genome. Out of which, 7 regions were aligned to each other while the remaining 6 regions were not (suggesting it to be unique between them). Among all the conserved regions, a maximum of 12 ORFs were predicted in the 4137 to 7039 nucleotide region of *C. elegans*. It also identified 5 regions where no ORF was predicted. In the same alignment result, 20 ORFs were found in the 3095-6932 nucleotide region of *W. bancrofti* while 2 regions were identified to have no ORFs. Most of the ORFs showed functional similarity with the 12 protein coding genes of their respective genome. Two hypothetical proteins namely WUBG_19143 (of *W. bancrofti* in the 1574-1819 nucleotide region) and DI535_26975 (of *C. elegans* in the 8655-9429 nucleotide region) have also been identified. In the 12153-13187 nucleotide region of *W. bancrofti*, one ORF showed functional similarity with the neuronal IgCAM of *C. elegans*. A multiple C2 and transmembrane domain-containing protein 2 isoform X1 has been predicted in one of the ORF of 7029-10006 nucleotide region of *W. bancrofti* (Table 2).

In the alignment result of *B. malayi* to *C. elegans*, 13 conserved regions were identified in which 7 regions were aligned to one another while the remaining 6 were unique between them. A maximum of 25 ORFs were predicted in the 2590-9950 nucleotide region of *C. elegans* while 7 regions didn't show any ORF. Similarly, 6 regions of *B. malayi* didn't have any ORF in them. No full-length PCGs in ORFs other than 12 PCGs of mitochondria have been found in their respective genomes (Table 3).

In *W. bancrofti* and *B. malayi* alignment, 6 conserved regions were identified in which 5 regions were aligned to each other while only one was left. Maximum 33 ORFs were predicted in the 4500-11090 nucleotide region of *W. bancrofti* and a multiple C2 and transmembrane domain-containing protein 2 isoform X1 has been predicted again (also predicted in the alignment of *C. elegans* and *W. bancrofti*) in one of the ORF of 4500-11090 nucleotide region of *W. bancrofti*. 27 ORFs were predicted in 4458-11075 nucleotide region of *B. malayi*. In one region (1019-1041 nucleotide region of *W. bancrofti* and 11076-11098 nucleotide region of *B. malayi*) no ORF was predicted for both the genomes (Table 4). The neuronal IgCAM of *C. elegans* was also predicted in one of the ORF in the 11095-13644 nucleotide region of *W. bancrofti*. Two uncharacterized proteins namely BM_BM5154 and BM_BM126 and one hypothetical protein of *Wolbachia* endosymbiont of *Mansonella perstans* (A filarial nematode) were identified in the 1019-4456 nucleotide region of *B. malayi*.

Smart BLAST could not assign functions for all the predicted ORFs and only those which showed similarity with the known protein were listed (Table 2-4).

3.3 Identification of intergenic regions

In the alignment result of *C. elegans* and *W. bancrofti*, a total number of 20 conserved intergenic regions have been identified (Table 5) which have aligned with each other showing identity ranging between 68 to 74%. The identified intergenic regions which are part of the non-coding region have sequence length ranging between 104 bp (smallest) to 333 bp (largest). The alignment of *C. elegans* and *B. malayi* have identified 22 intergenic regions with identity ranging between 67.8 to 74 (Table 6). The identified conserved intergenic regions have sequence length ranging between 98 bp to 277 bp. In case of alignment of *W. bancrofti* and *B. malayi* only one conserved intergenic region has been identified and aligned with each other showing highest sequence identity of 87.5%. UCSC genome browser comparison of the three mitochondrial genomes also reveals the conservation among the different nematodal species. Regions of high conservation corresponds to the coding regions while intergenic regions have relatively less conservation (Figure 2).

3.4 ORF

A total number of 63, 58, and 40 ORFs were identified in the complete mt genome of *W. bancrofti* (Table S1), *B. malayi* (Table S2), and *C. elegans* (Table S3) respectively

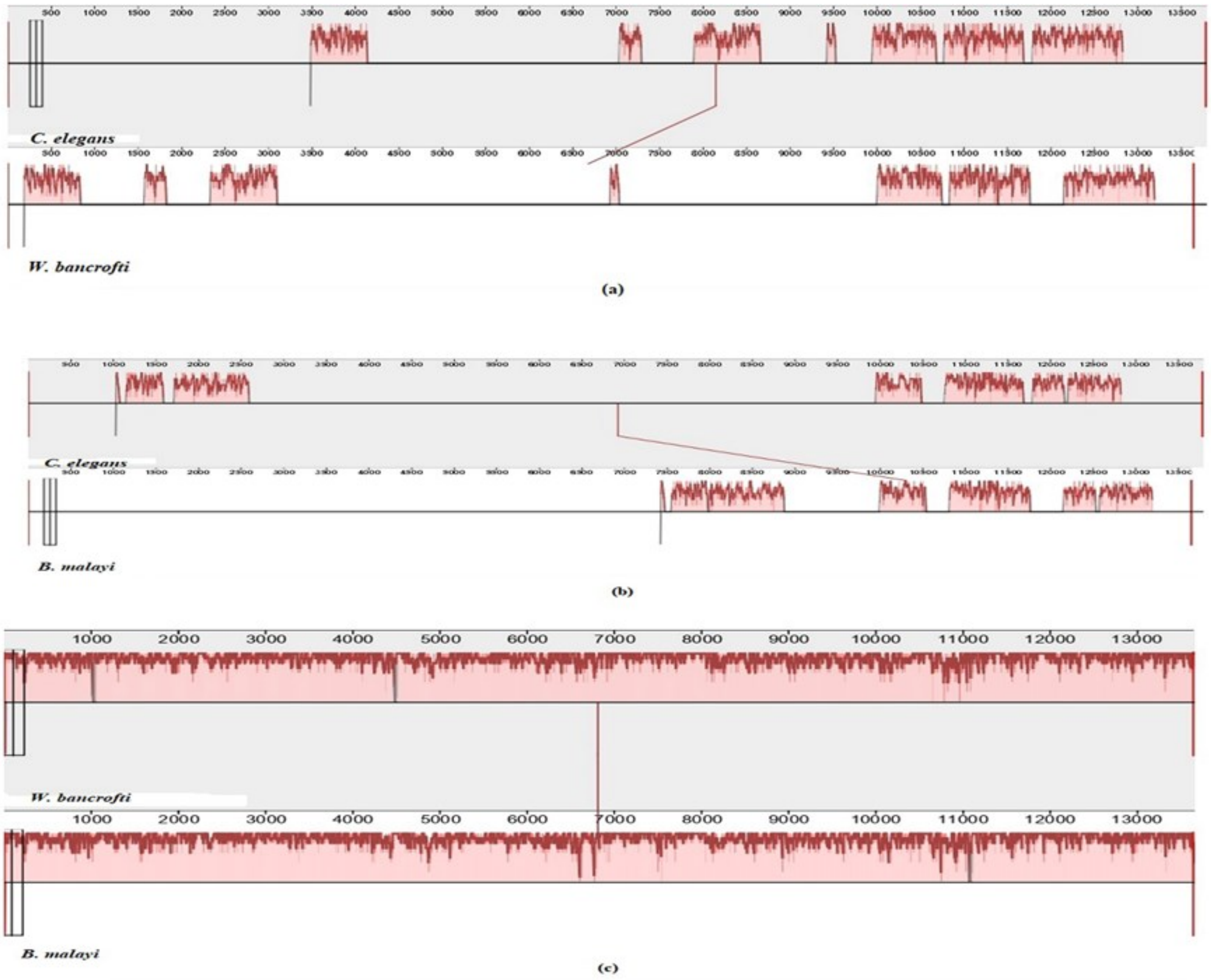

Figure 1 | (a) Alignment of *W. bancrofti* to *C. elegans*; (b): Alignment of *B. malayi* to *C. elegans*; (c): Alignment of *B. malayi* to *W. bancrofti* generated by the MAUVE viewer. The coloured bars inside the blocks are related to the level of sequence similarities. The line links the blocks with homology between two genomes that are aligned from top to bottom. The figure represents the genome alignment in which each panel represents one genome. The colourful blocks outline those regions of the genome sequence of one organism which have been aligned to the other genome sequence. The regions outside the coloured blocks/area of white regions depict the regions that have not been aligned, probably due to lineage specific sequences. The alignment panels of the *W. bancrofti* and *B. malayi* (c) genome alignment results are completely covered with the region of colour block depicting the highest level of sequence alignment as compared to the other two alignment results.

Table 1 | Comparison of nucleotide content of mtDNAs

Species	*W. bancrofti*	*B. malayi*	*C. elegans*
Family	*Onchocercinae*	*Onchocercinae*	*Rhabditidae*
Accession Number	NC_016186	AF538716	NC_001328
Length (bp)	13636	13657	13794
A %	20%	21%	31%
T%	55%	56%	47%
G%	18%	16%	14%
C%	7%	7%	8%
AT	75%	77%	78%

Table 2 | Alignment results of *W. bancrofti* to *C. elegans* (Backbone file results) showing the conserved regions generated by the Progressive Mauve program. ORFs predicted in the identified conserved regions followed by smart BLAST results for assigning the functions to ORFs. (NOTE- The differences in the no. of ORFs predicted and the results show that the smart BLAST could not predict functions of all the ORFs as no significant similarity was found with any known protein.)

S.No.	*C. elegans* nucleotide region (left end to right end)	No. of ORFs predicted	Smart BLAST results	*W. bancrofti* nucleotide region (left end to right end)	No. of ORFs predicted	Smart BLAST results
1.	3486-4136	2	Smart BLAST found no matches for both the ORFs	186-832	4	1.NADH dehydrogenase subunit 2 2. NADH dehydrogenase subunit 2
2.	7040-7286	1	Smart BLAST found no matches	1574-1819	1	hypothetical protein WUBG_19143 [*Wuchereria bancrofti*]
3.	7900-8654	4	1. cytochrome c oxidase subunit I 2. cytochrome c oxidase subunit I 3. cytochrome c oxidase subunit I 4. cytochrome c oxidase subunit I	2335-3094	4	1. Cytochrome oxidase subunit I 2. cbb3-type cytochrome c oxidase subunit I [*Wolbachia* endosymbiont of *Mansonella perstans*]
4.	9430-9521	0		6933-7028	0	
5.	9948-10677	2	Smart BLAST found no matches in both the ORFs	10007-10742	2	cytochrome c oxidase subunit 2
6.	10771-11682	2	Smart BLAST found no matches in both the ORFs	10837-11754	4	NADH dehydrogenase subunit 3
7.	11795-12823	0		12153-13187	6	1.NADH dehydrogenase subunit 5 2. NADH dehydrogenase subunit 5 3. neuRonal IGCAM [*Caenorhabditis elegans*]
8.	4137-7039	12	1.NADH dehydrogenase subunit 4 2. cytochrome b 3. cytochrome c oxidase subunit III 4. NADH dehydrogenase subunit 2 5. cytochrome c oxidase subunit III	0		
9.	7287-7899	2	1.NADH dehydrogenase subunit 4 2. NADH dehydrogenase subunit 4	0		
10.	8655-9429	4	1.cytochrome c oxidase subunit I 2. hypothetical protein DI535_26975]	0		
11.	9522-9947	0		0		
12.	10678-10770	0		0		
13.	11683-11794	0		0		
14.	0			833-1573	5	NADH dehydrogenase subunit 4
15.	0			1820-2334	2	NADH dehydrogenase subunit 4
	0			3095-6932	20	1.cbb3-type cytochrome c oxidase subunit I 2. cytochrome c oxidase subunit III 3. cytochrome b 4. cytochrome b 5. cytochrome c oxidase subunit 1 6. cytochrome b
16.	0			7029-10006	12	1.NADH dehydrogenase subunit 1 2. multiple C2 and transmembrane domain-containing protein 2 isoform X1
17.	0			10743-10836	0	
18.	0			11755-12152	0	

Table 3 | Alignment results of *B. malayi* to *C. elegans* (Backbone file results) showing the conserved regions generated by the Progressive Mauve program. ORFs predicted in the identified conserved regions followed by smart BLAST results for assigning the functions to ORFs. (NOTE- The differences in the no. of ORFs predicted and the smart BLAST results show that in the rest of the remaining ORFs no function could be assigned.)

S. No.	*C. elegans* nucleotide region (left end to right end)	No. of ORFs predicted	Smart BLAST results	*B. malayi* nucleotide region (left end to right end)	No. of ORFs predicted	Smart BLAST results
1.	1028-1069	0		7427-7466	0	
2.	1154-1583	1	Smart BLAST found no matches	7555-7976	1	Smart BLAST found no matches
3.	1715-2589	2	NADH dehydrogenase subunit 1	7997-8869	3	NADH dehydrogenase subunit 1
4.	9951-10485	1	Smart BLAST found no matches	9998-10534	3	1.cytochrome c oxidase subunit II 2. cytochrome oxidase subunit 2
5.	10763-11681	2	Smart BLAST found no matches in both the ORFs	10816-11758	4	NADH dehydrogenase subunit 3
6.	11795-12159	0		12158-12526	2	Smart BLAST found no matches in both the ORFs
7.	12210-12823	0		12576-13192	2	NADH dehydrogenase subunit 5
8.	1070-1153	0		0		
9.	1584-1714	0		0		
10.	2590-9950	25	1.NADH dehydrogenase subunit 4 2.NADH dehydrogenase subunit 2 3. NADH dehydrogenase subunit 4 4.cytochrome c oxidase subunit I 5.cytochrome c oxidase subunit I 6.ATP synthase F0 subunit 6 7. cytochrome c oxidase subunit I 8. cytochrome c oxidase subunit I 9.cytochrome b 10. cytochrome c oxidase subunit I 11. cytochrome c oxidase subunit III 12. cytochrome c oxidase subunit I 13. NADH dehydrogenase subunit 2 14. cytochrome c oxidase subunit III	0		
11.	10486-10762	1	Smart BLAST found no matches	0		
12.	11682-11794	0		0		
13.	12160-12209	0		0		
14.	0			7467-7554	0	
15.	0			7977-7996	0	
16.	0			8870-9997	5	No results found in any of the 5 ORFs
17.	0			10535-10815	0	
18.	0			11759-12157	0	
19.	0			12527-12575	0	

Table 4 | Alignment results of *B. malayi* to *W. bancrofti* (Backbone file results) showing the conserved regions generated by the Progressive Mauve program. ORFs predicted in the identified conserved regions followed by smart BLAST results for assigning the functions to ORFs. (NOTE- The differences in the no. of ORFs predicted and the smart BLAST results show that in the rest of the remaining ORFs no function could be assigned.)

S.No.	*W. bancrofti* nucleotide region (left end to right end)	No. of ORFs predicted	Smart BLAST results	*B. malayi* nucleotide region(left end to right end)	No. of ORFs predicted	Smart BLAST results
1	12-1018	4	1.NADH dehydrogenase subunit 2 2. NADH dehydrogenase subunit 2	3-1015	4	1.NADH dehydrogenase subunit 2 2. NADH dehydrogenase subunit 2
2	1042-4481	13	1.NADH dehydrogenase subunit 4 2. cytochrome oxidase subunit I 3. cbb3-type cytochrome c oxidase subunit I 4. cbb3-type cytochrome c oxidase subunit I [Wolbachia endosymbiont of Mansonella perstans] 5. cytochrome c oxidase subunit 1	1019-4456	17	1.Uncharacterized protein BM_BM5154 2. NADH dehydrogenase subunit 4 3. Uncharacterized protein BM_BM126 4. cytochrome c oxidase subunit I 5. cbb3-type cytochrome c oxidase subunit 6. hypothetical protein [*Wolbachia* endosymbiont of *Mansonella perstans*] 7. glutamate receptor ionotropic, kainate 3 8. cytochrome oxidase subunit 1
3	4500-11090	33	1.NADH dehydrogenase subunit 1 2. cytochrome c oxidase subunit 2 3. cytochrome c oxidase subunit III 4. cytochrome b 5. cytochrome b 6. cytochrome b 7. multiple C2 and transmembrane domain-containing protein 2 isoform X1	4458-11075	27	1.NADH dehydrogenase subunit 1 2. cytochrome c oxidase subunit III 3. cytochrome b 4. cytochrome c oxidase subunit III 5. cytochrome b 6. cytochrome c oxidase subunit II 7. cytochrome b
4	11095-13644	12	1.NADH dehydrogenase subunit 5 2.NADH dehydrogenase subunit 5 3.NADH dehydrogenase subunit 3 4.neuRonal IgCAM [*C. elegans*]	11099-13649	8	1. NADH dehydrogenase subunit 5 2. NADH dehydrogenase subunit 3
5	1019-1041	0		0		
6	0			11076-11098	0	

Table 5 | List of conserved intergenic regions identified by the alignment of *W. bancrofti* to *C. elegans* generated by Vista server

S. No.	*C. elegans* nucleotide region (left end CE right end)	*W. bancrofti* nucleotide region (left end right end)	Sequence length	Identity	
1.	1439-1588	7848-7997	152 bp	73.0%	Intergenic
2.	1785-1888	8080-8183	104 bp	71.2%	Intergenic
3.	1989-2130	8284-8425	142 bp	68.3%	Intergenic
4.	2286-2592	8583-8887	312 bp	67.9%	Intergenic
5.	4693-4818	4787-4912	126 bp	76.2%	Intergenic
6.	5233-5375	5327-5469	143 bp	70.6%	Intergenic
7.	6227-6344	6324-6441	118 bp	69.5%	Intergenic
8.	7016-7142	1550-1674	127 bp	74.0%	Intergenic
9.	7172-7295	1706-1833	128 bp	68.8%	Intergenic
10.	8004-8179	2445-2620	176 bp	73.3%	Intergenic
11.	8340-8672	2781-3113	333 bp	70.3%	Intergenic
12.	8703-8863	3144-3307	165 bp	70.9%	Intergenic
13.	8893-9074	3334-3516	183 bp	70.5%	Intergenic
14.	9109-9208	3550-3649	100 bp	70.0%	Intergenic
15.	9927-10148	9984-10207	224 bp	69.2%	Intergenic
16.	10183-10370	10242-10426	188 bp	68.6%	Intergenic
17.	10901-11029	10972-11095	132 bp	68.9%	Intergenic
18.	11221-11328	11283-11389	109 bp	70.6%	Intergenic
19.	11979-12135	12340-12500	161 bp	70.2%	Intergenic
20.	12493- 12614	12854- 12975	125 bp	68.0%	Intergenic

Table 6 | List of conserved intergenic regions identified by the alignment of *B. malayi* to *C. elegans* generated by Vista server

S. No.	CE nucleotide region (left end to right end)	BM nucleotide region (left end to right end)	Sequence Length	Identity	
1.	1161-1304	7566-7699	144 bp	68.1%	Intergenic
2.	1434-1588	7829-7982	156 bp	72.4%	Intergenic
3.	2002-2118	8283-8399	117 bp	69.2%	Intergenic
4.	2283-2461	8564-8742	179 bp	68.2%	Intergenic
5.	4562-4661	4618-4717	100 bp	72.0%	Intergenic
6.	4687-4807	4737-4857	121 bp	71.9%	Intergenic
7.	4831-4988	4881-5038	158 bp	67.7%	Intergenic
8.	5080-5177	5130-5227	98 bp	70.4%	Intergenic
9.	5221-5382	5271-5429	162 bp	68.5%	Intergenic
10.	6946-7135	1457-1646	190 bp	73.2%	Intergenic
11.	7167-7302	1678-1820	143 bp	69.9%	Intergenic
12.	8004-8179	2422-2597	176 bp	71.6%	Intergenic
13.	8442-8656	2860-3074	221 bp	70.6%	Intergenic
14.	8701-8852	3119-3270	152 bp	72.4%	Intergenic
15.	8928-9034	3346-3452	107 bp	72.0%	Intergenic
16.	9098-9213	3516-3631	116 bp	69.0%	Intergenic
17.	9941-10114	9988-10161	174 bp	72.4%	Intergenic
18.	10186-10342	10233-10387	159 bp	67.3%	Intergenic
19.	10739-11012	10792-11067	277 bp	74.0%	Intergenic
20.	11180-11328	11241-11394	154 bp	70.1%	Intergenic
21.	11970-12128	12336-12494	159 bp	71.1%	Intergenic
22.	12202-12344	12568-12707	143 bp	67.8%	Intergenic

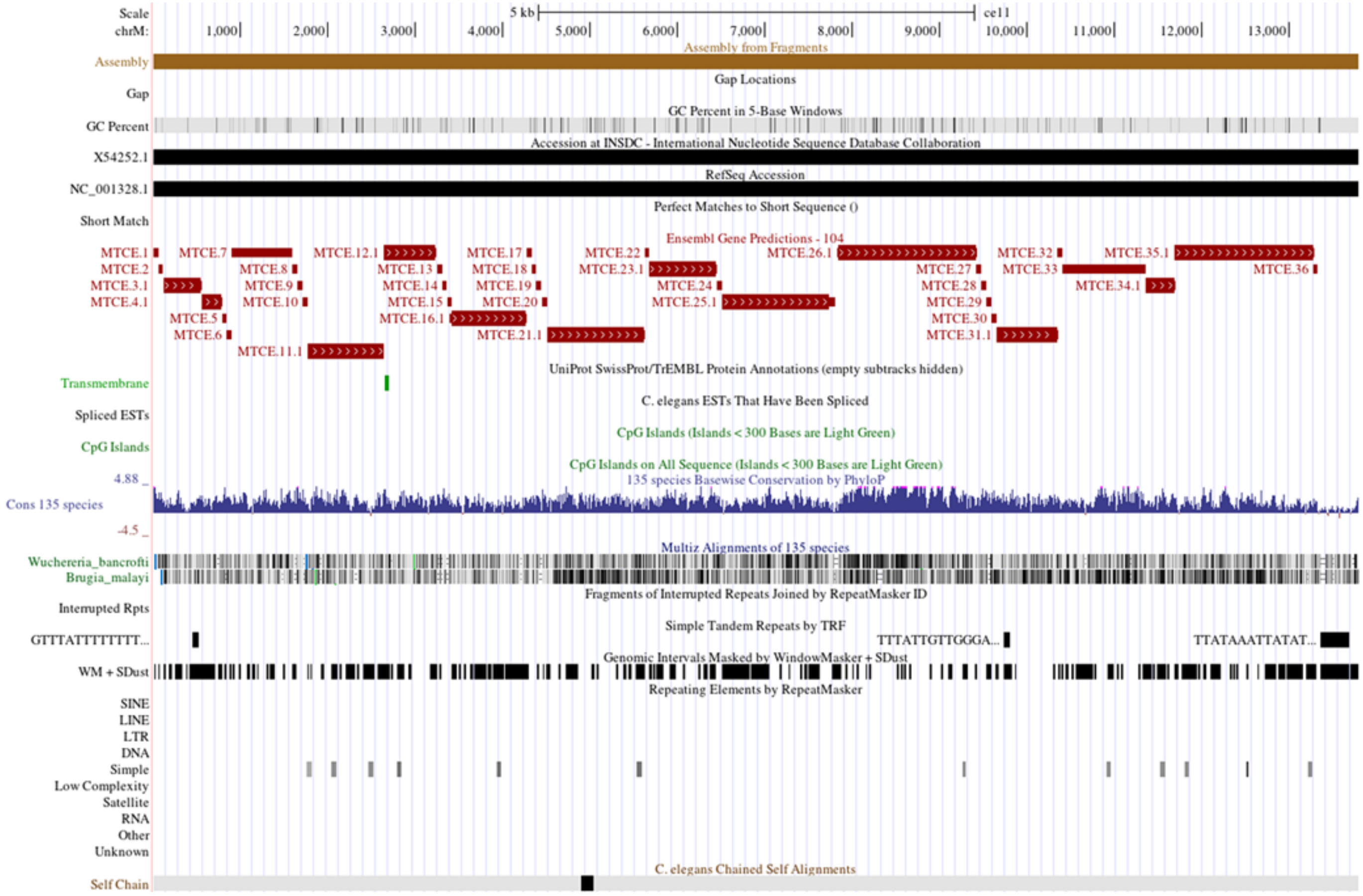

Figure 2 | The results depict the alignment of mitochondrial genomic data of *W. bancrofti* and *B. malayi* among the 135 available species for alignment in the browser. The peaks represent the degree of conservation among the two aligned genomes. The high-conserved areas are represented by dark regions in the genome panels of the species. Image prepared by UCSC genome browser (http://genome.ucsc.edu).

(Figure 3). After subjecting each ORF to BLASTP (protein-protein BLAST) only 28, 33, and 26 ORFs in *W. bancrofti*, *B. malayi* and *C. elegans* respectively had the functions while the remaining ORFs displayed no sequence similarity to any known proteins. Out of 28 ORFs in *W. bancrofti*, 17 ORFs were of already known 12 PCGs of mitochondria. While the remaining 11 ORFs were newly reported (Table 7). Similarly, in *B. malayi*, 17 ORFs showed the conserved genes present in mitochondria while the remaining 16 showed new results (Table 8). In the case of *C. elegans*, 9 results were new while the rest 17 ORFs showed similarity with the already known conserved genes of *C. elegans* (Table 9) (Figure 4). Although the ORF finder listed some of these regions as ORFs, they are most probably the non-coding regions of the mitochondrial genome. The ORFs and their subsequent blast were done to ascertain whether there is any difference at the mitochondrial gene coding level in these organisms.

3.5 Multiple sequence alignment and Phylogenetic relationships

Multiple sequence alignment results displayed by CLUSTALW for alignment of mt genomes of *C. elegans* with *W. bancrofti* and *B. malayi* shows significantly less alignment score (42) as compared to the alignment score of *W. bancrofti* and *B. malayi* (88).

The phylogenetic tree was constructed using the complete mt genome sequences of the species. The maximum likelihood method (Figure 5) clustered *W. bancrofti* and *B. malayi* in one distinct phylogenetic group while *C. elegans* was present in a different group. While these organisms are grouped into different clades than the *C. elegans*, they seem to share a common ancestor. These results showed that the two parasitic nematodes have more evolutionary relatedness to each other than *C. elegans*. All these three nematodes may have evolved from a common ancestor which explains the similarity in the mitochondrial genome of all three species.

3.6 Comparison of protein coding genes

All three nematode species contain the same 12 PCGs. As reported earlier, all the species lack ATP synthase subunit 8. For the validation of the amino acid sequence reterived from NCBI and PDB database alignment performed by pBLAST and 100% sequence similarity have been obtained for all the 12 PCGs. The alignment of mitochondrial protein coding genes of all three species shows the higher similarity between *W. bancrofti* and *B. malayi*. The sequence level similarity between genes from *C. elegans* and the other two organisms is less owing to the specific deletions and insertions in each

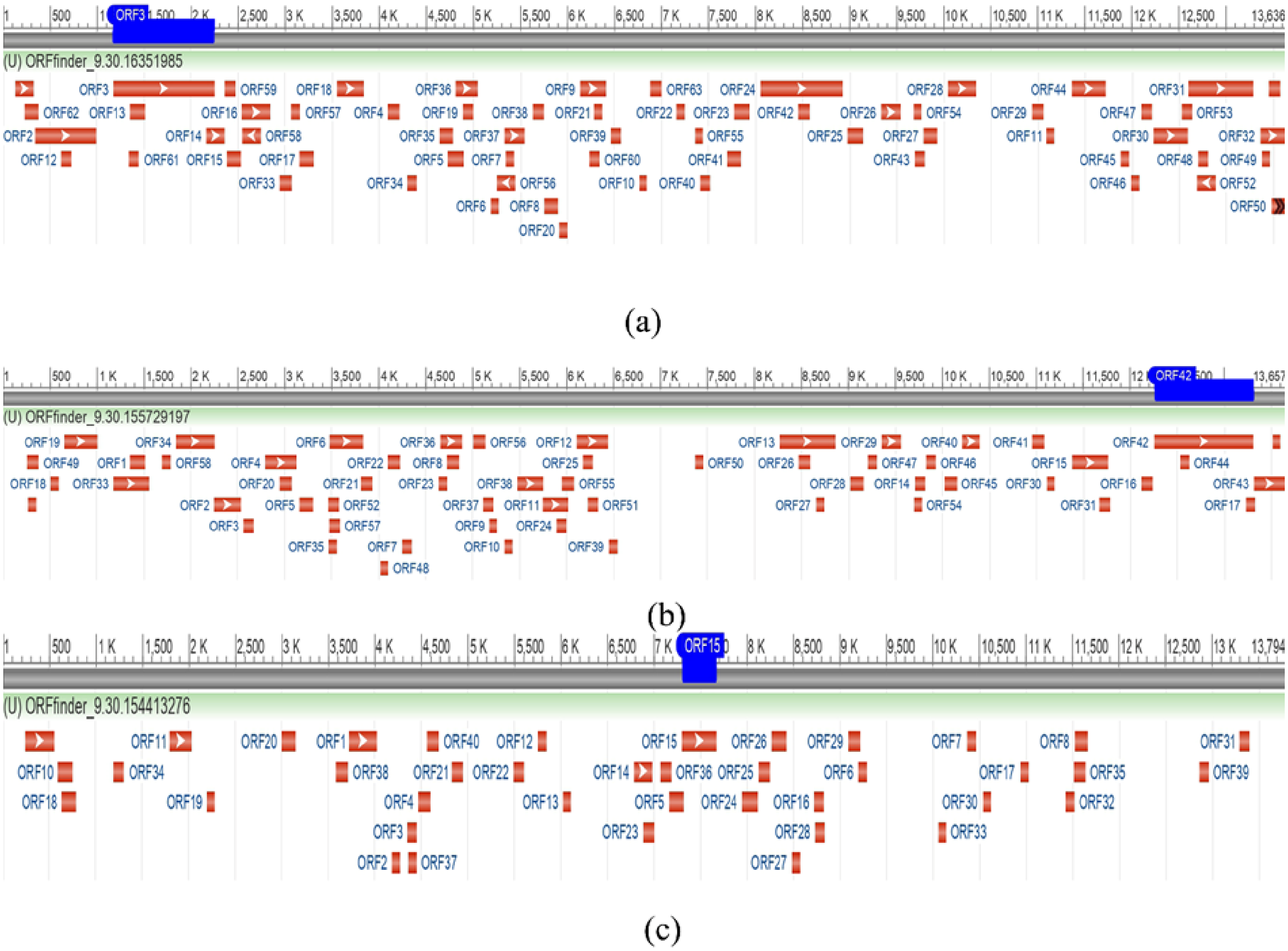

Figure 3 | Pictorial representation of all the ORFs predicted by ORF Finder tool of NCBI in the complete mitochondrial genome of (a) *W. bancrofti*; (b) *B. malayi*; (c) *C. elegans*.

Table 7 | List of new ORFs in *W. bancrofti* (Protein BLAST results)

S.NO.	Length of ORF (Nucleotide)	Length of ORF (Amino acid)	Function
1.	93	30	Helix-loop-helix protein 3
2.	87	28	Large envelope protein
3.	84	27	Vesicle transport protein GOT1A
4.	84	27	Meiotically up-regulated gene 73 protein
5.	81	26	Endoplasmic reticulum-Golgi intermediate compartment protein 1
6.	81	26	Cytotoxic and regulatory T-cell molecule
7.	81	26	Cytochrome P450 85A1
8.	78	25	Protein Opaque1
9.	78	25	HAUS augmin-like complex subunit 8
10.	78	25	Olfactory receptor
11.	78	25	V-type proton ATPase 116 kDa subunit a2

Table 8 | List of new ORFs in *B. malayi* (Protein BLAST results)

S.No.	Length of ORF (Nucleotide)	Length of ORF (Amino acid)	Function assignment
1.	93	30	UPF0295 protein GK0479
2.	93	30	Metabotropic glutamate receptor-like protein A
3.	93	30	Neuromedin-B receptor
4.	90	29	Guanylate cyclase beta
5.	87	28	Protoheme IX farnesyltransferase
6.	84	27	Serine/threonine-protein kinase ppk1
7.	81	26	Schlafen family member 12-like
8.	81	26	AB hydrolase superfamily protein B1A11.02
9.	81	26	Serine/threonine-protein kinase irlC
10.	81	26	Epidermal patterning factor-like protein 6
11.	81	26	Endoplasmic reticulum junction formation protein lunapark
12.	78	25	Pre-rRNA-processing protein IPI1
13.	78	25	DNA-directed RNA polymerase subunit beta
14.	78	25	Cell division protein FtsQ
15.	78	25	Dihydroneopterin monophosphate aldolase
16.	78	25	C-C chemokine receptor type 2

Table 9 | List of new ORFs in *C. elegans* (Protein Blast Results)

S.No	Length of ORF (Nucleotide)	Length of ORF (Amino acid)	Function
1.	93	30	Elongation factor G
2.	93	30	Phosphoglucosamine mutase
3.	93	30	Putative phosphoesterase GWCH70_0799
4.	90	29	Envelope glycoprotein O
5.	87	28	Delta (7)-sterol 5(6)-desaturase
6.	84	27	Mitochondrial aspartate-glutamate transporter AGC1
7.	81	26	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase
8.	81	26	Protein glycosylation K
9.	78	25	Uncharacterized 24 kDa protein

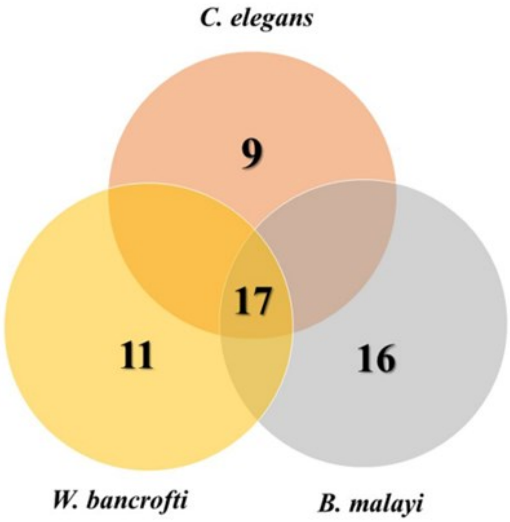

Figure 4 | Venn diagram representing numbers of functional common as well as unique ORFs in complete mt genomes of *C. elegans*, *W. bancrofti*, and *B. malayi*.

gene supporting this observation (Table S4). The sequence comparison shows the highest diversity of gene sequences among cytochrome C oxidase subunit 3 (*C. elegans* vs *W. bancrofti*) and NADH dehydrogenase subunit 6 (*C. elegans* vs *B. malayi*). Codon usage analysis using the sequence manipulation suite [17] for a single gene (NADH dehydrogenase subunit 1) reveals some important differences in codon usage in these three organisms. For proline, *C. elegans* preferred the codon CCA while the other two preferred CCT. Similarly, in *C. elegans*, CAA is preferred for glutamine, but *W. bancrofti* and *B. malayi* uses both CAG and CAA. For threonine, both *W. bancrofti* and *B. malayi* uses ACT while *C. elegans* prefer ACA and ACT (Table 10). These codon biases suggest that the parasitic nature of the *W. bancrofti* and *B. malayi* have been adapted for different codons for some of the amino acids.

4. Discussion

In this study, an attempt has been made to compare the mt genomes of filarial parasites *Wuchereria bancrofti* and *Brugia malayi* to a free-living nematode *C. elegans*. Access to the publicly available multiple genomes in different databases has offered improvised gene prediction by comparing the conserved genomic regions of multiple species [18].

The AT nucleotide content of reference genome *C. elegans* is 78 %. The AT nucleotide content of *W. bancrofti* was calculated to be 75 % consistent with the earlier reports [19]. While for *B. malayi*, it is 77% slightly more than the previous report of 75.5 % [20].

With the help of complete mt genome alignment, a total of 13 conserved regions have been identified in all three species. These regions are having variable number of ORFs within them. Meanwhile, a total of 20 and 22 conserved intergenic regions in *W. bancrofti* and *B. malayi* respectively have also been identified which are part of the non coding regions that can be found within genes. While in the complete mt genome a total number of 32,35 and 26 functional ORF have been predicted in *W. bancrofti*, *B. malayi* and *C. elegans* respectively. The total number of ORFs of these species has not been reported earlier in any previous study. Among all the identified ORFs, 17 ORFs were found to be common in all the three genomes studied.

The MSA is a fundamental part of comparative sequence analysis [21] that has been performed with the help of CLUSTALW in this study. The difference in the CLUSTALW alignment score depicts the sequence identity difference between *C. elegans* and the other two species. The sequence similarity depicted by the alignment score of *C. elegans* to *W. bancrofti* and *B. malayi* was almost half of the alignment score of *W. bancrofti* and *B. malayi* indicating that their sequence similarity/relatedness is much higher than each other as compared to *C. elegans*.

The complete mt genome of total of 62 species was used to construct the phylogenetic tree through the Maximum likelihood method. All the species compared were clustered according to their free-living nature and host preferences (either being a plant, animal, or human parasite). The phylogenetic analysis depicts a close relationship between *W. bancrofti* and *B. malayi*. Both the species were present in the same phylogenetic clade and causes the same disease (LF) in humans. Such a similar finding regarding *W. bancrofti* and *B. malayi* has also been reported previously [11] [19] by using the concatenated nucleotide sequences of only twelve PCGs of nematodes. *C. elegans* is grouped into separate clade but share a common ancestor with the other two studied nematodes.

In a study of the mt genome sequence of 5 nematode species that were either *Wolbachia* dependent or independent parasites, it was observed that the species were remarkably similar on their sequence level despite their dependency on *Wolbachia* for their survival [11]. While the mitochondrial sequences of *W. bancrofti* and *B. malayi* are found to be similar in respect of their size, AT content and encode the same 12 PCGs, we have found the unique conserved non-coding regions that are present only in either of the genome. These unique regions may carry the difference between the free living and the parastic organism.

5. Concluding Remarks

W. bancrofti and *B. malayi* are genetically similar to each other but are divergent from the model species *C. elegans* even though they have evolved from a common ancestor. There was an early divergence of these two species from *C. elegans* but still, they all contain the same 12 PCGs in their mt genome. Analysis of the mt genome of *W. bancrofti* and *B. malayi* showed that it contains some unique conserved regions. These conserved regions may not contain any protein coding genes but are conserved at their sequence level. Some new unique (partial) ORFs have also been

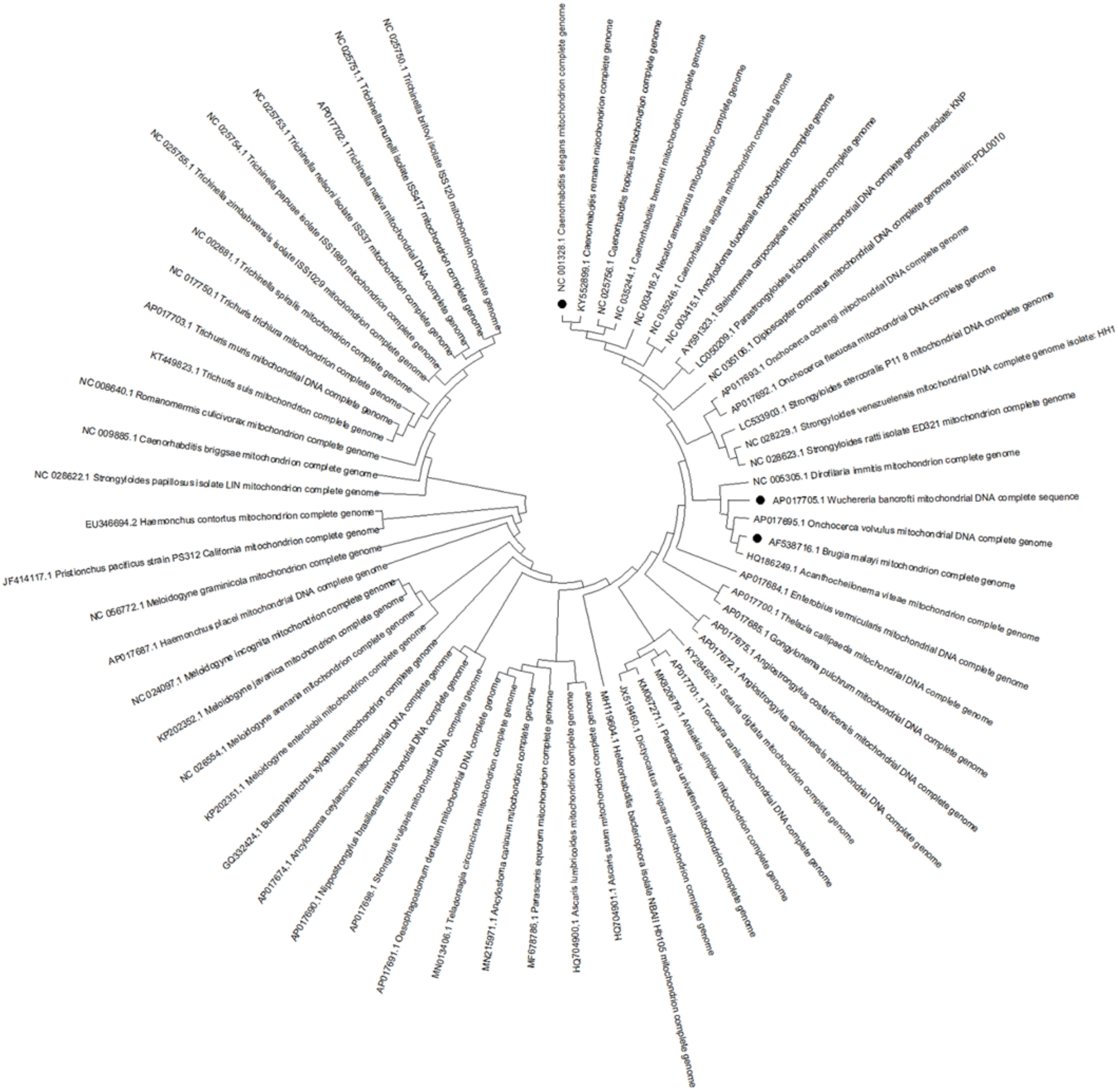

Figure 5 | Evolutionary analysis by Maximum Likelihood method in MEGA X. The evolutionary history was inferred by using the Maximum Likelihood method and General Time Reversible model. All the species compared were clustered according to their free-living nature and host preferences (either being a plant, animal, or human parasite). The tree constructed depicts a close relationship between *W. bancrofti* and *B. malayi*. Both species were present in the same phylogenetic clade. *C. elegans* is grouped into separate clade but share a common ancestor with the other two studied nematodes.

Table 10 | Codon usage analysis using the sequence manipulation suite [17] for a single gene (NADH dehydrogenase subunit 1)

S.No.	Amino Acid	Codons	Fraction		
			CE	WB	BM
1.	Ala	GCG	0.08	0.11	0.20
		GCA	0.23	0.0	0.0
		GCT	0.54	0.89	0.50
		GCC	0.15	0.00	0.30
2.	Cys	TCT	1.0	0.93	0.83
		TGC	0.0	0.07	0.17
3.	Asp	GAT	1.0	1.0	1.0
		GAC	0.00	0.0	0.0
4.	Glu	GAG	0.33	0.67	0.25
		GAA	0.67	0.33	0.75
5.	Phe	TTT	1.0	0.98	0.98
		TTC	0.0	0.02	0.02
6.	Gly	GGG	0.25	0.05	0.05
		GGA	0.50	0.81	0.05
		GGT	0.25	0.10	0.76
		GGC	0.00	0.05	0.14
7.	His	CAT	1.00	0.5	1.0
		CAC	0.00	0.5	0.0
8.	Ile	ATA	0.26	0.19	0.15
		ATT	0.62	0.77	0.85
		ATC	0.12	0.04	0.00
9.	Lys	AAG	0.11	0.83	0.5
		AAA	0.89	0.17	0.5
10.	Leu	TTG	0.12	0.49	0.34
		TTA	0.67	0.40	0.45
		CTG	0.00	0.00	0.02
		CTA	0.05	0.00	0.07
		CTT	0.16	0.11	0.11
		CTC	0.00	0.00	0.00
11.	Met	ATG	1.00	1.00	1.00
12.	Asn	AAT	0.88	1.0	1.0
		AAC	0.13	0.0	0.0
13.	Pro	CCG	0.00	0.00	0.00
		CCA	0.63	0.14	0.00
		CCT	0.13	0.86	0.86
		CCC	0.25	0.00	0.14
14.	Gln	CAG	0.00	0.40	0.60
		CAA	1.00	0.60	0.40
15.	Arg	AGG	0.14	0.15	0.00
		AGA	0.52	0.31	0.30
		CGG	0.05	0.08	0.10
		CGA	0.00	0.00	0.00
		CGT	0.29	0.46	0.60
		CGC	0.00	0.00	0.00
16.	Ser	AGT	0.18	0.25	0.35
		AGC	0.05	0.00	0.00
		TCG	0.00	0.00	0.00
		TCA	0.32	0.08	0.08
		TCT	0.41	0.63	0.58
		TCC	0.05	0.04	0.00
17.	Thr	ACG	0.14	0.00	0.00
		ACA	0.43	0.00	0.00
		ACT	0.29	1.00	1.00
		ACC	0.14	0.00	0.00
18.	Val	GTG	0.05	0.18	0.00
		GTA	0.32	0.09	0.00
		GTT	0.64	0.73	0.94
		GTC	0.00	0.001	0.60
19.	Trp	TGG	0.00	1.0	1.0
20.	Tyr	TAT	0.81	0.89	0.83
		TAC	0.19	0.11	0.17
21.	END	TGA	0.67	0.00	1.00
		TAG	0.00	0.00	0.00
		TAA	0.33	1.00	0.00

identified in these species which have not been reported earlier. The analysis of the intergenic regions between these organisms showed a range of conserved regions between all three nematodes. The study identified these common conserved regions in these mitochondrial genomes which may explain their evolutionary and lifestyle differences.

Supplementary material:

Supplementary Table S1
Supplementary Table S2
Supplementary Table S3
Supplementary Table S4

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