

Table S1:

Primers used in the present study to amplify the complete mt genome of PNG and Indian *W. bancrofti* isolate. Numbers assigned to primer sets represent the first position to which the forward primer was predicted to anneal. F and R designations that appear in the primer names indicate transcription in the forward and reverse directions, respectively.

Primer name	Primer sequence (5'-3')
41F	TCGATTAAAAGATTGTATATTAT
41R	CATCAACATCTCCAAACTAA
701F	TTAATTTTGTAGTTTGGAGAT
701R	AATAGAAGAATAAGCAGCCA
1751F	TGTAAGTCTTTGGCTGCTT
1751R	AATACCAACGGTATGTAAAC
2721F	TTTGGATGTTATAATTTTAGG
2721R	TCAATCATTAAATAATTAATAAT
3691F	GTTACTTTTATTGGTTTTATATT
3691R	CATACTACCAAATTCACA
4651F	GCTAGATTTACTTTAAGTTATA
4651R	GATAATGACCAGCCCAAG
5611F	CAATAACTATCAAGTTATGATA
5611R	ATTCTAAAAATCGTCAATAATC
6425F	GTAGTAAATTACATAATTTTAA
6425R	GGATACTAATCCAGTTCA
7441F	GATTTTGGTTTTGGTTGTATT
7441R	CTAAAAATCCCAGATAATATAA
8461F	TGGGTGTTTCTGTATATTTTA
8461R	GATACGTAAAGTCAAAGCAA
9441F	GAGTTTTTTGATGAGTGGTG
9441R	AACTCTAAAGCAATAGGTATAA
10421F	TTTGTGGTGCTAATCATAGTT
10421R	AACAAGATAAACCGCTCTGT
11420F	ATTGAACTTAATATTAGTTTAG
11420R	ATCAAACCACCCATACTC
12381F	TATTTACGGTTCTTTTTATATG
12381R	CCTTACTACAACAACCACTA
13119F	GGTAGTCAGGATTATCGTG
13119R	CGAGTTAAACCCAAAATTAG

Table S2:Codon usage (%) reported for the 12 mitochondrial protein-coding genes - PNG *W. bancrofti* isolate

aa	Codon	N	%	aa	Codon	N	%	aa	Codon	N	%	aa	Codon	N	%		
Phe	TTT	619	17.9	Ser (UCN)	TCT	159	4.6	Tyr	TAT	214	6.2	Cys	TGT	101	2.9		
	TTC	19	0.5			TCC	4	0.1		TAC	13	0.4		TGC	2	0.1	
Leu (UUR)	TTA	171	4.9		TCA	6	0.2	Stop	TAA	5	0.1	Trp	TGA	31	0.9		
	TTG	247	7.1		TCG	2	0.1	Stop	TAG	2	0.1		TGG	42	1.2		
Leu (CUN)	CTT	30	0.9	Pro	CCT	64	1.9	His	CAT	48	1.4	Arg	CGT	46	1.3		
	CTC	0	0.0			CCC	1	0.0		CAC	4		0.1		CGC	0	0.0
	CTA	5	0.1			CCA	7	0.2	Gln	CAA	19		0.5		CGA	3	0.1
	CTG	5	0.1			CCG	3	0.1		CAG	33		1.0		CGG	6	0.2
Ile	ATT	185	5.4	Thr	ACT	82	2.4	Asn	AAT	98	2.8	Ser (AGN)	AGT	121	3.5		
	ATC	12	0.3			ACC	4	0.1		AAC	7		0.2		AGC	3	0.1
Met	ATA	59	1.7		ACA	1	0.0	Lys	AAA	19	0.5		AGA	17	0.5		
	ATG	90	2.6		ACG	0	0.0		AAG	51	1.5		AGG	17	0.5		
Val	GTT	272	7.9	Ala	GCT	72	2.1	Asp	GAT	79	2.3	Gly	GGT	176	5.1		
	GTC	6	0.2			GCC	6	0.2		GAC	5		0.1		GGC	12	0.3
	GTA	25	0.7			GCA	2	0.1	Glu	GAA	22		0.6		GGA	20	0.6
	GTG	19	0.5			GCG	1	0.0		GAG	38		1.1		GGG	25	0.7

Table S3:Nucleotide composition (%) of PNG *W. bancrofti* isolate mt genome subsets

mt genome subset	No. of nt	A	C	G	T	A+T
Entire sequence	13,637	20.1	7.2	18.1	54.5	74.6
Protein-coding genes	10,377	17.7	7.5	19.1	55.7	73.4
Codon position	1st	22.2	7.9	22.6	47.3	69.5
	2nd	19.0	12.0	18.0	51.0	70.0
	3rd	11.9	2.8	16.8	68.5	80.4
Ribosomal RNA	1,644	26.2	6.6	15.8	51.4	77.6
Transfer RNA	1,245	30.3	6.1	15.8	47.8	78.1
AT-rich region	267	33.3	7.1	9.0	50.6	83.9

Table S4:

Nucleotide composition (%) of each protein-coding gene - *W. bancrofti* PNG isolate.

Gene	A	C	G	T	A+T
<i>nad2</i>	15.4	4.6	19.4	60.5	75.9
<i>nad4</i>	15.0	6.7	19.2	59.1	74.1
<i>cox1</i>	19.2	11.3	20.9	48.6	67.8
<i>nad6</i>	18.3	3.5	16.3	61.8	80.1
<i>cob</i>	18.8	8.6	18.6	54.0	72.8
<i>cox3</i>	22.9	6.9	18.7	51.4	74.3
<i>nad4L</i>	16.0	3.7	15.2	65.0	81.0
<i>nad1</i>	17.0	8.0	19.2	55.9	72.9
<i>atp6</i>	18.9	7.4	16.8	56.9	75.8
<i>cox2</i>	22.3	9.3	20.7	47.7	70.0
<i>nad3</i>	15.4	5.3	18.4	60.8	76.2
<i>nad5</i>	14.5	6.3	19.0	60.1	74.6

Table S5:

Codon usage (%) reported by codon family for the 12 mt protein-coding genes - PNG *W. bancrofti* isolate.

Amino acid	Codon	No. of codons	Codon usage (%)
Non-polar			
Alanine	GCN	81	2.4
Isoleucine	ATY	197	5.7
Leucine	CTN	40	1.2
Leucine	TTR	418	12.1
Methionine	ATR	149	4.3
Phenylalanine	TTY	638	18.5
Proline	CCN	75	2.2
Tryptophan	TGR	73	2.1
Valine	GTN	322	9.3
Subtotal		1,993	57.8
Polar			
Asparagine	AAY	105	3.0
Cysteine	TGY	103	3.0
Glutamine	CAR	52	1.5
Glycine	GGN	233	6.8
Serine	AGN	158	4.6
Serine	TCN	171	5.0
Threonine	ACN	87	2.5
Tyrosine	TAY	227	6.6
Subtotal		1,136	33.0
Acidic			
Aspartate	GAY	84	2.4
Glutamate	GAR	60	1.7
Subtotal		144	4.1
Basic			
Arginine	CGN	55	1.6
Histidine	CAY	52	1.5
Lysine	AAR	70	2.0
Subtotal		177	5.1
Total		3,450	100