

First Blast result showing high match with Duck Hepatitis B virus and for the second blast when filtering only eukaryotes we will see all matches are from Aves(birds), Neognathae, mostly *melopsittacus undulatus*.

DHBV: ***Duck hepatitis B virus***, abbreviated **DHBV**, is part of the genus *Avihepadnavirus* of the *Hepadnaviridae*, and is the causal agent of duck hepatitis B.

DHBV is a small DNA virus with a diameter of 40–45 nm. The viral envelope is made up from host cell lipid, with viral surface antigens (DHBsAg). The icosahedral nucleocapsid within, is composed of the virus core antigen (DHBcAg) and surrounds the DNA genome and viral polymerase. The viral genome is a circular double stranded DNA molecule about 3000 base pairs long.

Neognathae (/niˈɒgnəθiː/; from Ancient Greek νέος (*néos*) 'new, young', and γνάθος (*gnáthos*) 'jaw') is an infraclass of birds, called **neognaths**, within the class *Aves* of the clade Archosauria. Neognathae includes the majority of living birds; the exceptions being the tinamous and the flightless ratites, which belong instead to the sister taxon Palaeognathae. There are nearly 10,000 living species of neognaths.

The high similarity between bird genomes and the Duck hepatitis B virus (DHBV) isn't due to the birds inheriting the virus directly into their own DNA. Instead, it's a result of two separate factors:

1. Shared Evolutionary History:

- DHBV belongs to the Hepadnaviridae family, which has infected birds for millions of years. Over time, both the virus and birds have co-evolved, adapting to each other's presence.
- This co-evolution led to DHBV developing mechanisms to exploit specific features of bird biology for its own replication and survival.
- As both birds and DHBV diverged into different species and strains, they carried a "memory" of this shared evolutionary history in their genomes. This resulted in some degree of sequence similarity, particularly in genes crucial for the virus-host interaction.

2. Selective Pressure and Functional Constraints:

- Certain viral genes responsible for essential functions, like entering host cells or evading the immune system, are under strong selective pressure to remain effective.
- This pressure ensures that even as the virus and birds evolve, these key genes retain similar structures and functions to maintain their effectiveness.

- Additionally, some functional constraints might limit the possible variations in these genes, leading to convergent evolution where different viruses independently arrive at similar solutions.

☒ select all 100 sequences selected
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[Graphics](#)
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Description	Scientific Name	Taxid	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/> Duck hepatitis B virus, complete genome	Duck hepatitis B virus	12639	100%	0.0	100.00%	3021	K01834.1
<input checked="" type="checkbox"/> Duck hepatitis B virus isolate 31, complete genome	Duck hepatitis B virus	12639	99%	0.0	99.53%	3021	AY250901.1
<input checked="" type="checkbox"/> Duck hepatitis B virus isolate 102, complete genome	Duck hepatitis B virus	12639	99%	0.0	99.50%	3021	AY250902.1
<input checked="" type="checkbox"/> Duck hepatitis B virus isolate Indiana, complete genome	Duck hepatitis B virus	12639	100%	0.0	99.40%	3021	AF493986.1
<input checked="" type="checkbox"/> Duck hepatitis B virus, complete genome	Duck hepatitis B virus	12639	99%	0.0	99.40%	3021	AF047045.1
<input checked="" type="checkbox"/> Duck hepatitis B virus isolate ST10, complete genome	Duck hepatitis B virus	12639	99%	0.0	99.40%	3021	AY294028.1
<input checked="" type="checkbox"/> Duck hepatitis B virus isolate 8, complete genome	Duck hepatitis B virus	12639	99%	0.0	99.40%	3021	AY250903.1
<input checked="" type="checkbox"/> Duck hepatitis B virus strain DHBV-XY, complete genome	Duck hepatitis B virus	12639	99%	0.0	99.30%	3021	HQ214130.1
<input checked="" type="checkbox"/> Duck hepatitis B virus strain SCP01, complete genome	Duck hepatitis B virus	12639	99%	0.0	99.26%	3021	KM676220.1
<input checked="" type="checkbox"/> Duck hepatitis B virus isolate D1, complete genome	Duck hepatitis B virus	12639	99%	0.0	99.23%	3021	AY294029.1
<input checked="" type="checkbox"/> Duck hepatitis B virus, complete genome	Duck hepatitis B virus	12639	99%	0.0	99.23%	3021	AF505512.1
<input checked="" type="checkbox"/> Duck hepatitis B virus, complete genome	Duck hepatitis B virus	12639	100%	0.0	99.16%	3021	M60677.1
<input checked="" type="checkbox"/> Duck hepatitis B virus, complete genome	Duck hepatitis B virus	12639	100%	0.0	99.13%	3021	AY294656.1
<input checked="" type="checkbox"/> Duck hepatitis B virus isolate SD-02, complete genome	Duck hepatitis B virus	12639	99%	0.0	98.90%	3021	MF471769.1
<input checked="" type="checkbox"/> Duck hepatitis B Virus DNA complete genome	Duck hepatitis B virus	12639	100%	0.0	98.80%	3021	X74623.1
<input checked="" type="checkbox"/> Duck hepatitis virus B genome	Duck hepatitis B virus	12639	100%	0.0	98.76%	3021	X12798.1
<input checked="" type="checkbox"/> Duck hepatitis B virus isolate 410, complete genome	Duck hepatitis B virus	12639	100%	0.0	94.65%	3021	MW176097.1
<input checked="" type="checkbox"/> Duck hepatitis B virus isolate DHBV-GD-056, complete genome	Duck hepatitis B virus	12639	100%	0.0	94.62%	3021	HQ132730.1
<input checked="" type="checkbox"/> Duck hepatitis B virus isolate 414, complete genome	Duck hepatitis B virus	12639	100%	0.0	94.58%	3021	MW176098.1
<input checked="" type="checkbox"/> Duck hepatitis B virus isolate 3, complete genome	Duck hepatitis B virus	12639	100%	0.0	94.41%	3021	DQ195079.1
<input checked="" type="checkbox"/> Duck hepatitis B virus strain Y190303HN, complete genome	Duck hepatitis B virus	12639	99%	0.0	94.19%	3021	OP762450.1

Descriptions

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100 sequences selected ?

Organism	Blast Name	Score	Number of Hits	Description
Avihepadnavirus	viruses		101	
• Duck hepatitis B virus	viruses	5522	99	Duck hepatitis B virus hits
• Snow goose hepatitis B virus	viruses	3646	2	Snow goose hepatitis B virus hits

Sequences producing significant alignments

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	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	Melopsittacus undulatus isolate 4 endogenous budgerigar hepatitis B virus element 2 (eBHBV2) .complete se...	Melopsittacus u...	616	616	52%	1e-170	74.09%	3856	JQ978784.1
<input checked="" type="checkbox"/>	Melopsittacus undulatus isolate 2 endogenous budgerigar hepatitis B virus element 2 (eBHBV2) .complete se...	Melopsittacus u...	616	616	52%	1e-170	74.09%	3853	JQ978782.1
<input checked="" type="checkbox"/>	Melopsittacus undulatus isolate 1 endogenous budgerigar hepatitis B virus element 2 (eBHBV2) .complete se...	Melopsittacus u...	616	616	52%	1e-170	74.09%	3856	JQ978781.1
<input checked="" type="checkbox"/>	TPA: Melopsittacus undulatus endogenous budgerigar hepatitis B viruses element 2 (eBHBV2) .complete seq...	Melopsittacus u...	612	612	51%	1e-169	74.17%	3856	BK008521.1
<input checked="" type="checkbox"/>	Melopsittacus undulatus isolate 4 clone SH4L endogenous budgerigar hepatitis B virus element 1 (eBHBV1) ...	Melopsittacus u...	555	555	47%	2e-152	74.08%	4865	JQ978780.1
<input checked="" type="checkbox"/>	Melopsittacus undulatus isolate 3 clone SH3L endogenous budgerigar hepatitis B virus element 1 (eBHBV1) ...	Melopsittacus u...	555	555	47%	2e-152	74.08%	4865	JQ978779.1
<input checked="" type="checkbox"/>	Melopsittacus undulatus isolate 2 clone SH2Ld endogenous budgerigar hepatitis B virus element 1 (eBHBV1) ...	Melopsittacus u...	555	555	47%	2e-152	74.08%	4865	JQ978778.1
<input checked="" type="checkbox"/>	Melopsittacus undulatus isolate 1 clone SH1L endogenous budgerigar hepatitis B virus element 1 (eBHBV1) ...	Melopsittacus u...	555	555	47%	2e-152	74.08%	4865	JQ978774.1
<input checked="" type="checkbox"/>	Melopsittacus undulatus isolate 2 clone SH2La endogenous budgerigar hepatitis B virus element 1 (eBHBV1) ...	Melopsittacus u...	549	549	47%	1e-150	74.15%	4859	JQ978775.1
<input checked="" type="checkbox"/>	TPA: Melopsittacus undulatus endogenous budgerigar hepatitis B viruses element 1 (eBHBV1) .complete seq...	Melopsittacus u...	549	549	47%	1e-150	74.04%	4865	BK008520.1
<input checked="" type="checkbox"/>	Melopsittacus undulatus isolate 2 clone SH2Lb endogenous budgerigar hepatitis B virus element 1 (eBHBV1) ...	Melopsittacus u...	544	544	47%	5e-149	74.08%	4858	JQ978776.1
<input checked="" type="checkbox"/>	Caprimulgus europaeus genome assembly .chromosome: Z	Caprimulgus eur...	372	372	22%	3e-97	77.38%	82627501	OU015527.1
<input checked="" type="checkbox"/>	Taeniopygia guttata endogenous zebra finch hepadnavirus fragment I .genomic sequence	Taeniopygia gutt...	307	307	13%	7e-78	80.65%	644	HQ116577.1
<input checked="" type="checkbox"/>	Psittacula echo genome assembly .chromosome: 15	Psittacula echo	219	219	18%	4e-51	74.50%	12757604	OY725435.1
<input checked="" type="checkbox"/>	Caprimulgus europaeus genome assembly .chromosome: 22	Caprimulgus eur...	193	193	6%	2e-43	84.16%	9157100	OU015546.1
<input checked="" type="checkbox"/>	Anthus pratensis pratensis marker 6 genomic sequence: and endogenous virus endogenous virus ZHBV .com...	Anthus pratensis...	122	122	5%	3e-22	80.89%	971	KC750131.1
<input checked="" type="checkbox"/>	Carpodacus erythrinus erythrinus MAST3 gene .partial sequence: and endogenous virus endogenous virus Z...	Carpodacus eryt...	113	113	4%	2e-19	81.08%	1994	KC750109.1
<input checked="" type="checkbox"/>	Fringilla coelebs genome assembly .chromosome: 24	Fringilla coelebs	108	108	4%	8e-18	80.27%	8088918	OY740748.1

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20 sequences selected?

Organism	Blast Name	Score	Number of Hits	Description
Neognathae	birds		22	
• Psittaciformes	birds		14	
• • Melopsittacus undulatus	birds	616	13	Melopsittacus undulatus hits
• • Psittacula echo	birds	219	1	Psittacula echo hits
• Caprimulgus europaeus	birds	372	2	Caprimulgus europaeus hits
• Taeniopygia guttata	birds	307	1	Taeniopygia guttata hits
• Anthus pratensis pratensis	birds	122	1	Anthus pratensis pratensis hits
• Carpodacus erythrinus erythrinus	birds	113	1	Carpodacus erythrinus erythrinus hits
• Fringilla coelebs	birds	108	1	Fringilla coelebs hits
• Poecile palustris palustris	birds	102	1	Poecile palustris palustris hits
• Chloropsis aurifrons aurifrons	birds	99.0	1	Chloropsis aurifrons aurifrons hits

Descriptions	Graphic Summary	Alignments	Taxonomy
Reports	Lineage	Organism	Taxonomy
20 sequences selected ?			
Description	Score	E value	Accession
Melopsittacus undulatus (budgerigar) [birds]	▼ Next	▲ Previous	◀ First
Melopsittacus undulatus isolate 4 endogenous budgerigar hepatitis B virus element 2 (eBHBV2), complete sequence	616	1e-170	JQ978784
Melopsittacus undulatus isolate 2 endogenous budgerigar hepatitis B virus element 2 (eBHBV2), complete sequence	616	1e-170	JQ978782
Melopsittacus undulatus isolate 3 endogenous budgerigar hepatitis B virus element 2 (eBHBV2), complete sequence	616	1e-170	JQ978783
Melopsittacus undulatus isolate 1 endogenous budgerigar hepatitis B virus element 2 (eBHBV2), complete sequence	616	1e-170	JQ978781
TPA_exp: Melopsittacus undulatus endogenous budgerigar hepatitis B viruses element 2 (eBHBV2), complete sequence	612	1e-169	BK008521
Melopsittacus undulatus isolate 4 clone SH4L endogenous budgerigar hepatitis B virus element 1 (eBHBV1), putative Pr	555	2e-152	JQ978780
Melopsittacus undulatus isolate 3 clone SH3L endogenous budgerigar hepatitis B virus element 1 (eBHBV1), putative Pr	555	2e-152	JQ978779
Melopsittacus undulatus isolate 2 clone SH2Ld endogenous budgerigar hepatitis B virus element 1 (eBHBV1), putative Pr	555	2e-152	JQ978778
Melopsittacus undulatus isolate 1 clone SH1L endogenous budgerigar hepatitis B virus element 1 (eBHBV1), putative Pr	555	2e-152	JQ978774
Melopsittacus undulatus isolate 2 clone SH2Lc endogenous budgerigar hepatitis B virus element 1 (eBHBV1), putative Pr	555	2e-152	JQ978777
Melopsittacus undulatus isolate 2 clone SH2La endogenous budgerigar hepatitis B virus element 1 (eBHBV1), putative Pr	549	1e-150	JQ978775
TPA_exp: Melopsittacus undulatus endogenous budgerigar hepatitis B viruses element 1 (eBHBV1), complete sequence	549	1e-150	BK008520
Melopsittacus undulatus isolate 2 clone SH2Lb endogenous budgerigar hepatitis B virus element 1 (eBHBV1), putative Pr	544	5e-149	JQ978776
Caprimulgus europaeus (Eurasian nightjar) [birds]	▼ Next	▲ Previous	◀ First
Caprimulgus europaeus genome assembly, chromosome: Z	372	3e-97	OU015527
Caprimulgus europaeus genome assembly, chromosome: 22	193	2e-43	OU015546

TABLE 1 Results of the BLAST analysis of the P ORFs of avian hepadnaviruses

Species	GenBank accession no.	Contig length (bp)	P length (amino acids)	Similarity (%)	Genome type	Flanking gene(s)	E value	Reverse BLAST (E value)
<i>Melopsittacus undulatus</i> (budgerigar)	AGAI01066647	52,555	418	65	Complete	<i>PCBD1, GH1</i>	0.0	DHBV (0.0)
			324	46			1e-78	DHBV (0.0)
			108	62			4e-32	RGHBV (5e-40)
	AGAI01070398	34,567	377	66	Complete	<i>PCBD1</i>	4e-140	RGHBV (2e-179)
			265	49			5e-57	DHBV (4e-73)
			156	65			1e-59	DHBV (1e-69)
	AGAI01048473	59,743	110	55	Partial	<i>PCBD1</i>	3e-32	CHBV (9e-40)
	AGAI01069060	4,174	198	42	Partial	<i>LOC100548410</i>	5e-29	HBBV (3e-35)
	AGAI01070370	182,598	135	46	Partial	<i>PCBD1</i>	1e-27	ShHBV (1e-34)
	AGAI01068110	134,081	105	55	Partial	<i>PCBD1</i>	3e-26	DHBV (5e-32)
	AGAI01067768	139,808	108	61	Partial	<i>PCBD1</i>	3e-26	DHBV (1e-25)
	AGAI01046846	42,041	95	56	Partial	<i>PCBD1</i>	2e-24	DHBV (4e-30)
	AGAI01056960	185,067	85	53	Partial	<i>PCBD1</i>	1e-17	StHBV (2e-24)
	AGAI01048462	27,912	84	50	Partial	<i>Aanat</i>	2e-15	RGHBV (6e-19)
	AGAI01067853	33,178	114	44	Partial	<i>CR1</i>	5e-13	StHBV (7e-21)
	AGAI01070664	32,569	90	46	Partial	<i>LOC100232143</i>	2e-12	RGHBV (7e-17)
	AGAI01050253	40,494	91	48	Partial	<i>PCBD1</i>	9e-10	StHBV (5e-22)
<i>Taeniopygia guttata</i> (zebra finch)	ABQF01038718	71,638	404	58	Complete	<i>LOC100217595</i>	9e-138	DHBV (3e-156)
	ABQF01051978	1,732	159	58	Partial	ND ^a	2e-48	DHBV (4e-54)
	ABQF01047718	82,878	206	47	Partial	<i>ATP2B2</i>	8e-44	PHBV (5e-53)
	ABQF01007435	128,889	108	42	Partial	<i>LOC100221519</i>	2e-43	SGHBV (6e-22)
	ABQF01039383	26,988	139	51	Partial	<i>LOC100228257</i>	2e-43	DHBV (3e-34)
	ABQF01051981	3,171	79	71	Partial	ND	1e-25	RGHBV (1e-30)
	ABQF01105392	2,838	137	52	Partial	ND	3e-23	CHBV (4e-35)
	ABQF01097021	4,156	91	56	Partial	ND	6e-20	RGHBV (3e-24)
	ABQF01026236	39,254	91	55	Partial	<i>LOC100225966</i>	3e-19	DHBV (2e-24)
	ABQF01051706	13,577	81	54	Partial	ND	6e-17	SGHBV (2e-20)
	ABQF01033534	67,953	100	43	Partial	<i>LOC100224031</i>	2e-09	RGHBV (5e-12)

^a ND, no data.

