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 (/niˈpgnəθiː/; 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:

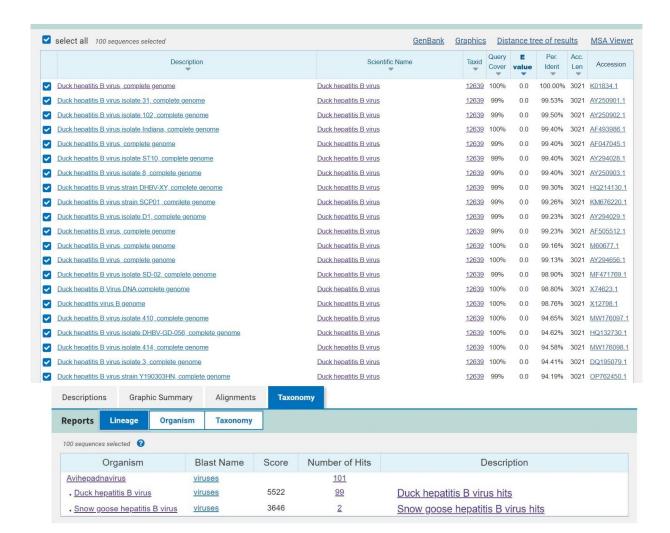
1. Shared Evolutionary History:

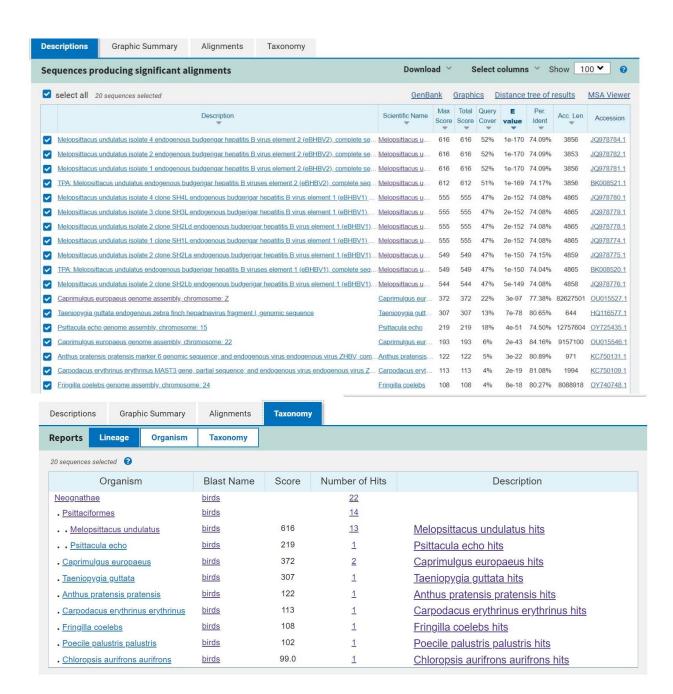
- DHBV belongs to the Hepadnaviridae family, which has infected birds for millions
 of years. Over time, both the virus and birds have co-evolved, adapting to each
 other's presence.
- This co-evolution led to DHBV developing mechanisms to exploit specific features of bird biology for its own replication 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 virushost 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.





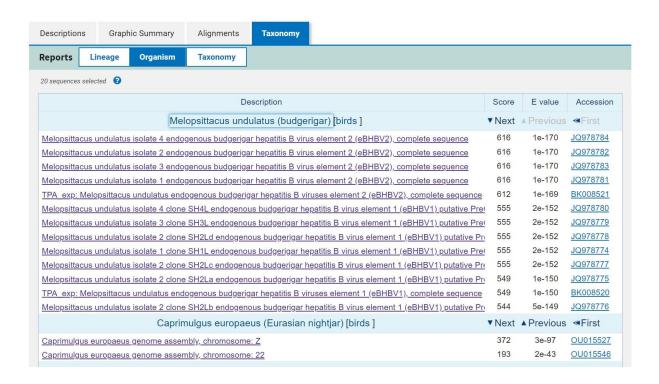


TABLE 1 Results of the BLAST analysis of the P ORFs of avian hepadnaviruses

	GenBank	Contig	P length	Similarity	Genome	Flanking		Reverse BLAST
Species	accession no.	length (bp)	(amino acids)	(%)	type	gene(s)	E value	(E value)
Melopsittacus undulatus (budgerigar)	AGAI01066647	52,555	418	65	Complete	PCBD1, GH1	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	PCBD1	4e - 140	RGHBV (2e-179)
			265	49			5e-57	DHBV (4e-73)
	AGAI01058091	67,933	156	65	Partial	PCBD1	1e-59	DHBV (1e-69)
	AGAI01048473	59,743	110	55	Partial	PCBD1	3e - 32	CHBV (9e-40)
	AGAI01069060	4,174	198	42	Partial	LOC100548410	5e-29	HHBV (3e-35)
	AGAI01070370	182,598	135	46	Partial	PCBD1	1e-27	ShHBV(1e-34)
	AGAI01068110	134,081	105	55	Partial	PCBD1	3e-26	DHBV (5e-32)
	AGAI01067768	139,808	108	61	Partial	PCBD1	3e-26	DHBV (1e-25)
	AGAI01046846	42,041	95	56	Partial	PCBD1	2e - 24	DHBV (4e-30)
	AGAI01056960	185,067	85	53	Partial	PCBD1	1e-17	StHBV (2e-24)
	AGAI01048462	27,912	84	50	Partial	Aanat	2e-15	RGHBV (6e-19)
	AGAI01067853	33,178	114	44	Partial	CR1	5e-13	StHBV (7e-21)
	AGAI01070664	32,569	90	46	Partial	LOC100232143	2e - 12	RGHBV (7e-17)
	AGAI01050253	40,494	91	48	Partial	PCBD1	9e-10	StHBV (5e-22)
Taeniopygia guttata (zebra finch)	ABQF01038718	71,638	404	58	Complete	LOC100217595	9e-138	DHBV (3e-156)
	ABQF01051978	1,732	159	58	Partial	ND^a	2e - 48	DHBV (4e-54)
	ABQF01047718	82,878	206	47	Partial	ATP2B2	8e - 44	PHBV (5e-53)
	ABQF01007435	128,889	108	42	Partial	LOC100221519	2e - 43	SGHBV (6e-22)
	ABQF01039383	26,988	139	51	Partial	LOC100228257	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	LOC100225966	3e-19	DHBV (2e-24)
	ABQF01051706	13,577	81	54	Partial	ND	6e-17	SGHBV (2e-20)
	ABQF01033534	67,953	100	43	Partial	LOC100224031	2e-09	RGHBV (5e-12)

a ND, no data.