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Review Article

A Comprehensive Review on Epidemiological Insights of Infectious Bronchitis Virus in South Asian Region

Bilal Javid*, Tahira Kamal, Farhana Amin, Muhammad Naeem Riaz and Hafiz Muhammad Bilal Akhtar
National Institute for Genomics and Advanced Biotechnology, NARC, Islamabad, Pakistan
*For correspondence: bilaljavid824@gmail.com
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Abstract

Infectious bronchitis virus (IBV) is a highly mutating virus that affects both vaccinated and unprotected chicken flocks and causes enormous economic losses worldwide, so it is very critical to gain a deeper understanding of this virus. It is classified as gamma corona virus which belongs to family of coronaviridae. It leads to infectious bronchitis in poultry which is a contagious disease. The upper respiratory tract and reproductive tract are mostly affected by this disease. There are many strains which have been identified globally and cause nephritis along with other complications. The occurrence of different strains is the result of recombination and mutation in the viral genome, which makes it very difficult to identify and control. This virus contains three major structural proteins that are encoded by the virus, one of which is the highly variable spike (S) glycoprotein. The S1 portion surface protein of IBV virus is involved in hem-agglutination and pathogenicity due to the presence of virus neutralizing epitopes. The amplification trough RT-PCR and S1 glycoprotein sequence analysis made the diagnosis of Infectious bronchitis virus possible. The phylogenetic analysis of different strains of S1 gene helps in identifying the similarity index of this virus with other related virus strains. The objective of current review is to deliver an overview of the IBV variants or strains those are currently in circulation in commercial poultry in South Asian region and it focuses on the point that particular vaccine should be prepared according to the prevailing local strain of particular area. In order to develop effective vaccine, vaccine matching is very crucial process because of the rapidly changing nature of infectious bronchitis virus. The details about IBV types provided here are taken from published articles and Submissions at Gene Bank. The phylogenetic analysis was conducted to check the relationship between different IBV strains in some South-Asian countries.

Keywords: IBV; Genetic type; S1 gene; South Asia; Vaccine matching; Phylogenetic analysis

Introduction

One of the most economically significant diseases of poultry is infectious bronchitis virus (Uddin *et al.* 2016). This virus is a continuously evolving with an envelope that carries a positive-sense, single-stranded RNA genome. It is classified within the Gamma coronavirus genus of the Coronaviridae family. The poultry industry worldwide has faced remarkable economic losses due to IBV-accompanying conditions such as tracheitis, proventriculitis, nephritis, salpingitis and significant decrease in egg production (Zhang *et al.* 2020). The important structural proteins are encoded by the IBV genome which are N protein (nucleocapsid), M (membrane-protein), S (spike-glycoprotein) and E (small membrane-protein). IBV can cause harm to the host's kidneys, reproductive system, and respiratory tract by replicating within the epithelium of numerous organs (Wit *et al.* 2019). IBV strains are categorized into 35 lineages having seven genotypes using a novel classification technique (GI to GVII) (Valastro *et al.* 2016; Chen *et al.* 2017; Jiang *et al.* 2017; Ma *et al.* 2019). It is typical to see the disease in vaccinated chickens also, which has a significant negative economic impact globally (Sumi *et al.* 2012). Respiratory diseases such as tracheal rales, coughing, and sneezing, as well as excessive mucus formation and accumulation in the bronchi, decreased broiler growth, nephritis, urolithiasis, and permanent oviduct damage, which results in high mortality rates and abnormal egg production (Worthington *et al.* 2008; Bickerton *et al.* 2018). The size of IBV viral genome is approximately 27.6 kb having 5 prime and 3 prime non-coding regions (Abro *et al.* 2012a). It contains three most important structural proteins that are encoded by the virus, one of which is the highly variable spike (S) glycoprotein, which is interpreted as a pre-protein or protein prior to being fragmented into the N-terminal (S1) and the C-terminal (S2) glycol-polypeptides (Farsang *et al.* 2002). The portion of surface protein (S1) of IBV virus is involved in hem-agglutination and pathogenicity due to the presence of virus neutralizing epitopes (Abro *et al.* 2012b). The S1 protein's antigenic determinants alter, resulting in the creation of novel

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strains and genotypes (Promkuntod *et al.* 2015). IBV serotypes differ in their S1 glycoprotein by around 20 to 25%. On the other hand, variations of up to 50% have been noted, which has an impact on cross-protection against virus strains that are developing or reoccurring (Ennaji *et al.* 2020). The S1 gene of IBV is most frequently addressed in molecular epidemiological investigations to describe (*e.g*., genotyping) and comprehend the spread of the virus because of its genetic diversity (Bande *et al.* 2017). It is possible to determine the path of the virus distribution and identify the strains of the virus that are most common in a given location by using sequencing and phylo-genomics (Zulperi *et al.* 2009). However, because IBV is an extremely fluctuating coronavirus, the current occurrence of novel strains significantly reduces the efficacy of IBV vaccines (Fan *et al.* 2018). The vaccines' low cross-protection rates unavoidably impede the disease's prevention and control (Jordan 2017). IBV can take many different forms that are difficult to manage. Their vaccines sometimes do have the ability of cross protection. Attenuated live vaccines are given to broilers and pullets, and killed vaccines are typically given to layers and breeders. Effective control requires the identification of the virus that causes the disease and the subsequent administration of an appropriate vaccine against it (Cavanagh and Naqi 2003). The emergence of new serotypes as a result of some changes in amino acid sequence is due to the immunological stress triggered by extensive use of vaccines. The other filed strains emerge due to the consequence of mixed infection or decline of most prevailing serotype (Liu *et al.* 2006). Numerous IBV serotypes have been identified globally, and there is minute to no cross-immunity between the various antigenic variants (Cavanagh 2007). This results in an increasing number of immunological failures and large financial losses for the chicken sector Chen *et al.* 2017).

Molecular characterization of BV in India

A study was conducted in India to identify and characterize two strains of the infectious bronchitis virus (IBV) from field occurrences in broiler chickens in 2008 and 2010 which were India/LKW/56/IVRI/08 and India/NMK/72/IVRI/10, respectively. The two Indian IBV isolates presented 73% similarity among them according to nucleotide sequencing analysis, while India/LKW/56 and India/NMK/72 were 99% similar with the 4/91 (it is pathogenic strain in the UK), JP/Wakayama/2/2004 (Japan), and TA03 (China). The presence of 4/91 (793/B) IBV nephron-pathogenic variant existing in India was confirmed for the very first time. Phylogenetic Analysis revealed that the isolate India/LKW/56/IVRI/08 formed a group with THA280252 (Thailand), and the isolated strain, India/NMK/72/IVRI/10 formed a separate group with 4/91 pathogenic (UK) (Sumi *et al.* 2012). The furthermost prevalent IBV variants identified in India since 1991 were the (India/Mass/16-V-AD/07) in Mass genotype and 793B strain (Elankumaran *et al.* 1999). The strain India/PDRC/Pune/9/99 and various nephro-pathogenic variants or strains of Infectious Bronchitis were recognized in 1991 (Bayry *et al.* 2005). The five IBV strains were identified and described as Anand isolates. These isolates were isolates in Gujrat, India and were compared with already isolated field strains of IBV in Gujrat (Patel *et al.* 2015). These isolates with other strains are given in Table 1. Another study found that 20 field strains of IBV were examined in India between 2003 and 2011 using RT-PCR and sequencing of the S1 gene's HVR I and HVR II. The three isolates (I. IND-TN-168-06, II. IND-TN-280-10, III. IND-TN-290-11) out of 20 were totally new variants which matched with GI-24 lineage. The Fourteen isolates (a. IND-113-03, b. IND-114-03, c. IND-TN-04-03, d. IND-TN-20-03, e. IND-TN-92-03, f. IND-TN-95-03, g. IND-TN-97-03, h. IND-TN-98-03, i. IND-AP-151-05, j. IND-KA-152-05, k. IND-TN-162-06, l. IND-TN-163-06, m. IND-TN-270-09, n. IND-TN-183-09) were grouped in GI-1 lineage. The further two (02) field isolates (I. IND-TN-174-07, II. IND-TN-175-07) grouped into the GI-13 genetic lineage (Raja *et al.* 2020). Some published IBV isolates of India with accession numbers are given in Table 1.

Molecular characterization of IBV in China

In 2019, HeN-1/China/2019, HeN-2/China/2019, and HeN-101/China/2019 were shown to be three extremely aggressive IBV strains in China. The recently found IBV strain was closely linked to the ck/China/I0529/17 strain and classified into the GI-19 genotype clade on the basis of genetic sequence and phylogenetic study of the full S1 gene, despite the fact that the gross pathological demonstration of two IB outbreaks was divergent. This work shed light on recently occurring IBV epidemics in poultry with IBV vaccinations and identified the genetic traits of three virulent GI-19 IBV strains, demonstrating the necessity of implementing appropriate preventative measures and management tactics. After Molecular detection, four IBV strains were isolated comprising HeN-101/China/2019, and HeN-102/China/2019, HeN-1/China/2019, HeN-2/China/2019. After complete sequencing the complete S1 gene Hen-1 and Hen-2 strains showed 99.9% similarity, while Hen-101 and Hen-102 showed 100 similarities exploring the fact that these two outbreaks were triggered by single IBV strain (Zhang *et al.* 2020). In 2018, ck/CH/LDL/150434–I (LDL/150434–I), ck/CH/LDL/150434–II (LDL/150434–II), and ck/CH/LDL/150434–III (LDL/150434–III) are the three distinct IBV genotypes/serotypes that were identified in chicken (Han *et al.* 2018). The Novel IBV strain, ck/CH/LGX/111119 was identified in 2017 and grouped in GI-28 lineage. This new novel strain may be the result of the recombination of IBVs in LX4 genotype and non-identifies IBV strain, or S1 gene of unidentified IBV or mutations in S1 gene of IBVs of LX4 genotype (Chen *et al.* 2017). Nine distinct genetic families, including Mass- and 793B-type

Table 1: Prevalence of different isolates of infectious bronchitis virus in India. The given isolates of IBV have different levels of similarity index of S1 gene sequence. This table contains the already published Indian IBV isolates with different Antigenic variations

Country	Strain	Type	Gene Bank No#	Reference
	India/ LKW/56/IVRI/08	Mass	HM163471	Sumi *et al*. (2012)
India	India/Mass/16-V-AD/07	Mass	HM179146	Elankumaran *et al*. (1999)
	India/NMK/72/ IVRI/10	4/91	HM748585	Sumi *et al*. (2012)
	India/PDRC/Pune/9/99	(Unique)	AY091551	Bayry *et al*. (2005)
	ANAND/GUJ/IBV1/2013	Cluster I	KJ577258	Patel *et al*. (2015)
	ANAND/GUJ/IBV2/2013		KJ577259	
	ANAND/GUJ/IBV3/2013		KJ577260	
	ANAND/GUJ/IBV4/2013		KJ577261	
	ANAND/GUJ/IBV5/2013		KJ577262	
	IND-TN-168-06	Variant IBV	JX966396	Raja *et al*. (2020)
	IND-TN-290-11	(GI-24)	JX966403	
	ND-113-03	(Mass 41 IBV)	JX966392	
	IND-114-03	GI-1	EF165593	
	IND-TN-04-03		EF165596	
	IND-TN-20-03		EF165597	
	IND-TN-92-03		EF165598	
	IND-TN-95-03		EF165599	
	IND-TN-97-03		EF165600	
	IND-TN-98-03		EF165601	
	IND-AP-151-05		JX966393	
	IND-KA-152-05		EF165595	
	IND-TN-162-06		JX966394	
	IND-TN-163-06		JX966395	
	IND-TN-270-09		JX966400	
	IND-TN-183-09		JX966399	
	IND-TN-174-07	UK 4/91 IBV	JX966397	
	IND-TN-175-07	(GI-13)	JX966398	
	IND-284-10	Indian nephron-pathogenic IBV	JX966402	

viruses, reported in China: LX4, LDT3, LHLJ, BJ, LDL, N1/62, and LSC (Han *et al.* 2011). The wider distribution and high pathogenicity make the IBVs of LX4 and LDL groups more significant among all the identified genetic groups. The different strains were published with Gene Bank No. as China/LX4/QX/99 (AF193423), China/LDT3/03 (AY702975), China/LHLJ/95I (DQ167141), China/BJ/97 with (AY31965), China/LDL/Q1/98 (AF286302), China/N1/62/JAAS/04 (AY839140), China/LSC/99I (DQ167147), China/793B/Sichuan/06 (GQ844991), China/Mass-H120/ SDLY0612/06 (EU857816) and Taiwan/LDL/Q1-3374/05 (DQ402364) (Jackwood 2012). In 2019 and 2020, two isolates of IBV, designated CK/CH/TJ1904 and CK/CH/NP2011, from many poultry farms in the provinces of Tianjin and Fujian were recovered, respectively. The CK/CH/TJ1904 and CK/CH/NP2011 strains whole genome sequences have been added to Gene Bank under the accession numbers MW815494 and MW815495 (Sun *et al.* 2021). For the previous 20 years, the QX (GI-19) genotype has dominated the Chinese population. It was initially identified in Qingdao, China, in 1996 (Xu *et al.* 2018) (Zhao *et al.* 2016). China's Guangxi province reported the first isolation of a GVI-1 strain in 2007. The strain, dubbed TC07-2, differed significantly from six other key genotypes in terms of evolution (Li *et al.* 2010). The respiratory tract tropism observed in GVI-1 strains may be caused by extensive gene 3 and S recombination (Ren *et al.* 2019). The S1 glycoprotein gene nucleotide sequences of the avian infectious bronchitis virus (IBV) strains Gray and JMK were identified and cross-referenced with previously published IBV sequences (Kwon and Jackwood 1995). The new IBV GDTS13 strain was evaluated for vaccine production, which was common and most prevalent in 2016-2017 in southern China, GVI-1 is now the most common IBV genotype. Some published IBV isolates of China with accession numbers are given in Table 2. The Phylogenetic study was conducted on the basis of whole S1 gene sequences among 16 strains and 156 reference strains. In this experiment, GI-1 includes the mentioned strains as reference like Mass 41 and H120 having accession numbers AY561711, FJ888351, respectively (Chen *et al.* 2021).

Molecular characterization of IBV in Pakistan

A trail was conducted to examine clinical samples of IBV in Pakistan, 358 out of 905 samples were found to be positive, with serotype distributions of Mass strain (43%), 4/91strain (51%), and various IBV variants (5%), respectively. A variant Pak-973 was recovered from Broiler Breeder flock through molecular characterization. IBV isolate was given name as KX013102_NARC/973_Pakistan_2015. The phylogenetic study presented 93% resemblance with KF360983_23/B/2008_India. After sequencing the Pak-973 isolate, a difference of almost 7% was noticed with the rest of the variants and serotypes. The 13 Amino acid substitutions also made pak-973 different from rest of the isolates. The amino acid mutations were found on the hyper variable region 1 and hyper variable region 2s, which made

Table 2: Prevalence of different isolates of infectious bronchitis virus in China. The given isolates of IBV have different levels of similarity index of S1 gene sequence. This table contains the already published Chinese IBV isolates with different Antigenic variations

Country	Strain	Type	Gene Bank No#	Reference
	China/LX4/QX/99	LX4	AF193423	Jackwood (2012)
China	China/LDT3/03	LDT3	AY702975	
	China/LHLJ/95I	LHLJ	DQ167141	
	China/BJ/97	BJ	AY319651	
	China/LDL/Q1/98	LDL	AF286302	
	China/N1/62/JAAS/04	Subgroup 1	AY839140	
	China/LSC/99I	LSC	DQ167147	
	China/793B/Sichuan/06	793B	GQ844991	
	China/Mass-H120/ SDLY0612/06	Mass	EU857816	
	Taiwan/LDL/Q1-3374/05	N1/62	DQ402364	
	CK/CH/GD/GDJM1206	GVI-1	MN193597	Chen *et al.* (2021)
	CK/CH/GD/GDSB1214	GVI-1	MN193599	
	CK/CH/GD/BJSN17	GVI-1	MN193588	
	HeN-1/China/2019	G-19	MN055627	Zhang *et al.* (2020)
	HeN-2/China/2019	G-19	MN055628	
	HeN-101/China/2019	G-19	MN635798	
	ck/CH/LDL/150434–I	Mass	KT736031	Han *et al.* (2018)
	ck/CH/LDL/150434–II	LDT3	KT736032	
	ck/CH/LDL/150434–III	TWI like	KX077987	
	ck/CH/LGX/111119	GI-28	KX640829	Chen *et al.* (2017)
	CK/CH/TJ1904	GV1	MW815494	Sun *et al.* (2021)
	CK/CH/NP2011	GV1	MW815495	
	DY07	Genotype -I	GQ265927	Li *et al.* (2010)
	MN07	Genotype--I	GQ265946	
	DY05	Genotype -I	GQ265928	
	ZX07	Genotype--I	GQ265949	
	LZ07	Genotype II	GQ265944	
	NN04	Genotype-II	GQ265951	
	HY06	Genotype -III	GQ265941	
	CQ04-2	Genotype--III	GQ265953	
	TC07-2	Genotype -VI	GQ265948	
	Ck/CH/LSD/091003	QX like	HM194708	Ren *et al.* (2019)
	Ck/CH/LDL/091022	QX like	HM194640	
	Ck/CH/LJL/090330	QX Like	HM194674	
	CK/CH/GD/GDJM502	GI-19 lineage	MN193595	
	CK/CH/GD/GDSB1220	GI-19 lineage	MN193600	

the Pak-973 as new IBV strain. This study focused on the point that vaccine matching should be done before the selection of vaccine to control IB in commercial poultry (Rafique *et al.* 2018a). The majority of IBV isolates in Pakistan was grouped into GI-24 lineage and some were classified in GI-13. One isolate UAF-8 was placed in GI-1 lineage. This study evaluated the criteria using the 9 novel sequences for all Pakistani isolates of IBV that are currently available. The 8 sequences of IBV isolates out of 9 were grouped in GI-13 and one was placed in GI-24 lineage. The isolates from the liver, kidney, and respiratory tract are included in the GI-24 lineage and strains of GI-13 lineage are mostly linked to samples isolated from the reproductive and respiratory system (Saleem *et al.* 2024). The Pakistani IBV isolates from different areas are given in Table 1. Another study which was conducted in Pakistan revealed the unique IBV strain named as Pak-786. It showed link with GI-13 lineage that comprise the vaccine as well as highly pathogenic field strains. The study backs up the idea that a range of variants arise via random accidental mutation and genetic recombination, which may cause genetic drift, as a result of the widespread use of live IBV vaccination strains with different origins. The study's emerging strain of IBV highlights the necessity of including these variants in killed vaccine form into the affected region's immunization program (Rafique *et al.* 2018b). The most common strain of the infectious bronchitis virus was determined to be M-41, which was detected in 100% of layer flocks and roughly 67% of broiler flocks, with a total combined incidence of 88% in all flocks examined (Ahmed *et al.* 2007). Some published IBV isolates of Pakistan with accession numbers are given in Table 3.

Molecular characterization of IBV in Iran

A unique study demonstrated that samples were collected from (40) forty IB infected flocks from 4 different provinces of Iran. The samples were inoculated in to 9–11 days old chicken eggs (embryonated). After collection of fluid and RT-PCR, results showed that Four (04) isolates (IBV-83, IBV-29, IBV-80, and IBV-56) had high similarity (98.56 to 99.59%) to 4/91 serotype which belongs to (Pakistani strain) GI-13 lineage. Following phylogenetic analysis (on comparison of Nucleotide sequence), three isolates (IBV-80, IBV-16, and IBV-17) were classified as belonging to the GI-19 lineage (QX-like viruses), as they had 98 to 99% of the

Table 3: Prevalence of different isolates of infectious bronchitis virus in Pakistan. The given isolates of IBV have different levels of similarity index of S1 gene sequence. This table contains the already published Pakistani IBV isolates with different Antigenic variations

Country	Strain	Type	Gene bank No.	Reference
Pakistan	NARC/973_Pakistan_2015	**(GI-24)**	KX013102	Rafique *et al.* (2018a)
	IBV17/QAU/Pakistan/Talagang/2017 lung/trachea		MH703657	
	IBV/Ahad51 2018 Pakistan liver		MW464186	
	IBV/Ahad559 2019 Pakistan liver		MW464189	
	CK/PAK/UDL/MS-05/LHR/2020 Pakistan lung trachea kidney		OL763345	
	CK/PAK/UDL/MS-02/RWPD/2020 Pakistan lung trachea kidney		OL763342	
	CK/PAK/UDL/MS-03/MULT/2020 Pakistan lung trachea kidney		OL763343	
	CK/PAK/UDL/MS-06/LHR/2020 Pakistan lung trachea kidney		OL763346	
	CK/PAK/UDL/MS-04/MULT/2020 Pakistan lung trachea kidney		OL763344	
	CK/PAK/UDL/MS-01/ABTD/2020 Pakistan lung trachea kidney		OL763341	
	UAF-10 2020 Pakistan kidney		MW525215	
	UAF-9_2018 Pakistan lung		MW525214	
	IBV/Ahad 196 2018 Pakistan liver		MW464188	
	IBV/Ahad13 2018 Pakistan liver		MW464185	
	CK/PK/UVAS-GM-026-Lalamusa/2019 Pakistan		MK689242	
	IBV/Ahad4 2018 Pakistan liver		MW464184	
	IBV/Ahad3 2018 Pakistan liver		MW464183	
	IBV19/QAU/Pakistan/Rawalpindi/2017 Pakistan lung	**(GI-13)**	MH703659	
	IBV20/QAU/Pakistan/Rawalpindi/2017 Pakistan lung		MH703661	Saleem *et al.* (2024)
	IBV21/QAU/Pakistan/Rawalpindi/2017 Pakistan lung		MH703660	
	IBV18/QAU/Pakistan/Rawalpindi/2017 Pakistan lung		MH703858	
	IBVQ2/QAU/Pakistan/Rawalpindi/2017 Pakistan lung		MH703663	
	IBVQ1/QAU/Pakistan/Rawalpindi/2017 Pakistan lung		MH703662	
	IBV4/QAU/Pakistan/Rawalpindi/2017 Pakistan lung		MH703655	
	chicken/Pakistan/PATH-IX 2019 Pakistan tissue homogenate		MW856023	
	UAF-8 2020 Pakistan Liver	**(GI-1)**	MW525216	
	NARC/786_Pakistan_2013	**(GI-13)**	KU145467	Rafique *et al.* (2018b)

similarities to Iran and Iraq origin QX-like viruses. Two isolates IBV-34 and IBV-106, which belong to the GI-23 lineage (variant-2) share a 95–97% resemblance with Iranian variants of the GI-23 lineage. In this Current research, IBV was identified from 30% of the 40 flocks situated in diverse areas of Iran. Among these isolates, the 793/B serotype emerged as the most prevalent, with QX-like, variant-2 and Massachusetts isolates following in respective order of occurrence. It's noteworthy that all four lineages were identified to be actively circulating within these 40 flocks. The dominant IBV genotypes identified in specific regions of Iran include the GI-13, GI-19, and GI-23 lineages (Ghorbiani *et al.* 2020). In 1994, there was a report on the initial isolation of the IBV in Iranian chicken flocks. A study revealed that IBV isolates in Iran showed linkages to six different genetic groups. Group I had 40 field isolates (34%) that were most similar to Var2 (IS/1494/06 strain), Group II with 793/B serotype, Group III with QX like strain, Group IV with ISl720 strain, group V with Mass strain and Group VI showed similarity with IR1 genetic group (Najafi *et al.* 2016). Another molecular level study was conducted on infectious bronchitis virus in Iran to investigate the prevailing strains. This study documented Iran's first–ever identification of Q1 infectious bronchitis virus genotype which was originated from China from the proventriculus part of layers chickens. The newly identified strains were Iran/Q1/UT-PCR-N1/ 2019 and Iran/Q1/UT-PCR-N2/ 2019 linked to Q1 genotype. After sequencing both positive samples, the sequences were given the accession codes MN841015 and MN841016 for Iran/Q1/UT-PCR-N1/2019 and Iran/Q1/UT-PCR-N2/2019, respectively (Ghalyanchilangeroudi *et al.* 2020). Some published IBV isolates of Iran with accession numbers are given in Table 4.

Molecular characterization of IBV in Bangladesh

In this study, total 371 organ samples—the lungs, kidney, and trachea—were obtained from breeder, broiler, and layer chickens and placed in sterile zipper-lock bags., and Sonali breed (local) chickens that were exhibiting clinical respiratory signs from 9 sampling areas. After processing of swab solution (Homogenization, Suspension, Centrifugation and RNA Extraction), the next step was undergone RT-PCR. The S1 gene specified primer and probe were used in RT-PCR according to OIE guidelines as given in Anonymous (2004). Samples found to be highly positive for IBV using RT-PCR were inoculated into 9-day Specific pathogen free (SPF) chicken egg embryos according to OIE guideline and observed for dwarfing and curling. The next step was harvesting fluid, S1 gene sequence and phylogenetic analysis. Out of 371 samples, 65 (almost 17.5%) samples were positive for IBV in different areas of Bangladesh. The commercial layer was highly prevalent (42.2%) and broiler chicken showed lowest positive samples that were 16 out of 134 (11.9%). The prevalence of local breed Sonali and broiler breeder chicken was 17 and 14.9%, respectively. The results showed that Isolates of IBV were similar with a QX-like and Indian isolates (Bhuiyan *et al.* 2019). The total 5 isolates of IBV were found in Bangladesh which showed different level of similarity with

Table 4: Prevalence of different isolates of infectious bronchitis virus in Iran. The given isolates of IBV have different levels of similarity index of S1 gene sequence. This table contains the already published Iranian IBV isolates with different Antigenic variations

Country	Strain	Type	Genebank No.	Reference
Iran	IBV-34	GI-23	MK850426	Ghorbiani *et al*. (2020)
	1BV-106	GI-23	MK850429	
	1BV-80	GI-13	MK850432	
	1BV-83	GI-13	MK850428	
	1BV-29	GI-13	MK850425	
	1BV-56	GI-13	MK850431	
	1BV-8	GI-19	MK850423	
	1BV-17	GI-19	MK850424	
	1BV-16	GI-19	MK850430	
	1BV-35	GI-1	MK850427	
	IS-1494/UTIVO-27/2014	IS/1494/06 like	KT583593	
	IS-1494/UTIVO-66/2014 IS-1494/UTIVO-99/2014	(Variant2 like)	KT583597	(Najfi *et al.* 2016)
	IS-1494/UTIVO-90/2014		KT583598	
	IS-1494/UTIVO-97/2014 IS-1494/UTIVO-93/2014		KT583599	
	Iran/Variant 2/H840/14		KT583600	
	IS-720/UTIVO-15/2014		KT5835601	
	IS-720/UTIVO-114/2014		KP310028	
	IS-720/UTIVO-113/2014	IS720	KT583583	
	IR-Razi-HKM3-2010	like	KT283585	
	IR-Razi-HKM2-2010		KT583584	
	IR-I/H600/13		JN600612	
	IR-1/UTIVO-41/2015	**IR-1 like (Iran-**	JN600611	
	IR-1/UTIVO-117/2015	**strains cluster)**	KP310035	
	Iran/793B/UTIVO-1/2014		KT583580	
	Iran/793B/UTIVO-86/2014		KT583581	
	Iran/793B/UTIVO-48/2014	**4/91 like**	KT583572	
	Iran/793B/UTIVO-18/2014	**793B like**	KT583577	
	Iran/793B/UTIVO-108/2014		KT583576	
	IR-1062-GA		KT583573	
	IR-Razi-HKM4-2010		KT583579	
	Iran/QX/UTIVO-103/2015		AY544777	
	Iran/QX/UTIVO-6/2015		JN600613	
	Iran/QX/UTIVO-2/2015	**QX like**	KT583571	
	PCRLab/06/2012		KT583568 KT583567	
	Iran/Mass/UTIVO-111/2015		JX477827	
	Iran/Mass/UTIVO-22/2015		KT583566	
	Iran/Mass/UTIVO-46/2015	**Mass like**	KT583564	
	Iran/Mass/H650/13		KT583565	
	Iran/Q1/UT-PCR-N1/ 2019	Q1 Genetype	KP310053	
	Iran/Q1/UT-PCR-N2/ 2019	Q1 Genotype	MN841015 MN841016	Ghalyanchilangeroudi *et al.* (2020)

each other and hence these isolates were grouped after phylogenetic analysis. The two isolates of IBV were grouped in 4/91 type and two more isolates were grouped in Mass genotype. The remaining one was grouped in QX like genotype (Parvin *et al.* 2021). The IBV isolates are given with some other Bangladesh isolates in Table 5.

Molecular characterization of IBV in Afghanistan

According to first report on IBV in Afghanistan, between 2016 and 2017, IBV strains were found to be clustered into two different genotypes, LX4 (GI-19) and IS-1494 similar (GI-23) (34/45), according to phylogenetic analysis of all positive samples. The LX4 IBV (Afghan) is different from Iranian QX IBV. The Iraqi IBV (QX) showed almost 98.9% similarity with China QX like IBV stains. Regarding similarity to circulating strains in Iran and Iraq, IS-1494 had a 20% spread. It should be noted that frequent strains found in the area, such as Massachusetts and 793/B, were not found in this investigation. The study aimed to evaluate the percentage homology of partial sequences of nucleotide of the S1 genes of certain Afghan IBVs. The obtained nucleotide and sequences of amino acids can be found in the Gene Bank with accession numbers MF322853-MF322867 (Sadri *et al.* 2019). It is evident that there are many different IBV variations on the globe today. The challenges lie in classifying these variants and connecting the results to the most effective vaccination plan for protection. However, genotyping offers convenience and speed, the present review highlights requirement for a standardized way of performing genotyping because different groups use different parts such as the S1 region of the S gene for strain comparisons, which makes the interpretation of outcomes very difficult. Another important thing to keep in mind is that the level of cross-protection in a chicken is determined solely by the vaccination, not by genetic or antigenic variations as determined by genotyping or serotyping (Wit *et al.* 2011). Cross-protection studies indicate that flocks can be protected against IS-1494 and QX by using heterologous vaccines with different genotypes, such as Massachusetts and 4/91 (Habibi *et al.* 2017). Some published IBV isolates of Afghanistan with accession numbers are given in Table 6.

Table 5: Prevalence of different isolates of infectious bronchitis virus in Bangladesh. The given isolates of IBV have different levels of similarity index of S1 gene sequence. This table contains the already published Bangladeshi IBV isolates with different Antigenic variations

Country	Strain	Type	Gene Bank No#	Reference
Bangladesh	CK/ BD/IBV/NPHL1	QX like	MH631011.1	Bhuiyan *et al*. (2019)
	CK/BD/IBV/NPHL2	4/91 like	MH688060.1	
	CK/ BD/IBV/NPHL3	4/914/91 like	MH685740.1	
	IBV_CK/Bangladesh/LBM1/2020-HVR1-2 S1	4/91 like	MW971986.1	Parvin *et al.* (2021)
	IBV_CK/Bangladesh/LBM5/2020-HVR1-2 S1	Mass like	MW971987.1	
	IBV_CK/Bangladesh/LT46/2020-HVR1-2 S1	Mass like	MW971994.1	
	IBV_CK/Bangladesh/LT1/2020-HVR1-2 S1	QX like	MW971988.1	
	IBV_CK/Bangladesh/LT57/2020-HVR1-2 S1		MW971990.1	

Table 6: Prevalence of different isolates of infectious bronchitis virus in Afghanistan. The given isolates of IBV have different levels of similarity index of S1 gene sequence. This table contains the already published Afghani IBV isolates with different Antigenic variations

Country	Strain	Type	Gene bank No.	Reference
Afghanistan	Afghanistan/AFS21/2017	LX4 Like (GI-19)	MF322865	Sadri *et al*. (2019)
	Afghanistan/AFS14/2017	IS-1494 Like (GI-23)	MF322866	
	Afghanistan/AFS20/2017		MF322862	
	Afghanistan/AFS26/2017		MF322854	
	Afghanistan/AFS29/2017		MF322853	
	Afghanistan_AFS5_2017	LX4 Like	MF322867	
	IBV/Chicken/Afghanistan//AFS1/2016		MF322856	
	IBV/Chicken/Afghanistan//AFS7/2016		MF322857	
	IBV/Chicken/Afghanistan//AFS9/2016		MF322858	
	IBV/Chicken/Afghanistan//AFS15/2016		MF322859	
	IBV/Chicken/Afghanistan//AFS18/2016		MF322860	
	IBV/Chicken/Afghanistan//AFS19/2016		MF322861	
	IBV/Chicken/Afghanistan//AFS22/2016		MF322863	
	IBV/Chicken/Afghanistan//AFS23/2016		MF322864	

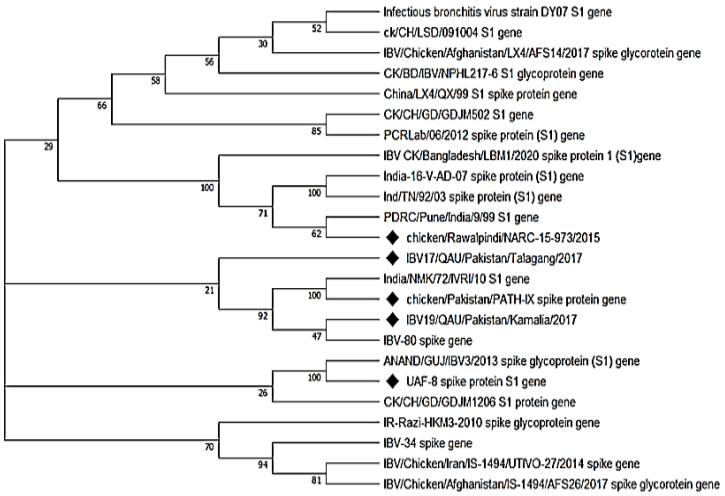

Fig. 1: Phylogenetic tree showing Antigenic diversity of the S1 gene for IBV strains generated using neighbor-joining 100 bootstrap replicates. The phylogenetic tree was constructed by using MEGA 11 software. Ten (05) Pakistani IBV strains were compared with IBV strains in selected countries of South-Asia. The Pakistani strains in this study were indicated by black arrows, The Fig. 1 contains the already published IBV isolates with different Antigenic variations in South-Asian region

Control strategies

The first step to control this economically significant disease in poultry requires identification of novel variant of IBV, which is linked to the disease outbreak in vaccinated birds. It is the need of an hour to develop a vaccine in order to control the newly circulating strain of IBV in particular area, because already available vaccines are unable to offer sufficient protection. The killed vaccines or attenuated live vaccines are usually developed for Novel IBV strain. It should be worth mentioning that new vaccine development approaches are obviously required in order to respond to disease outbreaks in a safe and timely manner.

Conclusion

Infectious bronchitis is a serious poultry disease with economic implications that mostly impacts countries with large poultry production (Bande *et al.* 2017), but it also affects poultry sectors globally (Jackwood and Wit 2013).

Currently, IBV strains are categorized using a phylogeny-based categorization approach developed by Valastro and colleagues. The phylogenetic tree given in Fig. 1 shows the antigenic diversity of S1 gene of infectious bronchitis virus in South Asian region. The IBV variants or strains are currently classified into eight genotypes (GI-GVIII), 39 different lineages (GI-1 to GI-31, GII-1, GII-2, GIII-1, GIV-1, GV-1, GVI-1, GVII-1 and GVIII-1) as well as a large number of inter-lineage recombinants that are not yet classified. Most IBV lineages are limited to specific geographic regions, while certain countries report the circulation of distinct lineages. On the other hand, the lineages GI-1, GI-13, GI-16, and GI-19 are widely distributed (Krisztina *et al.* 2022). The study conducted in Pakistan, evaluated the criteria using the 9 novel sequences for all Pakistani isolates of IBV. Eigth sequences of IBV isolates out of nine were grouped in GI-13 and one was placed in GI-24 lineage (Saleem *et al.* 2024). It suggested that Different IBV strains isolated and identified in Pakistan are diverse in terms of genetics, offering a base for re-combination and challenging the biological control protocols. Another study showed that IBV strain (Pak-973) has diverse mutations when matched with Mass and 4/91 strains which are being used as vaccine strains. The sequenced isolate Pak-973 varied from other serotypes by an average of 7%. These observable changes or substitutions in HVR1 and HVR2 ensure that this isolate is distinct from the vaccination strains that are used in vaccines. This demonstrates the importance of vaccine matching strategy before choosing a strain to use as a vaccine seed when introducing a novel IBV vaccination strain in a particular area. Conclusively, the major factors involved in the prevalence of Infectious bronchitis are occurrence of multiple strains of IBV, lower level of humoral immunity and emergence of novel IBV strains. This review presented a little contribution in demonstrating the similarity index between Pakistani IBV and strains of selected south Asian countries. This similarity index was established through phylogenetic analysis of different IBV strains. Furthermore, A detailed summary of the most recent findings regarding the genetic group distribution of avian coronavirus which may be helpful in vaccine production for different IBV strains circulating in selected South Asian countries. It is very important that vaccine matching should be done before vaccination. Vaccine matching is crucial for maintaining the efficacy of vaccines, as it allows researchers and healthcare professionals to stay ahead of the evolving nature of infectious agents and address emerging strains that might pose challenges to existing vaccine formulations.

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Author Contributions

BJ: Complete write up of original Article and Phylogenetic Analysis and collection of relevant data, TK: Idea and conceptualization, FA: Visualization (presentation of data, such as creating figures or tables), MNR: technical Support, HMBA: Proof-reading of review paper.

Conflicts of Interest

The authors have no conflicts of interest to declar.

Data Availability

The data used in this study can be obtained from the corresponding author upon a reasonable request.

Ethics Approval

Not applicable

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