



Mini Review

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Hebatitis B Virus Genotypes in Pakistan



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Mini Review

Hepatitis B virus (HBV) infection is one of the most common causes of human death worldwide [1-3]. HBV has ten genotypes alphabetized as A to J which are not uniformly distributed in different parts of the world. The genotypes are important in treatment of the infection as they influence the disease progression, baseline viral load and the patients' response to treatment.

Distribution of HBV genotypes in the world

According to Bonino et al. [2], who reviewed the global distribution of HBV genotypes, various HBV genotypes are not uniformly distributed all over the world. Further, their distribution is influenced by ethnic and geographical factors.

Genotype A is common in Brazil, North America, Northwest Europe, South Asia, Central Africa, Tunisia and Benin [2,4,5]. Genotype B is common in China, Hong Kong, Indonesia, Japan, Philippines, Taiwan, Thailand, Vietnam and United States of America. Genotype C is prevalent in Australia, Polynesia, Melanesia, Micronesia, Indonesia, China, Hong Kong, Vietnam, Thailand, Japan, Korea, Taiwan, India, Solomon Islands, Brazil and USA. Genotype D is predominant in Mediterranean region, Spain, Albania, Czech Republic, Russia, Turkey, Middle East, Iran, Afghanistan, India, Solomon Islands, Tunisia, Polynesia, Melanesia, Micronesia, Brazil and USA [6,7]. Genotype E is endemic to Africa where it occurs only in some countries of the Western part of the continent [6]. Genotype F is widely distributed in new world; it has been reported from Alaska, Argentina, Bolivia, Brazil, Central America, Polynesia, South America and USA [8,3]. Genotypes G has been recorded from North America, France and Germany while genotype H is confined to Central America, South America and Mexico [9,10]. Genotypes I and J are confined to Vietnam and Japan, respectively [11,12].

A number of studies in India showed that genotypes D and A are present in Western, Northern and mainland India while genotype C is present in the Eastern parts. In a study [13] on 62 HBV patients from Western India, the region along with Pakistani

borderline, genotype D was identified in 92% of the isolates while the remaining 8% were determined as genotype A. None of the other genotypes was recorded in the study. According to another study [14], who reviewed the distribution of HBV genotypes in India, the Northern and Western parts of India are prevailed with genotype D which is followed by genotype A but the Eastern parts of India have a different pattern where genotype C infections made almost equal proportion with genotypes A and D. A study having 1096 samples from nine different areas of China reported that genotypes C (53%) and B (41%) are most common in China [15]. They further identified genotype A, D and a mix infection with combination B+C in 1%, 4% and 1% of the samples respectively.

Prevalence and distribution of hbv genotypes in pakistan

Information regarding the various HBV genotypes in Pakistan and their distribution and prevalence is sketchy and somewhat contrasting. A few studies were conducted on the distribution of HBV genotypes in Pakistan and most of them are confined to some specific cities or areas like Karachi and Punjab. Table 1 summarises the available studies on HBV genotype prevalence in Pakistan, their sample size and sites of sampling along with their results. In brief, a study based on just 12 samples from Lahore reported the presence of only two genotypes; genotype C from nine samples which made 75% while remaining three were positive for genotype D [16].

Idrees et al. [17] studied HBV genotypes in 112 samples which they collect from four provinces of Pakistan and reported that genotype C is dominant with 41.1% prevalence. Genotypes A, B, D and mix genotypes were reported in 21.4%, 17.8%, 8.0% and 7.1% of the samples respectively. Similarly, Abbas et al. [18] performed genotyping of 109 samples from Karachi and reported that 107 (98.2%) of them had genotype D while remaining two (1.8%) were infected with a mixture of genotype A and D. None of the other genotypes were reported in this study.

Table 1: The prevalence of different HBV genotypes in published studies from Pakistan.

Source	Place of Sampling	Sample Size	Proportion of Genotype As % of Total Samples									
			A	B	C	D	E	F	Mix	Mixed Genotypes Combinations	UT*	
Mahmood et al. [25]	KP & FATA, AJK, Gilgit Baltistan, Sind, Punjab & FCT, Baluchistan	715 (99, 68, 93, 84, 311, 60)	55	4	6	509	1	-	-	124	A+D, A+B, B+D, C+D, E+D, A+B+D	
Mahmood et al. [24]	Islamabad	22	-	-	-	14	-	-	-	8	A+D	
Hanif et al. [23]	Karachi, Rawalpindi / Islamabad	200 (40, 160)	10	-	-	59	-	-	-	31	A+D	-
Awan et al. [7]	Punjab, KP, Sind, Baluchistan	300 (222, 36, 26, 15)	14	18	28	13	0.6	1.3	-	16	A+B+D, A+D+F, A+C, A+D, A+E, A+F, B+C, B+E, C+D	10.3
Ahmed et al. [21]	Punjab, Sind	236	0.8	-	5.9	93.2	-	-	-	-	-	-
Baig et al. [22]	A+D	-										
Baig et al. [22]	Karachi	315	20	-	-	70	-	-	-	10	A+D	-
Noorali et al. [20]	Karachi	180	-	-	-	84	-	-	-	16	B+D	-
Alam et al. [19]	Punjab, KP, Sind Baluchistan	110 (30, 28, 25, 18)	4.5	24.5	-	60	-	-	-	2.7	A+D, B+D	8.2
Abbas et al. [18]	Karachi	109	-	-	-	98.2	-	-	-	1.8	A+D	-
Idrees et al. [17]	Punjab, KP, Sind, Baluchistan	112 (Details not available)	21.4	17.9	41.1	8.0	-	-	-	7.1	Details not available	4.5
Abbas [16]	Lahore	12	-	-	75	25	-	-	-	-	-	-

*UT : Un-typeable

Another study described genotyping results for 101 samples which comprised 30 from Punjab [19], 28 from KP, 25 from Sind and 18 from Baluchistan. They identified genotype D in 65%, genotype B in 27% and genotype A in 5% of the samples. Mix genotype infections with combinations A+D and B+D were also reported in this study which were 2.7% of the samples. Yet another study reported that 84% of the 180 female patients in Karachi were infected with genotype D and the rest of 16% had mix infection with genotype B and D [20].

Ahmed et al. [21] conducted genotyping on 236 samples from Punjab and Sind provinces of Pakistan. The study reported that the dominant genotype is D with 93.2% of the samples followed by genotype C with 5.9% while genotype A was rare with only 0.8% of the samples. Sub-genotype D1 was found in 84% and D2 in 8% of the genotype D samples by complete genome sequencing. Genotype C samples belonged to sub genotype C2.

Baig et al. [22] studied 315 samples in Karachi from patients belonging to different ethnic groups. They found that 70% of the samples carried genotype D and 20% of the patients suffered

genotype A infection while 10% had mix infection involving genotypes B and D. Using 140 samples from Rawalpindi/ Islamabad, and 60 more from Karachi, a study [23] reported that 59% of the samples have genotype D, 10% have genotype A and 31% have mix infection involving genotype A and D.

However, the genotype profile seems to have been drastically altered by the study of Awan et al. [7] both in terms of the prevalence of genotypes A, B, C, and D and addition of two more genotypes. This study examined 300 samples including 222 from Punjab, 26 from Sind, 30 from Khyber Pakhtunkhwa and 16 from Baluchistan. Out of 300 samples, 269 (89.7%) were successfully genotyped. They identified six HBV genotypes with their prevalence as C(27.7%), B(18%), A(14.3%), D(13%), F(1.3%) and E(0.7%). This percentage is based on 202 single infection samples while mix genotype infections with nine different combinations were observed in 44 samples that make 14.7% of the prevalence.

A recently published smaller study [24] described that about 64 % of the studied HBV samples belong to genotype D while

remaining 36 % had a mixture of genotypes A and D. The study however, confirmed sub genotype D1 with complete genome sequencing of 4 out of the total 22 samples. The prevalence and distribution of HBV genotypes is almost confirmed in a conclusive study with a large number of samples from all over the Pakistan [25]. With a total of 715 samples from all 6 geopolitical regions of Pakistan, this study reported that genotype D is the predominant genotype in all regions of Pakistan with an overall prevalence of about 71 %. However, the mix infection with the combination of genotypes A+D was reported to be the second most prevalent infection in Pakistan with a percentage of 13.7. Genotype A, with an infection percentage of 7.7 was reported to be the third most common HBV genotype in Pakistan while about 3.6 % of the HBV infections were reported to be a mixture of genotypes with combinations other than A+D.

In conclusion, It is now clear that HBV/D is the most common genotype in all regions of Pakistan followed by the mix genotype infection with combination of A+D while the third most common HBV genotype in Pakistan is HBV/A.

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