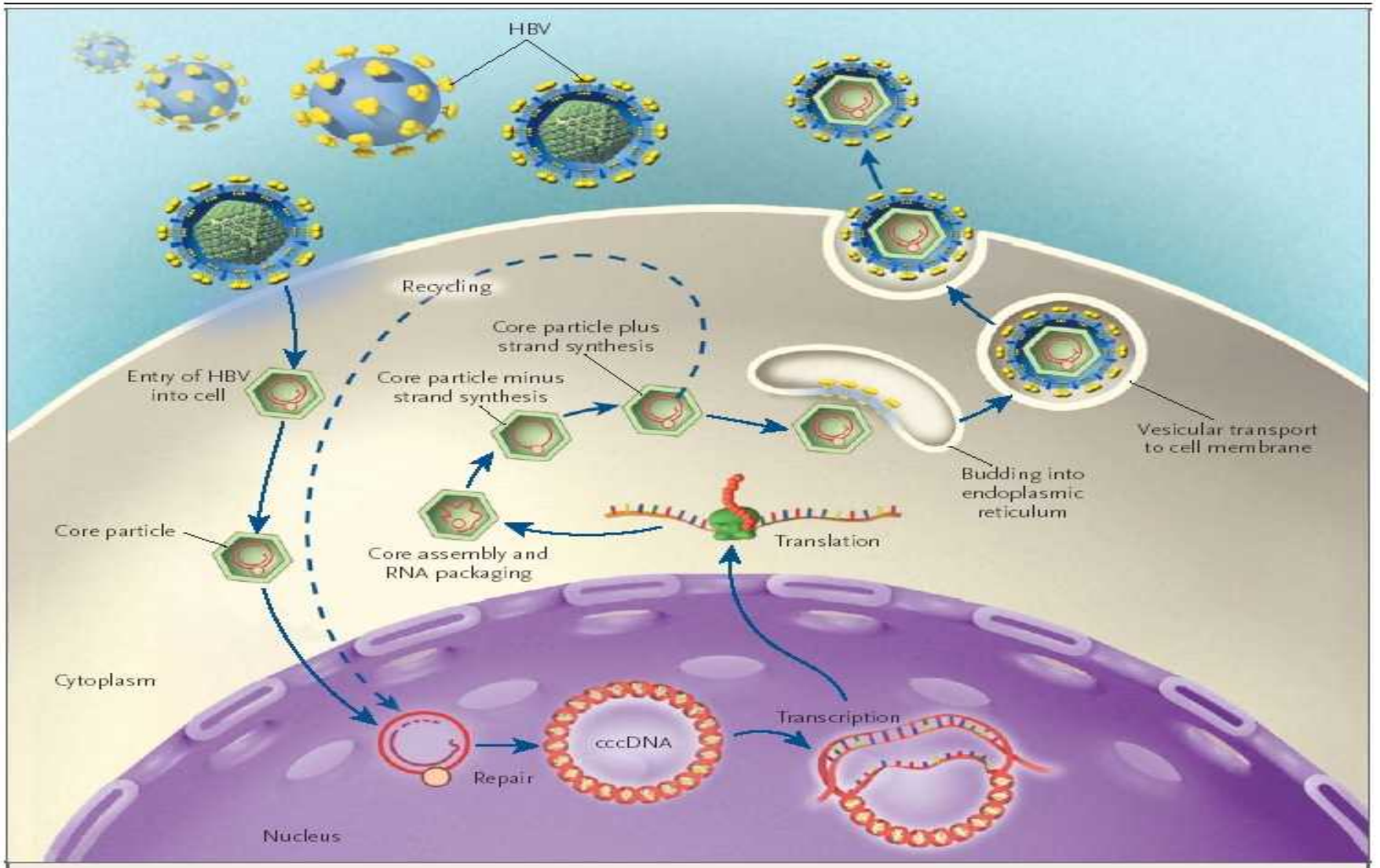
儿童乙肝的新认识(英文版）

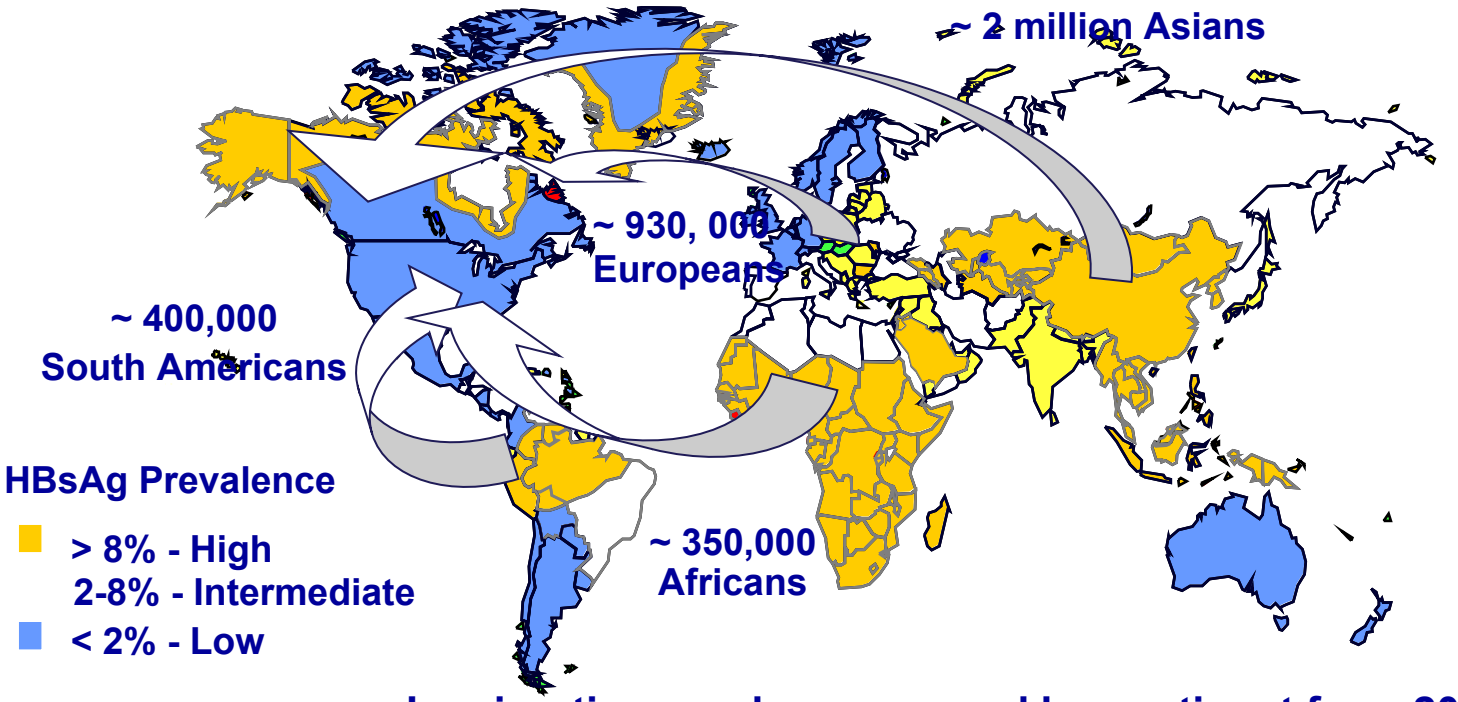


to cccDNA. The small, peach-colored sphere inside the core particle is the viral DNA polymerase.

EPIDEMIOLOGY

Chang MH

Prevalence of Chronic Hepatitis B



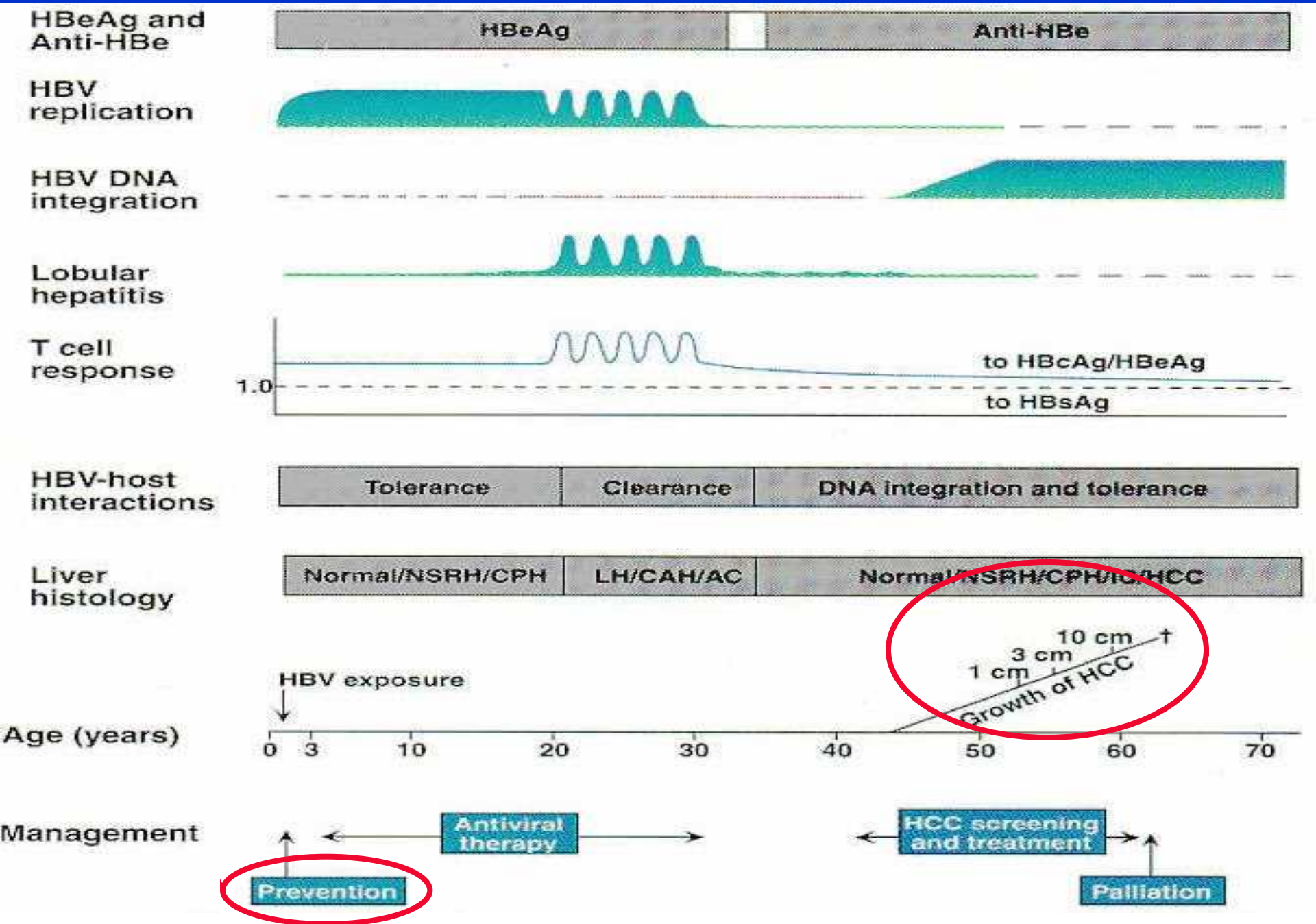
Immigration numbers summed by continent from 2019-2019

Centers for Disease Control. Hepatitis B fact sheet. Available at: cdc.gov/hepatitis. Accessed January 31, 2019. Mahoney FJ. Clin Microbiol Rev. 2019;12:351-366. Hepatitis B Foundation. Hepatitis B statistics. Available at: hepb.org/hepb/statistics.org. Accessed January 31, 2019.

NATURAL HISTORY OF HEPATITIS VIRUS INFECTION

Chang MH

Natural History of Hepatitis B



FACTORS AFFECTING THE CLINICAL COUSE OF HEPATITIS VIRUS INFECTION

- **Host**
  Age of Infection

- **Virus :**
  Genotype
  Mutants / Variants

- **Route of Infection**
- **Other Factors**

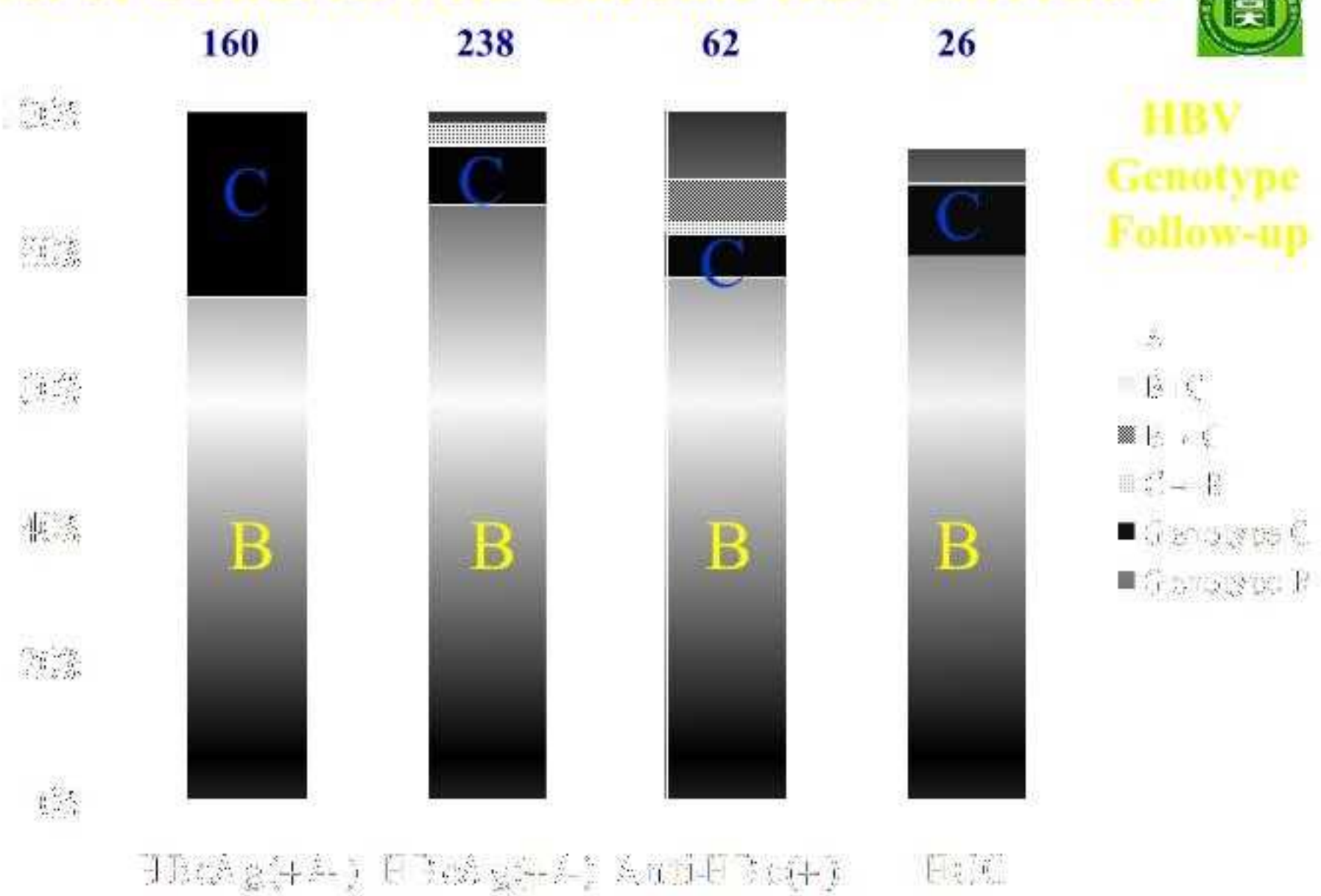
Age of Infection and Outcome

- Perinatal Transmission
- Childhood Infection
- Adolescent/Adult Onset Disease

HBV GENOTYPE AND HBeAg SEROCONVERSION

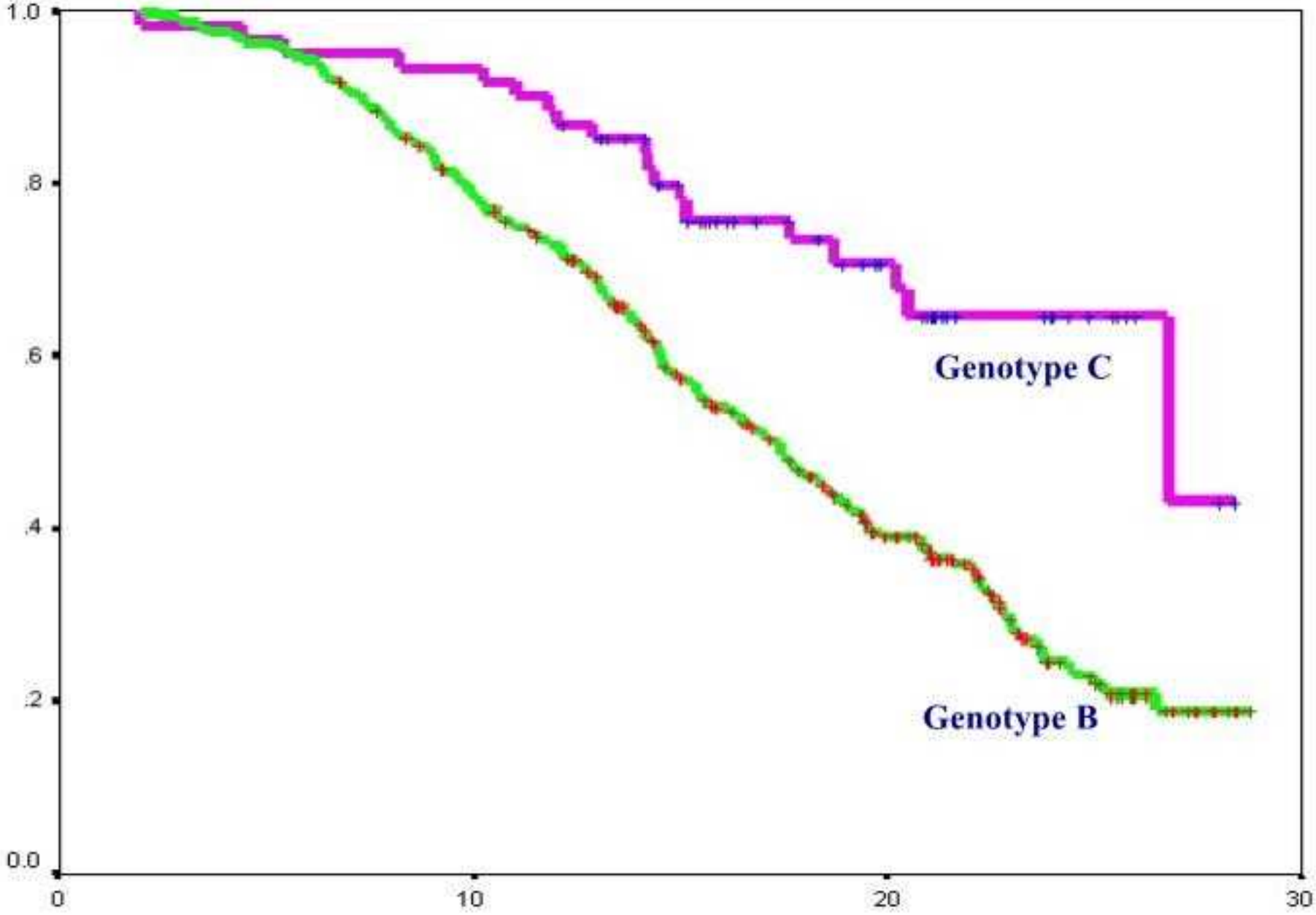
Worldwide Distribution of HBV Genotypes. The Size of the Capitals indicates the Relative Prevalence of the Genotypes

No. of Children with Chronic HBV Infection



Chang MH

Ni YH, Chang MH, et al. Gastroenterology 2019 ;127:1733-8.



Ni YH, Chang MH, et al. Gastroenterology 2019 ;127:1733-8.

HBV Genotype and Clinical Course in Children

- **Genotype C Delays HBeAg Seroconversion in Chronic HBV Infection in Children**
- **Genotype Changes : Rare**
- **Genotype B Dominates in Children with Chronic HBV Infection and HCC in Taiwan**

Ni YH, Chang MH, et al. Gastroenterology 2019 ;127:1733-8.

HBV VARIANTS / MUTANTS

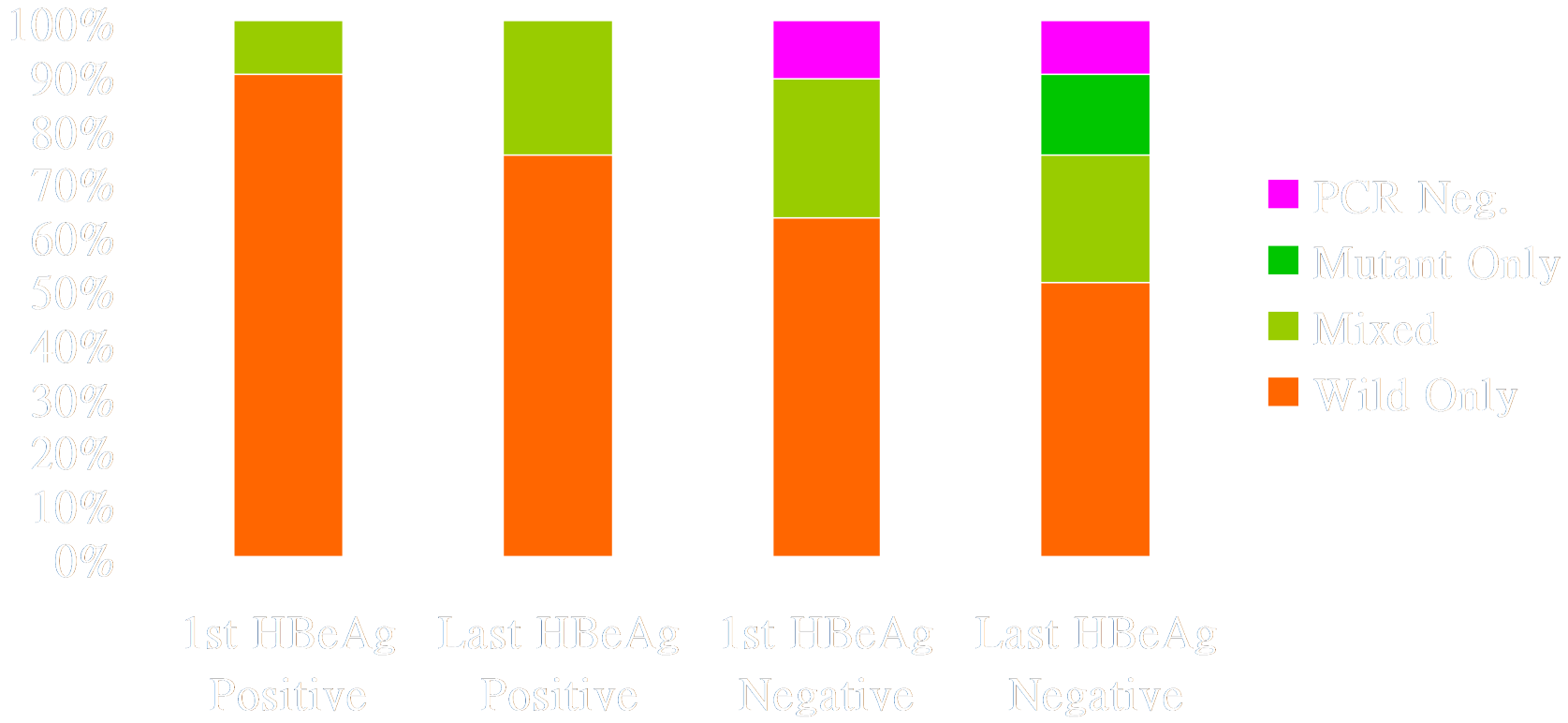
A Point Mutation at Codon 28 (Nucleotide 1896) of HBV Precore Gene

TGG → **TAG**

(Tryptophan) → **(Stop Codon)**

Leading to HBeAg Negative Strains

CHANGES OF HBV PRECORE GENE 1896 IN 80 HBsAg CARIER CHILDREN



Chang MH

Chang MH, et al. J Hepatol. 2019 ;28:915-22.

Peak ALT levels during follow-up in 3 groups with different patterns of HBV precore 1896

Peak ALT (IU/l)	Group 1 (*n*=37)	Group 2 (*n*=22)	Group 3 (*n*=21)	Total (*n*=80)
Mean	136	179	209	167
+- SD	+- 149	+- 141	+- 195	+-161

Group 1: Wild type throughout the whole course.

Group 2: Mutant after HBe seroconversion

Group 3: Mutant before HBe seroconversion.

- **ALT levels between groups, *p*=0.07.**

Chang MH, et al. J Hepatol 2019; 28: 915-22.

Comparisons of HBV Core Gene Between 31 Chronic Carriers and 12 HCC Children

Codon	Mutated Cases (No.) in HCC	Mutated Cases (No.) in Chronic carrier	Mutations	*P* value
Precore 28	58% (7)	52.2% (12)	W→X	0.73
Core 21	8% (1)	21.7% (5)	S→P or A	0.32
Core 65	33% (4)	17.3% (4)	L→W or V	0.29
Core 74	**33% (4)**	0	**S→G**	**0.0032**
Core 87	**33% (4)**	0	**S→G**	**0.0032**
Core 131	8% (1)	0	A→D	0.16
Core 143	33% (4)	4.3% (1)	L→P	0.015
Core 147	8% (1)	21.6% (5)	T→C or S	0.32
Core 159	**42% (5)**	0	**R→S**	**0.0006**
Core 182	**42% (5)**	**4.3% (1)**	**Q→X**	**0.0035**

Chang MH

Ni YH, et al. Gut 2019;52:122-5

Comparisons of HBV Core Gene Between 31 Chronic Carriers and 12 HCC Children - SUMMARY

- Core gene codon 21, 65, and 147 were the commonest mutation sites in children with chronic HBV infection. All were located in HBcAg epitopes of CTL.

- Codon 74, 87, and 159 mutations are found in HCC children, but not in the chronic infection group.

Ni YH, et al. Gut 2019;52:122-5

DISCUSSION

- **These mutations may help HBV to escape host immune pressure, to expand viral proteins, and finally bring in the cancer development.**

TREATMENT OF HEPATITIS B

CURRENT THERAPY FOR HEPATITIS B IS NOT SATISFACTORY