

Molecular characterization of hepatitis B virus strains infecting blood donors with high HBsAg and undetectable HBV DNA levels: implications for blood safety and screening policy

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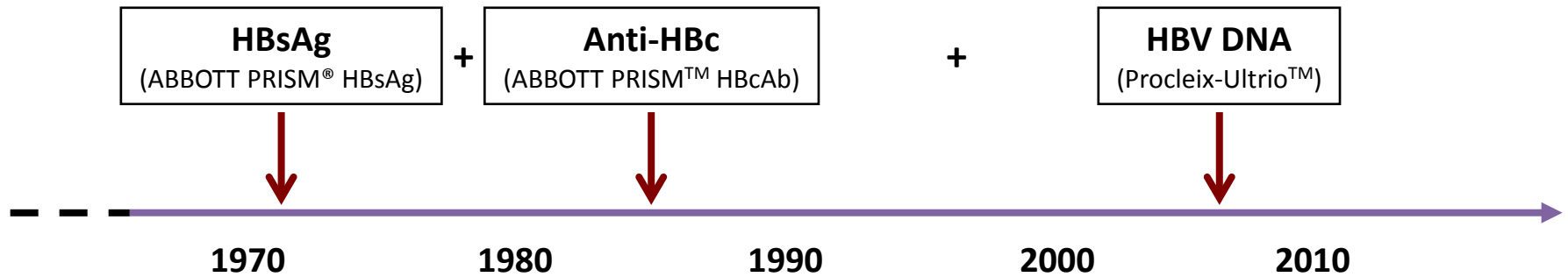
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Relative efficacy of HBV screening assays

HBV infection features	Detected by		
	HBsAg	Anti-HBc	HBV NAT
Window period	<i>No</i>	<i>No</i>	Yes
Primary OBI	<i>No</i>	<i>No</i>	Yes
2nd window period	<i>No</i>	Yes	Yes
Chronic infection	Yes	Yes	Yes
Anti-HBc+ OBI	<i>No</i>	Yes	Yes
Anti-HBs only OBI	<i>No</i>	<i>No</i>	Yes
Anti-HBc only	<i>No</i>	Yes	<i>No</i>
HBsAg only	Yes	?	<i>No</i>

HBV screening in French blood donations



- High sensitivity and adequate specificity
- Pre-seroconversion window period & occult infections
- **Estimated HBV residual risk: 1 in 4 millions donations**

But:

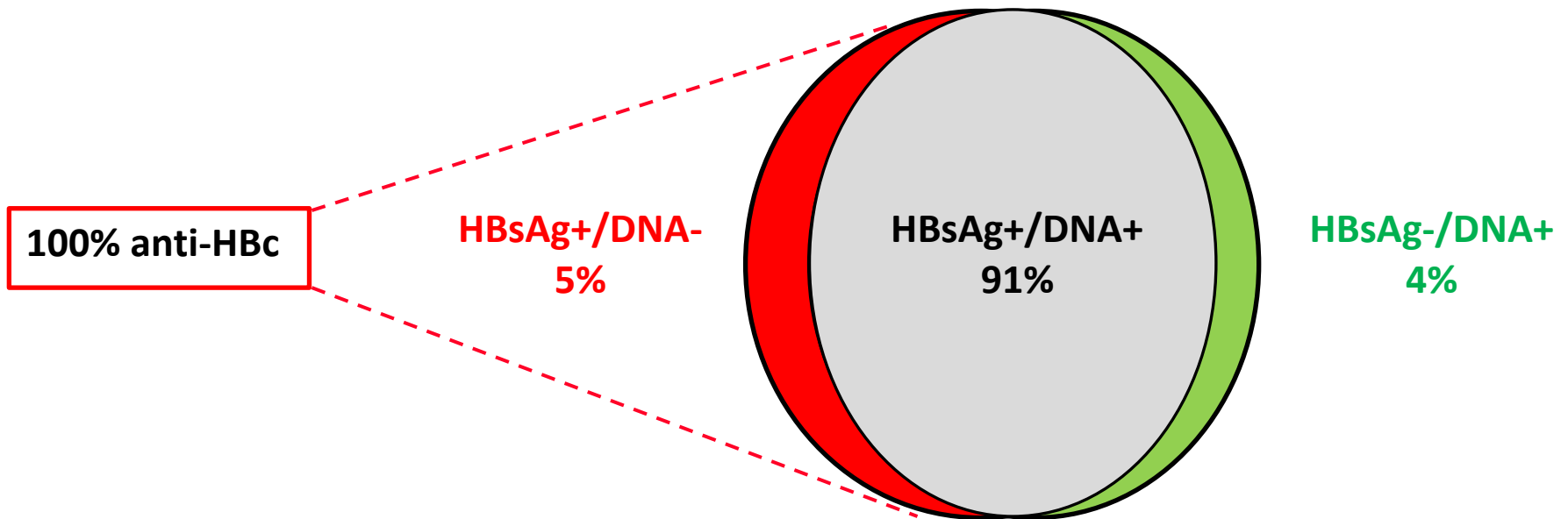
- High cost
- Redundancy of HBsAg and HBV DNA direct markers

Maintaining HBsAg testing?

- Cost reduction of blood testing
- Complementarity of anti-HBc and HBV DNA testing
(Enjalbert et al. Transfusion 2014;54:2485-95)
- Anti-HBc testing issues on blood availability in high endemic settings
- **Potential impact on blood safety?**

Distribution of HBV markers in French blood donors

- Period: 2010-2013
- Excluding overseas territories
- 10 186 279 donations tested → **806 HBV reactive** ($\approx 1/10,000$)



HBsAg & HBV DNA discrepant levels in 740 samples confirmed HBsAg+

Sample screening	Number (%)	HBV DNA load (IU/mL) (COBAS TaqMan HBV; LOQ 6 IU/mL)		
		Undetected	< 6	≥ 6
NAT* neg.	41 (5%)	13 (32%)	20 (49%)	8 (19%)
NAT pos.	699 (95%)			
• HBsAg < 100 IU/mL	58 (8%)	1 (2%)	12 (21%)	45 (77%)
• HBsAg > 100 IU/mL	641 (87%)	13 (2%)	27 (4%)	601 (94%)

*NAT: Procleix-Ultrio (LOD 12 IU/mL)

Hypotheses

- **Ratio: 1 viral particle / 1,000-10,000 HBsAg**

- Natural course of infection

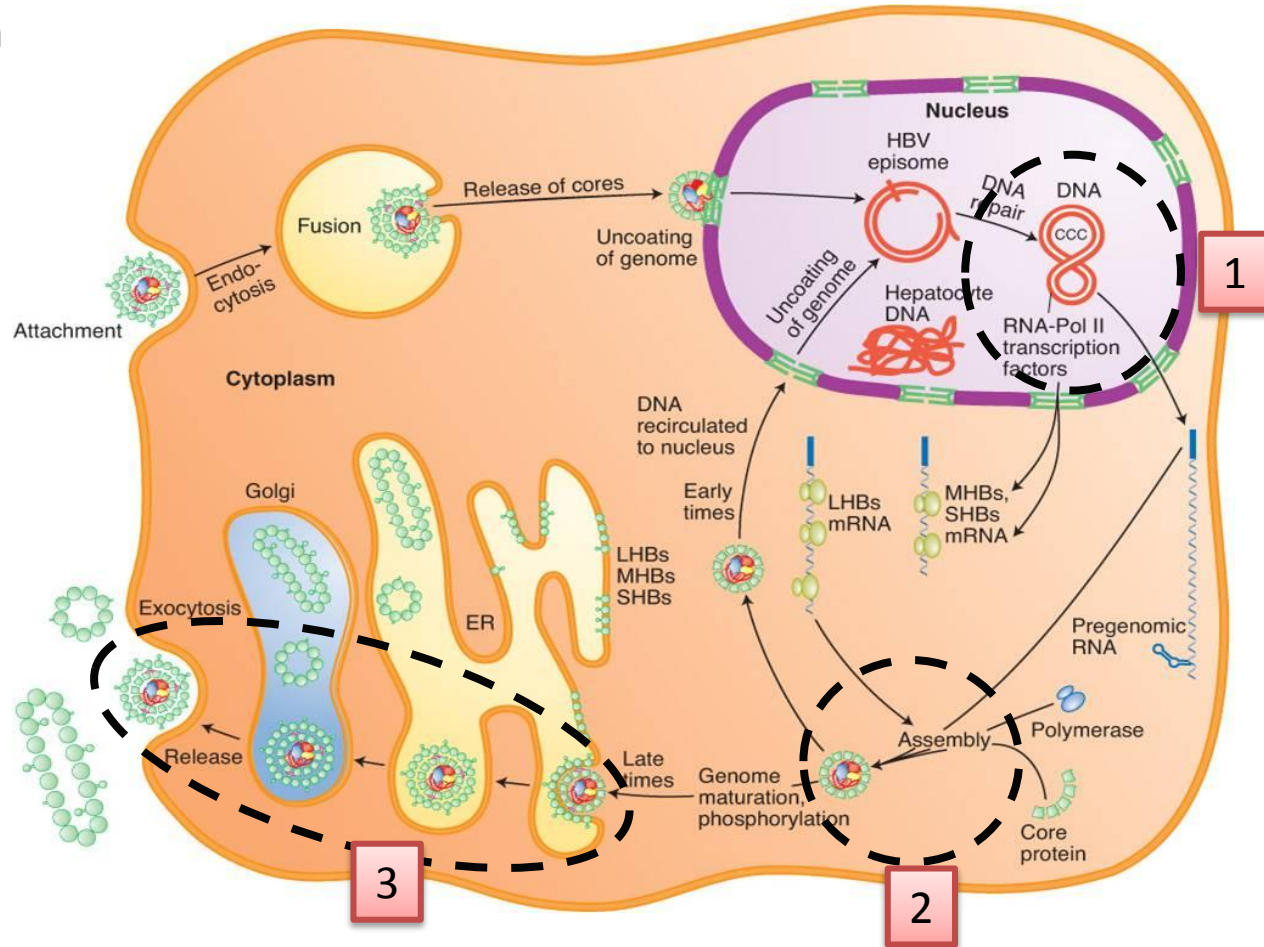
- HBV genotypes

- **Hypotheses:**

- NAT failure

- Impaired viral replication

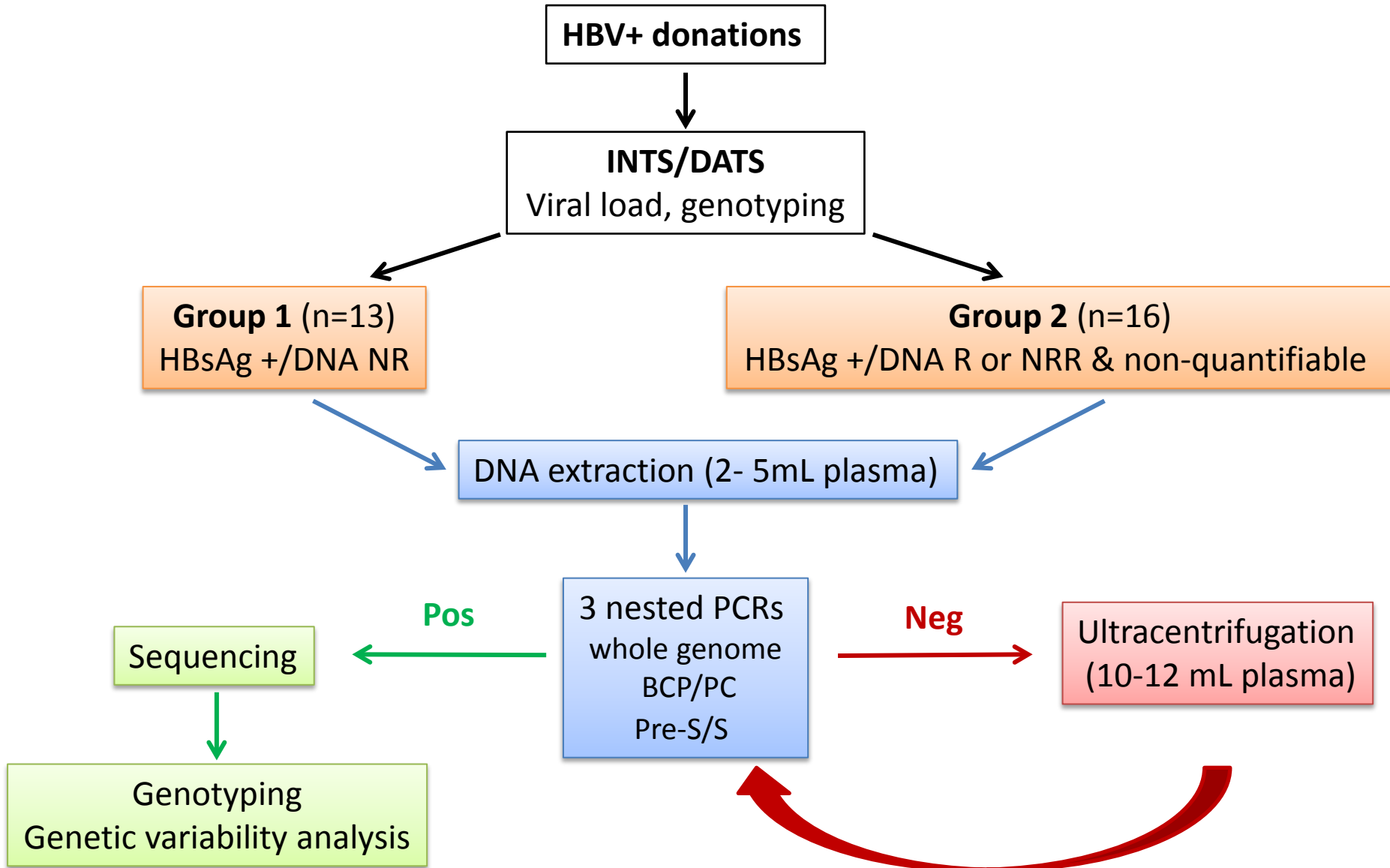
- **Infectivity?**



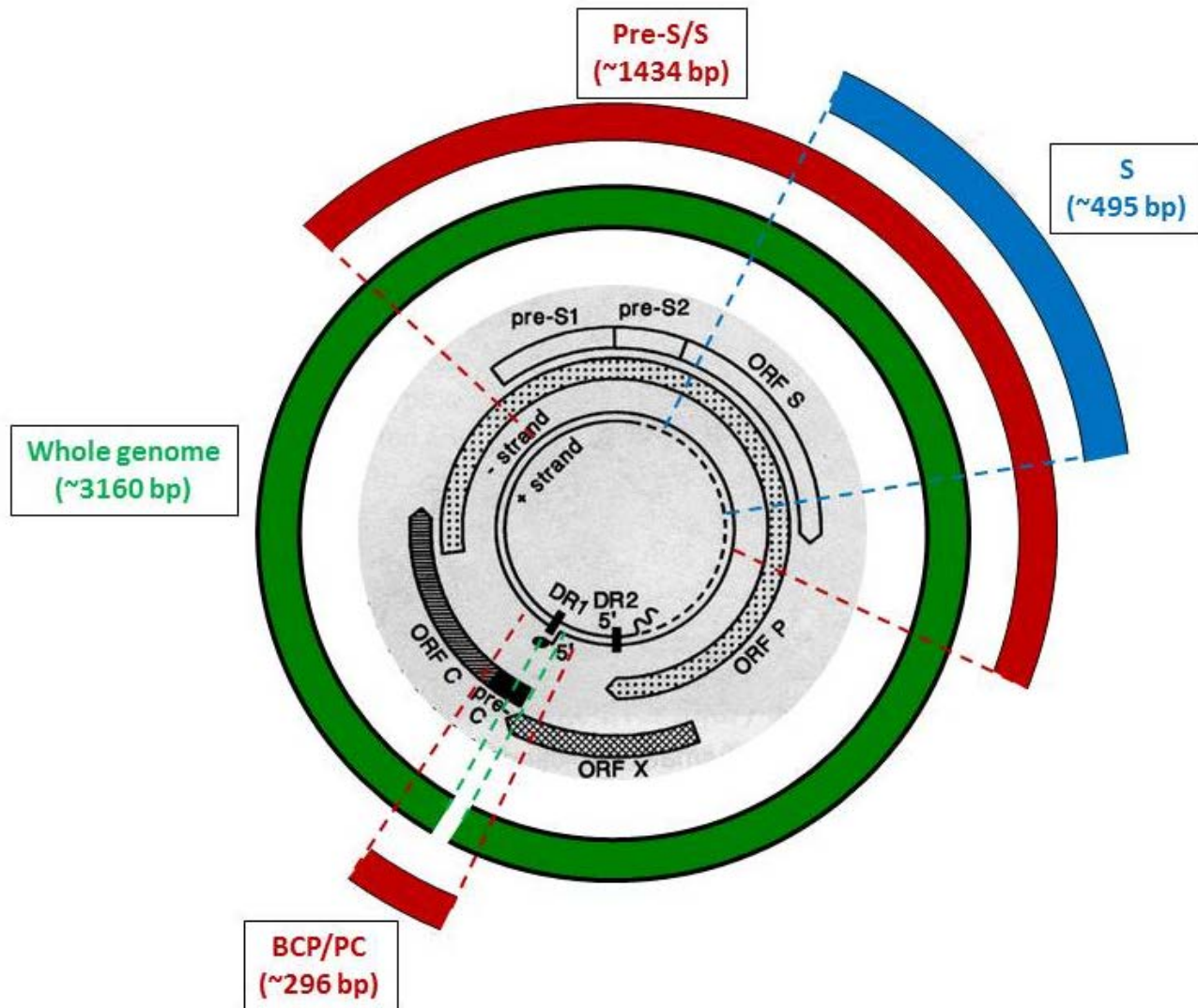
Objectives

- Prevalence of HBsAg+/ NAT non-reactive or non-repeatable reactive donations
- Detect and/or confirm HBV DNA presence
- Evaluate and compare performance of NAT assays to detect these samples
- Perform genetic characterization of the viral strains associated with this phenotype
- Evaluate viral replicative properties *in vitro* as a surrogate marker of infectivity

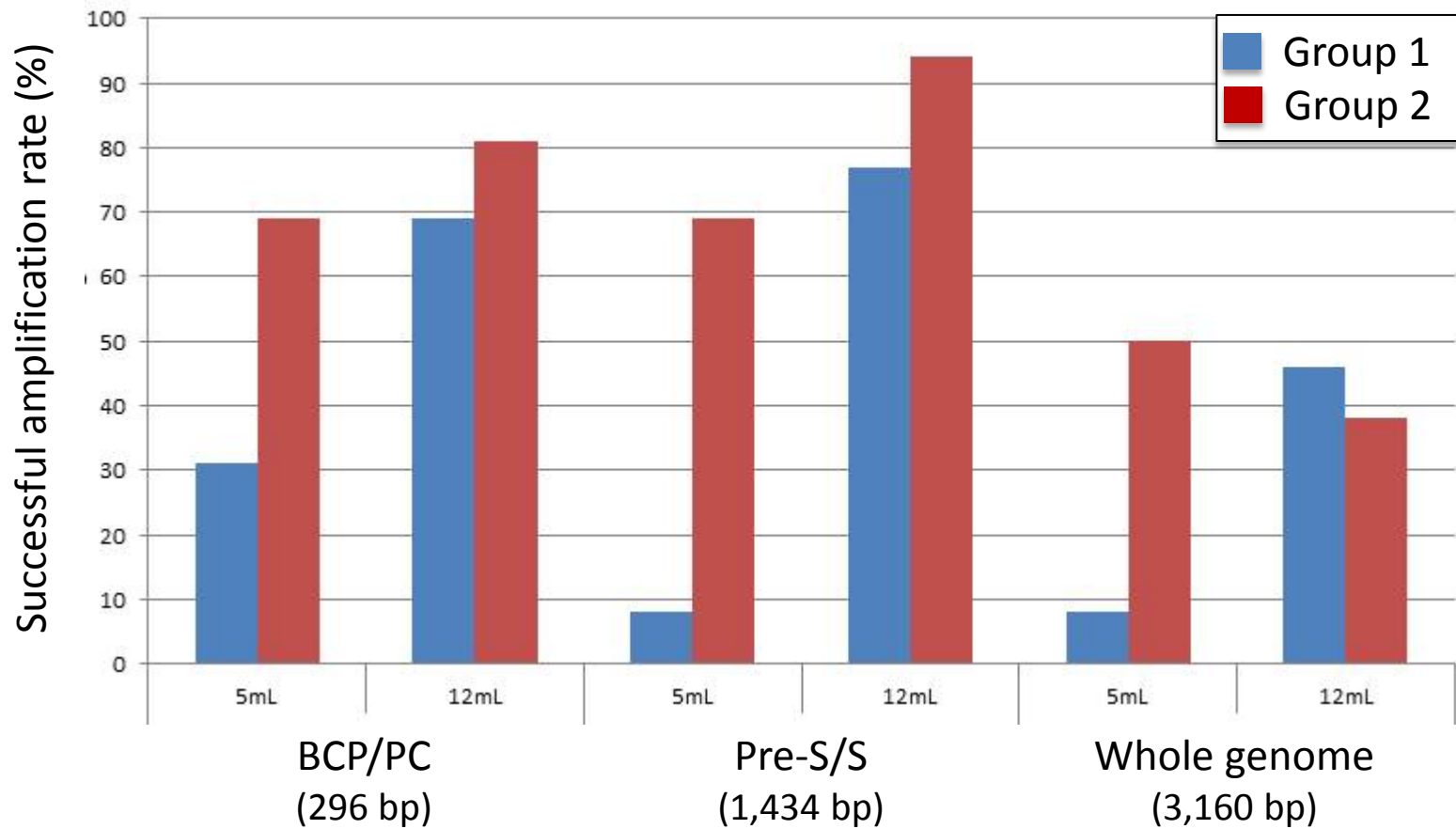
Study design



HBV DNA amplification



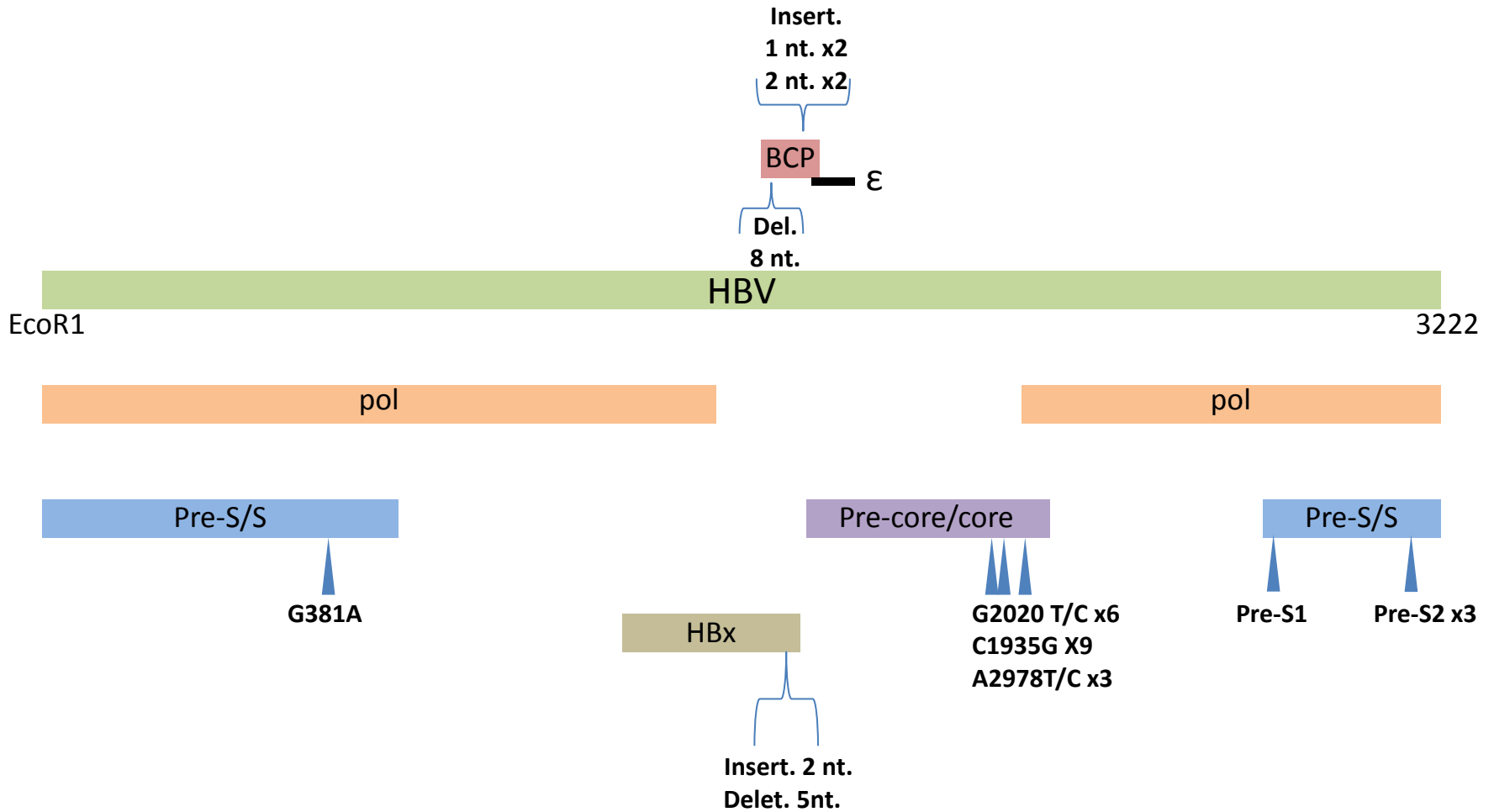
HBV DNA amplification performance



Preliminary results

	Group 1 (n = 13)	Group 2 (n = 16)	Total (n = 29)
Age (y) (mean; range)	34 (19 – 59)	35.5 (18 – 61)	34.8 (18 – 61)
HBsAg (ng/mL) (median; range)	1,355 (110 – 39,500)	2,113 (150 – 19,030)	1,881 (110 – 39,500)
HBV DNA confirmed	12 (92%)	15 (94%)	27 (93%)
HBV genotypes			
• A	-	9	9 (35%)
• B	1	-	1 (4%)
• C	2	1	3 (11%)
• D	7	2	9 (35%)
• E	1	3	4 (15%)

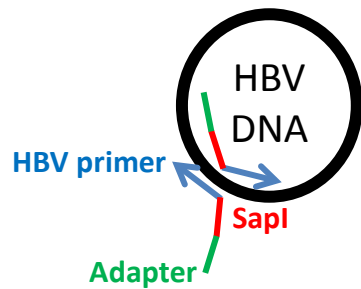
Sequences analysis



Construction of HBV replicons

Method 1

1st PCR amplification with HBV-specific primers



2nd PCR amplification using adapters



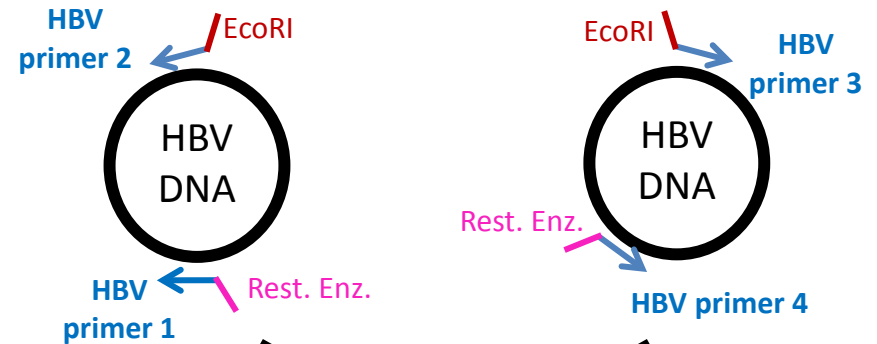
Huh7 transfection & re-circularization with SapI



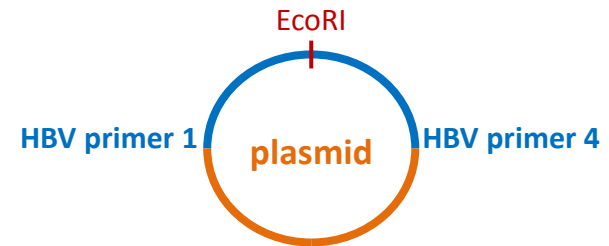
HBV genome expression & replication

Method 2

2 distinct PCR amplifications



Cloning of 1.2 HBV construct



Huh7 transfection



HBV genome expression & replication

Preliminary conclusions & perspectives

● Conclusions:

- Extremely low level of HBV DNA confirm in >90% of ID-NAT non-reactive blood donations with concomitant high HBsAg levels
- Phenotype not associated with donor age or HBV genotype
- Impaired viral replication rather than NAT failure is suggested
- Mutations potentially affecting viral replication identified

● Perspectives:

- Increase the number of samples and controls of various genotypes
- Collaborative study (Croatia, Poland, Switzerland, South Africa, Malaysia,...)
- Develop an *in vitro* HBV replication system
 - functional characterization of HBV variants
 - evaluation of infectious risk
 - increase knowledge about distinct molecular control of viral replication & HBsAg production → potential clinical implications
- Funding



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