

Hepatitis B Virus and Hepatitis Delta Virus infection in Colombian indigenous communities

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INTRODUCTION

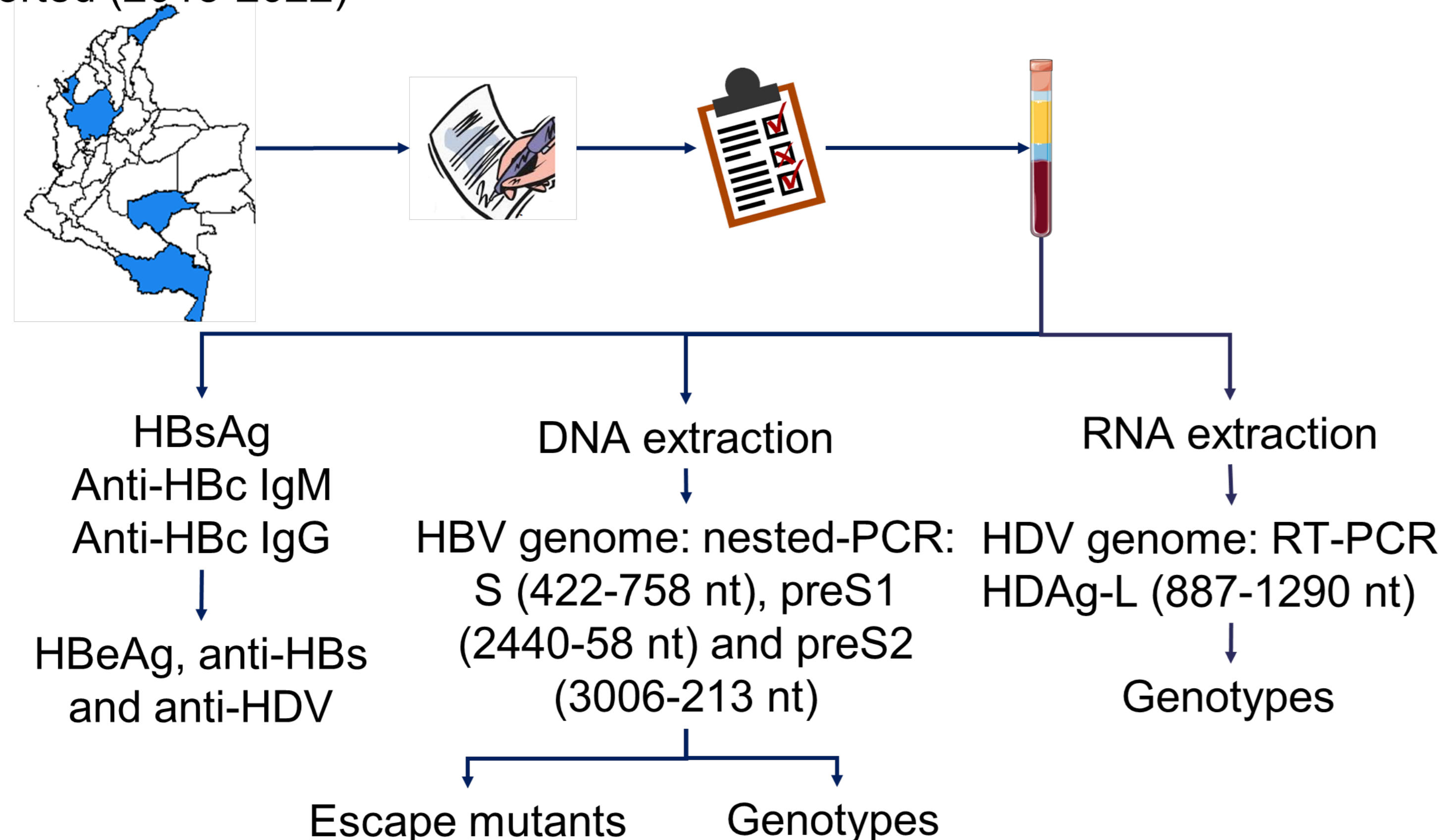
Despite the universal vaccine program, there are still high Hepatitis B prevalence regions such as the Amazon Basin. Indeed, the World Health Organization estimates 296 million people with chronic Hepatitis B Virus (HBV) infection and 820,000 deaths/year related to this infection over the world. Moreover, Hepatitis Delta Virus (HDV) affects 4.5% of individuals with chronic Hepatitis B. HDV is a satellite of HBV considering that the assembly of HDV virions depends upon the HBV surface antigen (HBsAg). HBV and HDV are particularly prevalent in indigenous communities from the Amazon Basin probably due to geographic, socioeconomic, and cultural factors that hinder access to the health system.

AIM

This study aims to characterize the serological and molecular markers of HBV and/or HDV infections in indigenous communities in four states in Colombia: Amazonas, Guaviare, Antioquia and La Guajira.

METHODS

Hepatitis B cases reported (2015-2022)



RESULTS

In total, 75 cases of Hepatitis B were included in the study. The mean age was 33 years old and 82.67% of participants were women.

Table 1. Serological markers of HBV cases in the study population

	Cases (n=75)				
HBsAg	+	+	-	-	-
Anti-HBc IgM	+	-	+	-	-
Anti-HBc Total	+	+	+	+	-
Total	1	47	1	5	21

Table 1. Molecular markers of HBV and HDV infection in the study population

Molecular Markers	Samples (n)	%
DNA HBV		
S	20/75	26,67
PreS1	3/20	15,00
PreS2	6/20	30,00
HBV Genotypes		
F1b	5/18	27,78
F3	7/18	38,89
D	6/18	33,33
RNA HDV		
HDAg	18/75	24,00
DNA-VHB y RNA-VHD	9/18	50,00
HDV Genotypes		
I	9/17	52,94
III	8/17	47,06

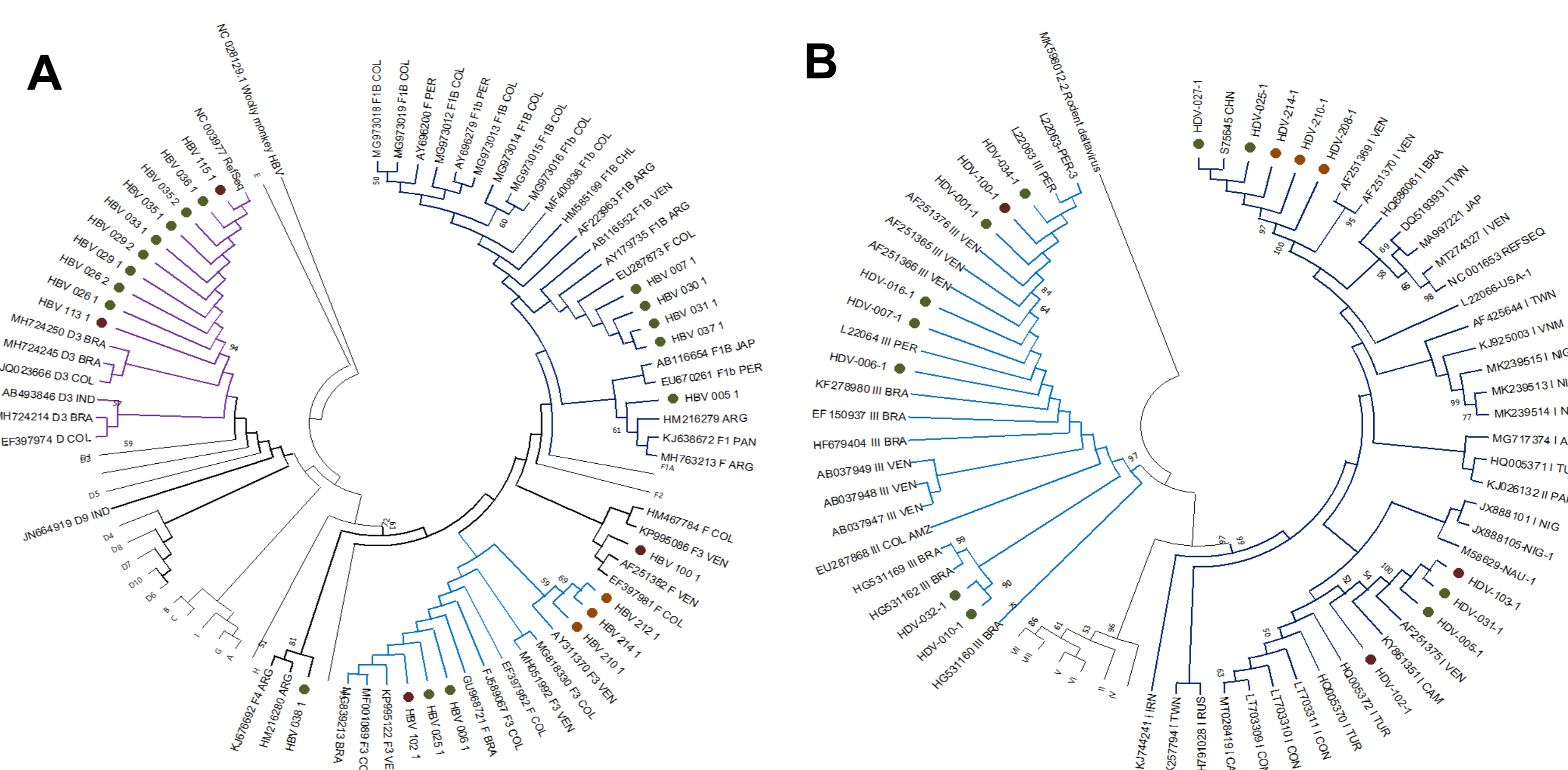


Figure 1. Phylogenetic analysis of HBV and HDV. **A. Phylogenetic analysis of HBV:** NC_004107 was used as outgroup. HBV ORF S generated by Maximum Likelihood with K2+G+I. **B. Phylogenetic analysis of HDV:** MK598012 was used as outgroup. HDV HDAg generated by Maximum Likelihood with GTR+G. The sequences of this study are indicated with circles. The sequences are denoted with the GenBank accession number, genotype, and country. The tree was generated using the software MEGA X. Bootstrap of 1000 replicates.

CONCLUSIONS

- The HBV and HDV co/superinfection prevalence was 24% in the study population.
- We identified the HBV Genotype F (5 samples subgenotype F1b and 7 subgenotype F3) and Genotype D (6 samples genotype D).
- The HDV Genotype III was characterized in 8 cases, and for the first time we identified the circulation of HDV Genotype I in Colombia.
- These results suggest that HBV and HDV infections continue to be a public health problem in indigenous people in Colombia.
- These results also show the importance to target this key population to invest resources in prevention, active search of cases, diagnosis and treatment.

Acknowledgment