

Prevalence and genotype distribution of hepatitis C virus in Georgia: A 2015 nationwide population-based survey

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INTRODUCTION

- Georgia is an Eastern European country with estimated high Hepatitis C (HCV) burden. However, country lacked updated, nationally representative data confirming disease burden¹.
- Georgia launched unprecedented HCV elimination program in April 2015, providing new DAAs at no cost to patients².
- A nationwide population-based Hepatitis C survey was conducted in 2015 to provide baseline data for the elimination program.

AIM

The survey aimed to:

- Estimate nationwide HCV prevalence
- Determine HCV genotype distribution
- Identify main risk factors for HCV infection in Georgia

METHOD

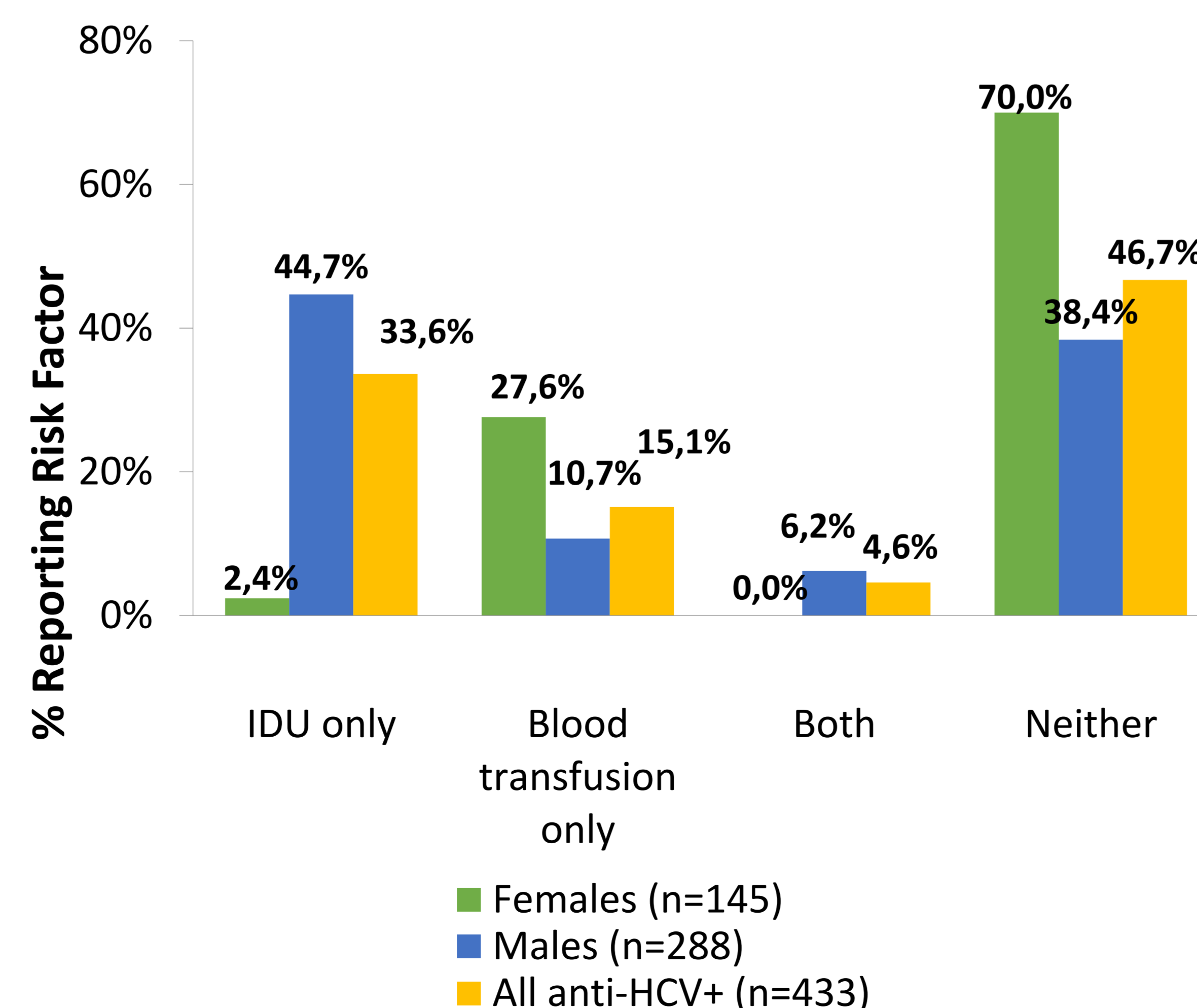
- The survey used a stratified, multi-stage cluster design (n=7,000) and included adults aged ≥18 years.
- A structured questionnaire collected data on socio-demographics, medical history, lifestyle information and HCV risk factors.
- Serum specimens were obtained and tested for anti-HCV antibody (anti-HCV). Positive samples were tested for HCV RNA and HCV genotype.
- Data were weighted using census data on sex, age, and geography. Descriptive analysis was conducted.

RESULTS

HCV Prevalence and Risk Factors

- National seroprevalence - **7.7%** (95% CI=6.7-8.9)
- Prevalence of chronic HCV infection - **5.4%** (95% CI=4.6-6.4)
- Two risk factors independently associated with anti-HCV+ status: history of injection drug use (IDU) (aOR=21.4, 95% CI=12.3-37.4), reported by 38.2% of anti-HCV positive participants, and ever receiving a blood transfusion (aOR=4.5, 95% CI=2.8-7.2), reported by 19.7% of participants;
- 46.7% of participants did not report either of these two risk factors. Among anti-HCV+ males, 50.9% reported history of IDU, 16.9% reported blood transfusion, and 38.4% reported neither risk factor.
- Among anti-HCV+ females, 2.4% reported IDU, 27.6% reported blood transfusion, and 70.0% reported neither risk factor (Figure 1).

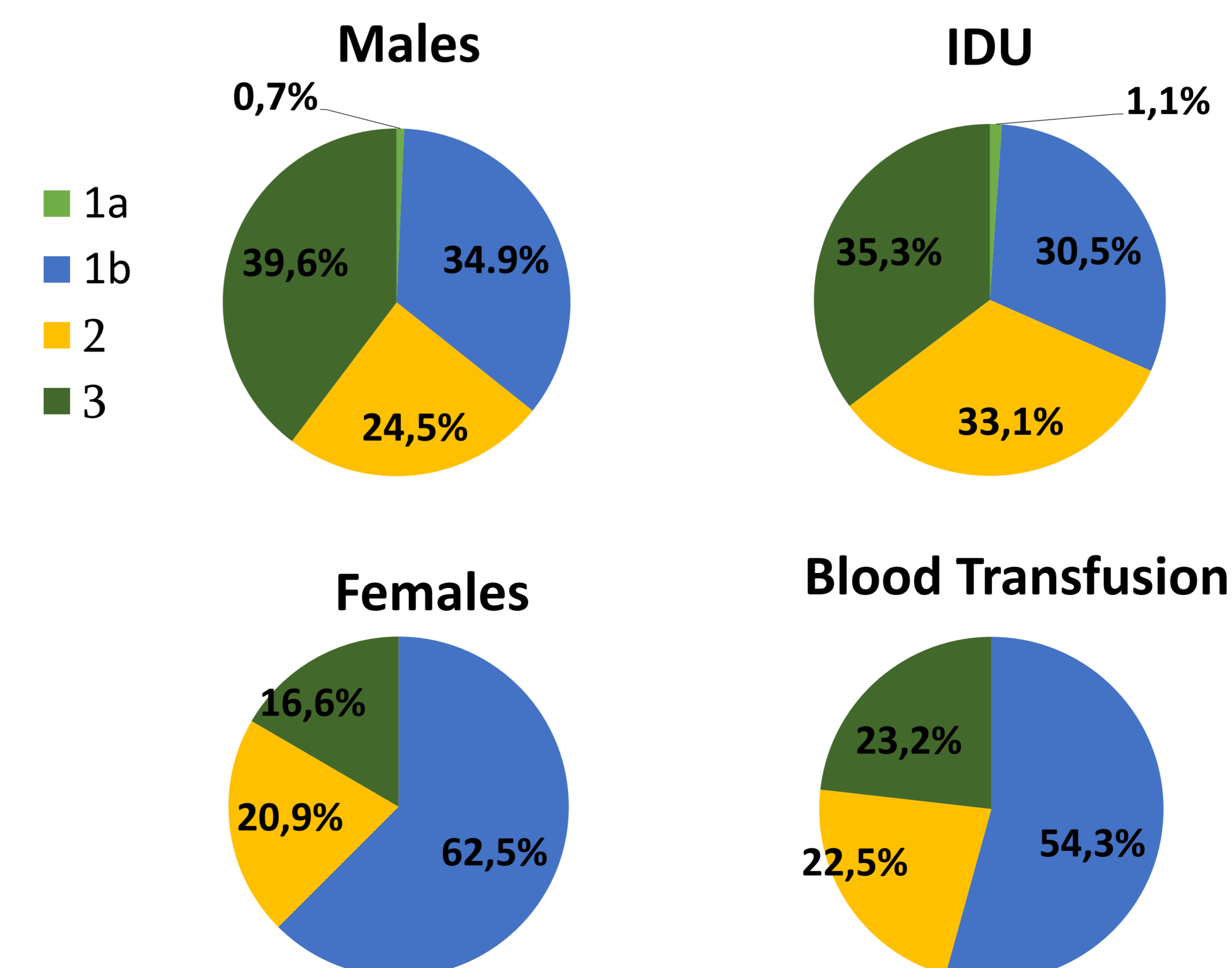
Figure 1: HCV Risk Factors Reported among Anti-HCV+ Participants



HCV Genotypes

- The most prevalent genotype nationally was GT1b (**40.5%**) followed by GT3 (**34.7%**), GT2 (**23.6%**) and GT1a (**0.6%**).
- 0.7% of participants had indeterminate genotype results.
- Genotype distribution varied by sex and reported risk factors, with GT3 most common among males (39.6%) and participants reporting history of IDU (35.3%).
- GT1b was more prevalent among females (62.5%) and participants reporting history of blood transfusion (54.3%) (Figure 2).
- Among participants not reporting either IDU or blood transfusion, GT3 was the most common among males (41.9%), and GT1b was most common among females (64.9%).

Figure 2: HCV Genotype by Sex and by Risk Factor



CONCLUSIONS

- HCV genotype distribution in Georgia varies by sex and reported risk factors.
- In the general population, genotypes 1 and 3 have similar prevalence
- Introduction of pangenotypic treatment regimens in the Georgian HCV elimination program would be beneficial.

ACKNOWLEDGEMENTS

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