

Distribution of Hepatitis C Virus Genotype and Associated Risk Factors in New Jersey, 2015 - 2018

Background:

Approximately 110,000 residents of New Jersey are chronically infected with hepatitis C (HCV). In recent years surveillance data show an increase in HCV among people who inject drug, especially young people. An increase in cases with genotype 3 has also been observed. HCV genotype can assist in HCV epidemiology and provide information related to liver disease severity and HCV treatment regimen.

This project studied the distribution of HCV genotypes, associated risk factors, and age in New Jersey which can provide context towards linking infected HCV cases to care.

Methods:

- HCV cases were evaluated using data from New Jersey Communicable Disease Reporting and Surveillance System (CDRSS), a web-based disease surveillance and case management system.
- Cases classified as acute and chronic HCV for the period 2015 to 2018 were used for this study. The total number of cases was 30,995; 4,123 cases (13.3%) had both risk factor and genotype data reported.
- Logistic regression was applied to determine the association between risk factors and genotypes.

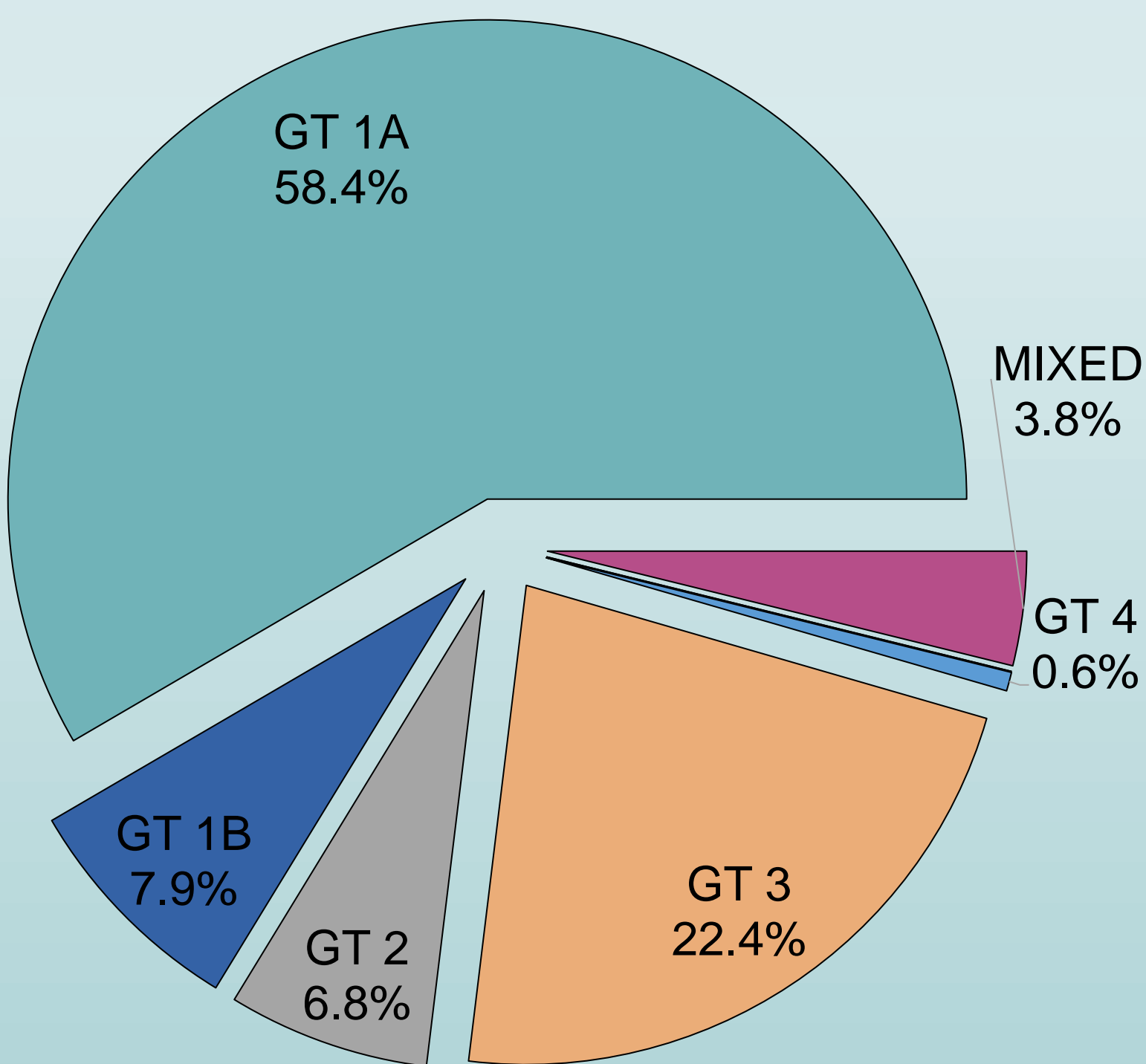


Fig 3. HCV genotype distribution for IDU, New Jersey, 2015-2018

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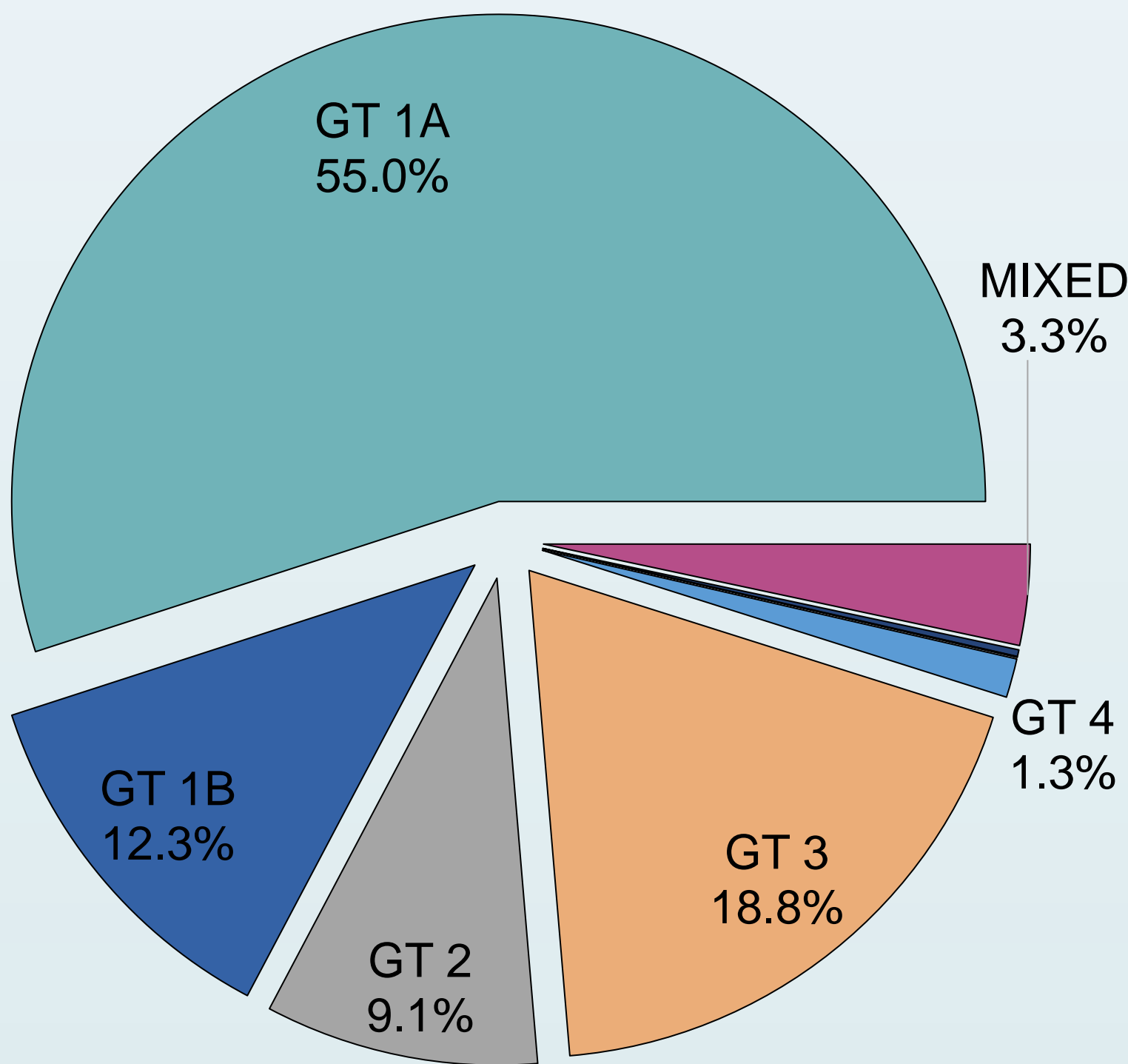


Fig 1. HCV genotype distribution for any risk factor, New Jersey, 2015-2018.

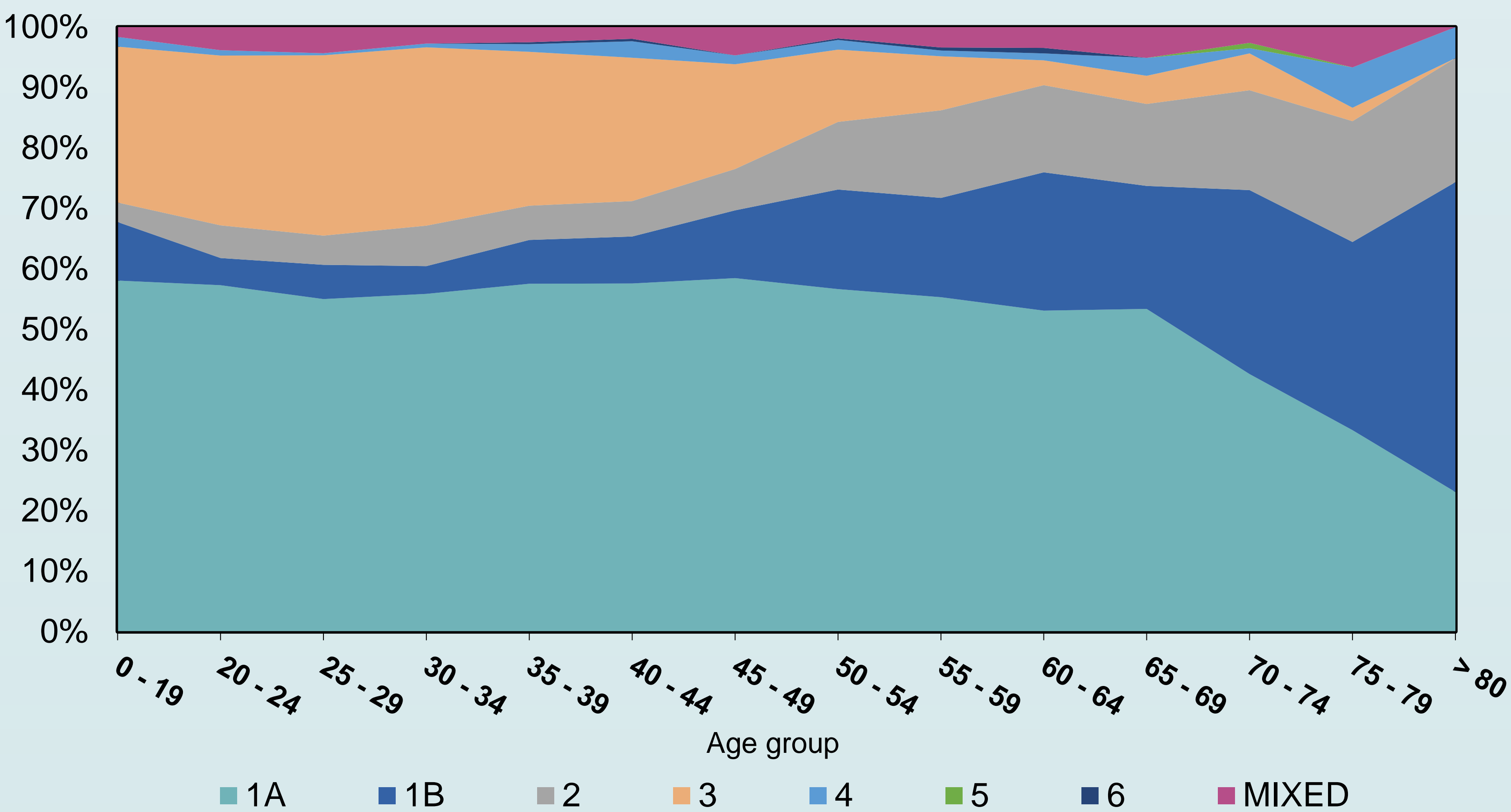


Fig 2. HCV genotype distribution by age, New Jersey, 2015-2018

Table 1. Odds ratio of becoming infected with HCV genotypes by risk factors, New Jersey, 2015-2018.

Risk factors	Genotype				
	1A	1B	2	3	MIXED
Injection drug use	*1.37 (1.21,1.57)	0.40 (0.32,0.49)	0.58 (0.47,0.73)	*1.66 (1.39,1.97)	*1.50 (1.01,2.23)
Tattoo or piercing	1.06 (0.91,1.23)	0.69 (0.54,0.88)	1.16 (0.90,1.50)	*1.26 (1.05,1.52)	0.58 (0.35,0.96)
Unprotected sex	1.16 (0.99,1.36)	0.94 (0.72,1.20)	1.08 (0.82,1.42)	0.91 (0.74,1.12)	0.66 (0.39,1.11)
Incarcerated	*1.49 (1.25,1.77)	0.66 (0.49,0.89)	0.67 (0.48,0.93)	0.90 (0.72,1.13)	0.54 (0.29,1.01)
Blood transfusion	0.67 (0.52,0.87)	*1.77 (1.31,2.38)	*1.92 (1.37,2.69)	0.39 (0.24,0.63)	1.69 (0.91,3.13)

* Significant with $\alpha=0.05$.
95% CI is given. (Genotype 4, 5 and 6 are not shown due to low case number)

Results:

- The top five risk factors were injection drug use (IDU) (57.4%), tattoo/piercing (23.9%), unprotected sex (20.9%), incarcerated (15.7%), and blood transfusion (7.1%).
- Genotype distribution greatest to least: 1A (55.0%), 3 (18.8%), 1B (12.6%), 2 (9.1%), mixed genotype (3.3%), 4 (1.3%), Figure 1.
- Genotype 1A or 3 were more prevalent in cases less than 50 years old, whereas genotype 1B or 2 were more common in older cases, Figure 2.
- IDU cases had higher odds for genotype 1A (OR=1.37, 1.21-1.57), genotype 3 (OR=1.65, 1.39-1.97) and mixed genotype (OR=1.50, 1.02-2.28), Table 1.
- In mixed genotype infection, IDU had more 1A/3 combination (Fisher's exact test, $p=0.005$).
- Cases with risk factors tattoo/piercing had higher odds for genotype 3. Cases ever incarcerated are more likely to get genotype 1A, less likely 1B or 2. Cases ever had blood transfusion were less likely to get 1A, more likely 1B or 2, Table 1.

Conclusion:

- This study provides an insight in the association among risk factor, age and genotype in New Jersey. Genotype 1A is most frequent (as seen nationally).
- Genotypes 1A or 3 is more common in cases less than 50 years old (mainly IDU), 1B or 2 is more common in older cases and IDU have more 1A/3 mixed infection.
- This New Jersey study highlights the need for HCV case risk factor classification, and genotype determination, to better tailor treatment regimens.