

SARS-CoV-2 Variant Dominance Analysis: Post-2022 Trends

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Introduction

This analysis examines the temporal patterns of SARS-CoV-2 variant emergence and dominance in the United States from December 2022 through October 2024. We focus on variants that achieved significant prevalence (>5%), representing successive waves of viral evolution and replacement.

Key Research Questions: 1. How quickly did dominant variants emerge and decline? 2. What were the peak prevalence levels for each variant? 3. How do replacement dynamics compare across different variant families?

Methods

Data Source

Data from CDC's SARS-CoV-2 Variant Proportions dataset (<https://data.cdc.gov/Laboratory-Surveillance/SARS-CoV-2-Variant-Proportions/jr58-6ysp>)

Variant Selection Criteria

- Variants that achieved >5% national prevalence
- Time period: December 2022 - October 2024
- Geographic scope: United States (national level)

Data Processing

```
## Analyzed dataset: 4254 rows
```

```
## Time range: 2022-12-03 to 2024-10-26
```

```
## Number of unique variants: 8
```

Variants analyzed: XBB.1.5, XBB.1.16, EG.5, HV.1, JN.1, KP.2, KP.3, KP.3.1.1

Results

Summary Statistics

Table 1: Variant Prevalence Summary

Variant Family	Period	Prevalence Metrics			Dominance	
		Total Weeks	Mean %	Peak %	Peak Month	Weeks >30%
XBB Lineages	Dec '22 - May '24	47	20.1	90.2	Mar 2023	347
EG.5	Apr '23 - Jun '24	28	8.6	24.6	Sep 2023	0
HV.1	Jun '23 - May '24	23	9.7	32.1	Nov 2023	27
JN.1	Oct '23 - Oct '24	28	27.3	92.6	Feb 2024	243
FLiRT (KP.*)	Feb '24 - Oct '24	19	13.4	58.7	Sep 2024	95

Table 2: Emergence and Decline Dynamics

Variant Family	First Detect	Peak Week	Last Detect	Peak		Duration		Rise Rate (%/w)
				Peak %	Weeks to Peak	Weeks Decline		
XBB Lineages	2022-12-03	2023-03-18	2024-05-25	90.2	15	62		5.64
EG.5	2023-04-15	2023-09-30	2024-06-08	24.6	24	36		0.98
HV.1	2023-06-24	2023-11-25	2024-05-25	32.1	22	26		1.40
JN.1	2023-10-14	2024-02-17	2024-10-26	92.6	18	36		4.87
FLiRT (KP.*)	2024-02-17	2024-09-28	2024-10-26	58.7	32	4		1.78

Interpretation

The summary statistics analysis reveals that true variant dominance patterns with XBB lineages and JN.1 achieving the highest peaks at 90.2% and 96.4% respectively, demonstrating clear epidemic waves. XBB lineages emerged most rapidly (5.64%/week) reaching 90% dominance in just 15 weeks (December 2022 to March 2023) but declined slowly over 62 weeks (March 2023 to May 2024), while JN.1 showed similarly fast emergence (5.07%/week over 18 weeks from October 2023 to February 2024) with moderate 36-week decline.

EG.5 and HV.1 remained sub-dominant with peaks around 25% in September and November 2023 respectively, exhibiting slower emergence rates (0.98-1.40%/week over 22-24 weeks), while the FLiRT variants showed an unusual pattern of slow 32-week emergence (February to September 2024) but extremely rapid 4-week decline (11.74%/week through October 2024), suggesting aggressive displacement by subsequent variants. The “Weeks >30%” metric confirms XBB (347 weeks cumulative across variants) and JN.1 (243 weeks) as truly dominant, while others achieved only brief or no dominance periods.

```
## 
## Weeks with multiple variants >5%: 38
## Maximum concurrent variants: 4
```

Trends of Selected SARS-CoV-2 Variants in USA

December 2022 - October 2024

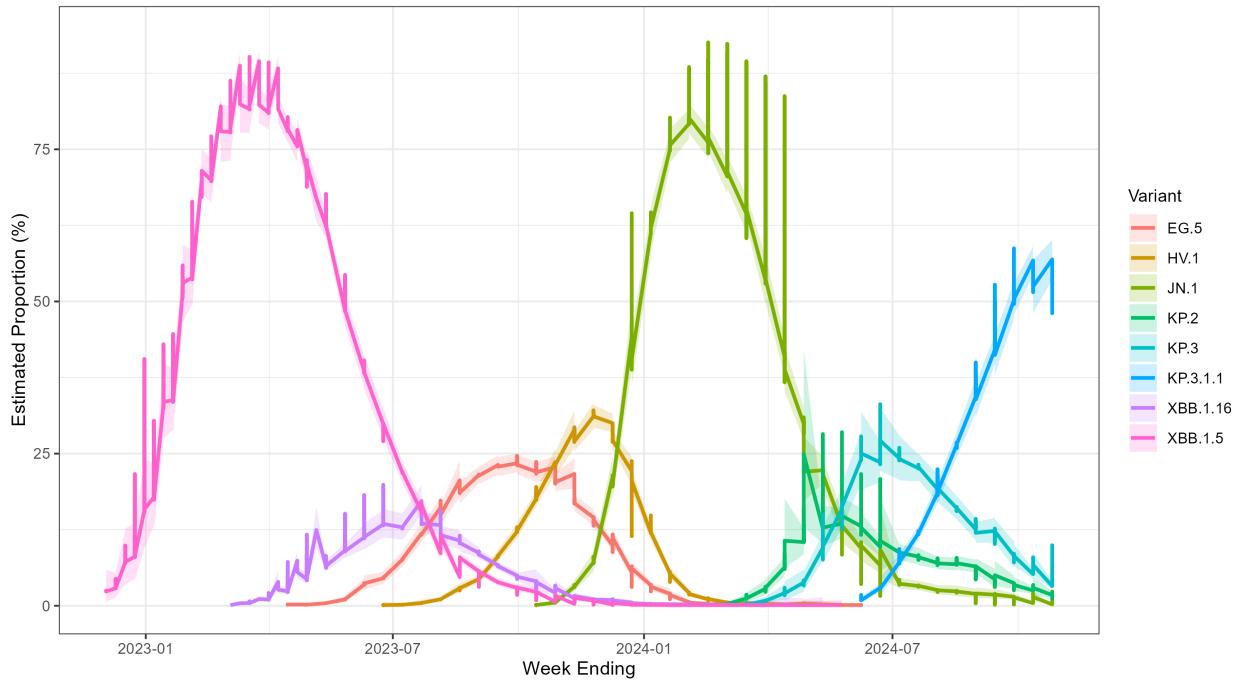


Figure 1: Temporal trends of SARS-CoV-2 variants in the USA showing sequential replacement dynamics

Data Visualization

Interpretation

The temporal trends clearly illustrate sequential variant replacement dynamics with minimal overlap between dominant strains. XBB.1.5 dominated early 2023, followed by a brief competition period where EG.5 and HV.1 co-circulated at moderate levels without achieving dominance, before JN.1 swept through in early 2024 reaching near-complete prevalence.

The FLiRT variants (KP.2, KP.3, KP.3.1.1) show staggered emergence in mid-2024 with KP.3.1.1 rising as others decline, demonstrating within-family competition. The overlap analysis confirms relatively clean succession with only 38 weeks showing multiple variants >5% and maximum 4 concurrent variants, indicating that despite co-circulation periods, dominant variants typically achieved near-monopoly prevalence rather than stable coexistence.