

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

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2025-11-05

## 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?

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## 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

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# Results

## Summary Statistics

Table 1: Variant Prevalence Summary

Variant Family	Period	Prevalence Metrics			Dominance	
		Total Weeks	Mean %	Peak %	Peak Month	Weeks >30%
<b>XBB Lineages</b>	Dec '22 - May '24	47	20.1	90.2	Mar 2023	347
<b>EG.5</b>	Apr '23 - Jun '24	28	8.6	24.6	Sep 2023	0
<b>HV.1</b>	Jun '23 - May '24	23	9.7	32.1	Nov 2023	27
<b>JN.1</b>	Oct '23 - Oct '24	28	27.3	92.6	Feb 2024	243
<b>FLiRT (KP.*)</b>	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	
<b>XBB Lineages</b>	2022-12-03	2023-03-18	2024-05-25	90.2	15	62	5.64
<b>EG.5</b>	2023-04-15	2023-09-30	2024-06-08	24.6	24	36	0.98
<b>HV.1</b>	2023-06-24	2023-11-25	2024-05-25	32.1	22	26	1.40
<b>JN.1</b>	2023-10-14	2024-02-17	2024-10-26	92.6	18	36	4.87
<b>FLiRT (KP.*)</b>	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.

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## Weeks with multiple variants >5%: 38

## Maximum concurrent variants: 4
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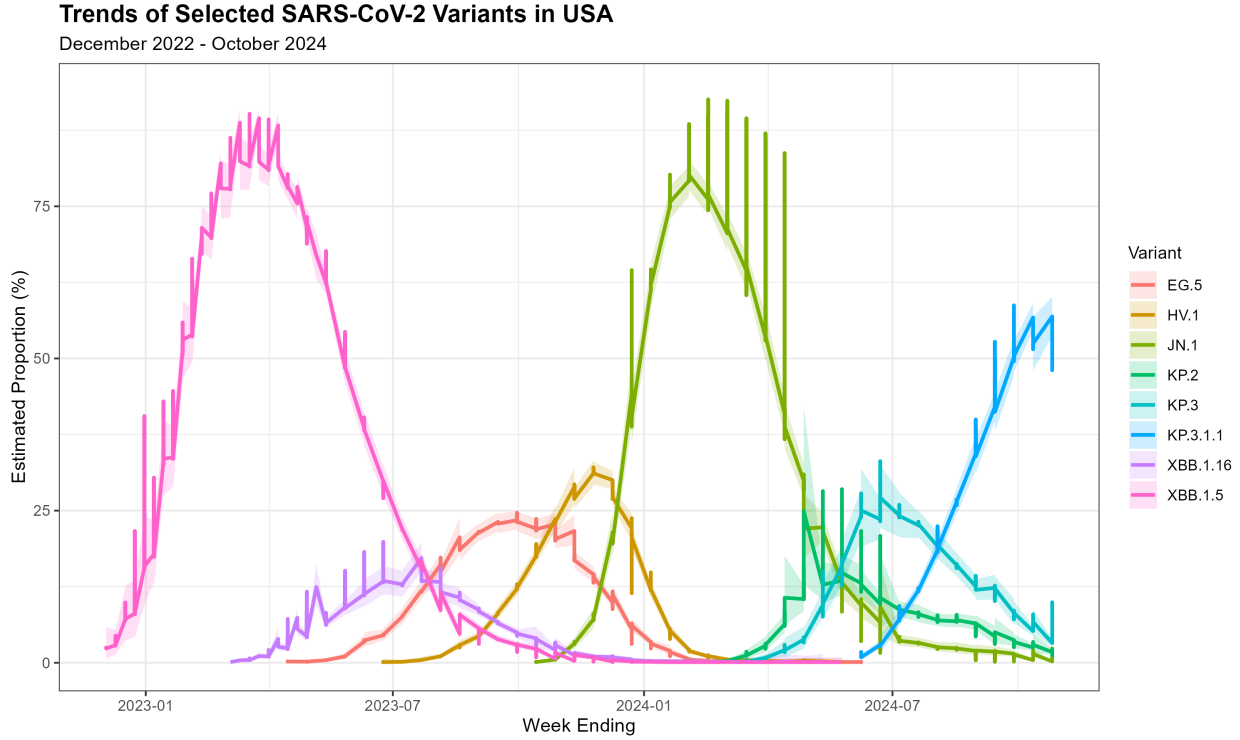


Figure 1: Temporal trends of SARS-CoV-2 variants in the USA showing sequential replacement dynamics

## 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.