

concerns about the potential emergence of new, more virulent clones, this has not been borne out by genomic studies which have linked cases in the 2022/2023 time window with lineages observed globally for more than a decade^{4,7,10}. Nevertheless, fundamental questions remain about how the pandemic may have affected global genomic patterns and how these changes may impact future RSV transmission patterns. Understanding this is essential for implementing effective control and prevention strategies.

Herein, we characterize the genetic diversity and diffusion dynamics of RSVA and RSVB strains in Florida, at the US and global level, including newly sequenced strains from Florida inpatient and outpatient pediatric cases sampled between August 2022 and March 2023. Our phylodynamic analysis reveals that, following the COVID-19 pandemic, both RSV types experienced a marked shift in the frequency of bottleneck events. This was accompanied by a significant increase in viral diversity within known epitope regions of the G protein, suggesting that the virus is actively adapting to a new genomic landscape, potentially influencing its transmission dynamics and disease severity.

Results

RSV Patient Demographics and Clinical Characteristics in Florida

In keeping with findings in other geographic areas^{6–8,10}, we observed an increased case numbers of pediatric RSV cases at a major medical center in Florida in the 2022/2023 “post-COVID-19” time period. To better understand the clinical, epidemiological and molecular implications of this upsurge, we evaluated a cohort of 48 pediatric patients who presented to UFHealth, between January 2022 and March 2023, with symptomatic bronchiolitis and a positive RT-qPCR for RSV. This cohort included both inpatients and outpatients aged 0-18 years. One patient presented as an outpatient twice and we removed the duplicate record leaving an analysis population of n=47.