

Sequence variability of the respiratory syncytial virus (RSV) fusion gene among contemporary and historical genotypes of RSV/A and RSV/B

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© 2017 Hause et al. This is an open access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited. Background: The fusion (F) protein of RSV is the major vaccine target. This protein undergoes a conformational change from pre-fusion to post-fusion. Both conformations share antigenic sites II and IV. Pre-fusion F has unique antigenic sites p27, δ , γ , and MPE8; whereas, post-fusion F has unique antigenic site I. Our objective was to determine the antigenic variability for RSV/A and RSV/B isolates from contemporary and historical genotypes compared to a historical RSV/A strain. Methods: The F sequences of isolates from GenBank, Houston, and Chile (N = 1,090) were used for this analysis. Sequences were compared pair-wise to a reference sequence, a historical RSV/A Long strain. Variability (calculated as %) was defined as changes