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**Research Topic: Molecular Investigation of Acute Respiratory Infection (ARI)  
Caused by Respiratory Syncytial Virus Among Children**

## **Abstract**

Acute respiratory infection (ARI) is the major cause of hospitalization and death among paediatric population globally. RSV is recognized as an important viral pathogen of ARI with global implications. RSV was first isolated in 1956 from a laboratory chimpanzee. Shortly within a year the virus was recognised as human pathogen identified from children with respiratory illness. It may cause a wide range of illness from mild cold to life threatening bronchiolitis, croup and pneumonia in infants, children and adults. Genetic and antigenic variations within the second hypervariable region of G protein gene could promote the frequent re-infections throughout the life of an individual. RSV is an enveloped, non-segmented, negative-sense, single stranded RNA genome. Classified into two antigenic groups; group A and B. In the present study respiratory syncytial virus was detected in the clinical samples collected from the symptomatic paediatric patients during the period of 2011 to 2015. Molecular characterization of the RSV strain was done followed by mutational analysis, entropy analysis, selection pressure analysis and evolutionary analysis.

## **Key findings**

- RSV was detected in 18.6% (93/500) of the samples by one step real time RT-PCR.
- The rate of infection was found to be higher 24.3% (59/243) amongst children in the first two years of their lives.

- Twenty seven of the samples (29%) were positive for group A and 66 samples (71%) for group B RSV. Group B RSV was found to be more predominant than group A RSV.
- The tMRCA of RSV-A and NA1 genotype suggested that they emerged in years 1953 (95% HPD, 1944-1961) and 2000 (95% HPD, 1996-2003), respectively.
- Bayesian skyline plot analysis showed that the effective population size of the Indian RSV-NA1 genotype was constant during the time period from 2009 to 2014.
- The tMRCA of group A, BA genotype and BA9 lineage were estimated to be the years 1955 (95% HPD; 1947-1962), 1995 (95% HPD; 1987-1997) and 2000 (95% HPD; 1998-2001), respectively.
- Bayesian and Network analysis reveals that the global BA9 lineage has three (I-III) distinct global sub-lineages.
- Bayesian skyline plot analysis showed significant variation in relative genetic diversity in RSV-BA9 lineage including contraction and expansion during the time period from 2002 to 2015.

### **Implication of the study**

The present investigation enhances our understanding of RSV infection, its epidemiological and population dynamics warranting steps towards its overall global surveillance. The NA1 genotype was dominated in the Indian scenario since 2008 and shows its complex global dissemination with no specific pattern. However the analysis of the BA9 lineage showed its global spread with three (I-III) sub-lineages. This study is envisaged to be useful for overall disease surveillance at the global level and policy planning and its implementation at the local level augmenting the much needed human health care system. This investigation will also be a step towards the vaccine design and development. Further, inclusion of both community and hospital based surveillance across different regions in India will provide information on its disease burden that might contribute to formulation of control measures.