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# The Molecular Epidemiology and Clinical Phylogenetics of Rhinoviruses among Paediatric Cases in Sydney, Australia.

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**Abstract**

Background Rhinoviruses (RV) represent the most common aetiological agent of all acute respiratory tract infections across all age groups and a significant burden of disease among children. Recent studies have shown that RV-A and RV-C species are associated with varying degrees of disease severity and clinical symptoms. Methods In this study, we uncovered potential associations between RV species and subtypes, and clinical disease severity using a matched dataset of 52 RV isolates sampled from children (<18 years) in Sydney, Australia between 2006 and 2009 using epidemiological and phylogenetic methods. Results We found that RV-C was significantly more likely to be isolated from paediatric cases under two years of age compared to RV-A, although no significant differences in recorded symptoms were observed. Significant phylogenetic-trait associations between age and the VP4/VP2 capsid protein phylogeny suggests age-specific variations in infectivity among subtypes might also be possible. Conclusions This study adds to the growing body of epidemiological evidence concerning RV. Improving surveillance and testing for RV, including routine whole genome sequencing may improve our understanding of the varied diseashe outcomes of RV species and subtypes. Future studies could aim to identify specific genetic markers associated with age-specific infectivity of RV which could inform treatment practices and public health surveillance of RV.

**Title:** The Molecular Epidemiology and Clinical Phylogenetics of Rhinoviruses among Paediatric Cases in Sydney, Australia.

**Running title** : Molecular Epidemiology of Rhinoviruses in Sydney

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**Declarations**

*Ethics approval and consent to participate*

The human sequence data used in this study were publicly available from GenBank. This study was approved by the UNSW Human Research Ethics Committee (HC17284).

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*Conflicts of interest*

CRM has received funding for investigator-driven research from Merck, GSK and Seqirus, and support for laboratory testing unrelated to this study from Pfizer. CRM has also been on advisory boards for the same companies. DCA, XC, MS, DD and JK have no competing interests to declare.

*Availability of data and materials*

All data generated or analysed during this study are included in this published article and its supplementary information.

*Authors' contributions*

DCA was a major contributor in data collection, analysis and writing the manuscript. MS, CRM, DD and JK have made substantial contributions to the conception and design of the study. MS and CRM revised the manuscript. XC contributed to data validation and manuscript submission. All authors read and approved the final manuscript.

*Patient consent statement*

Not applicable.

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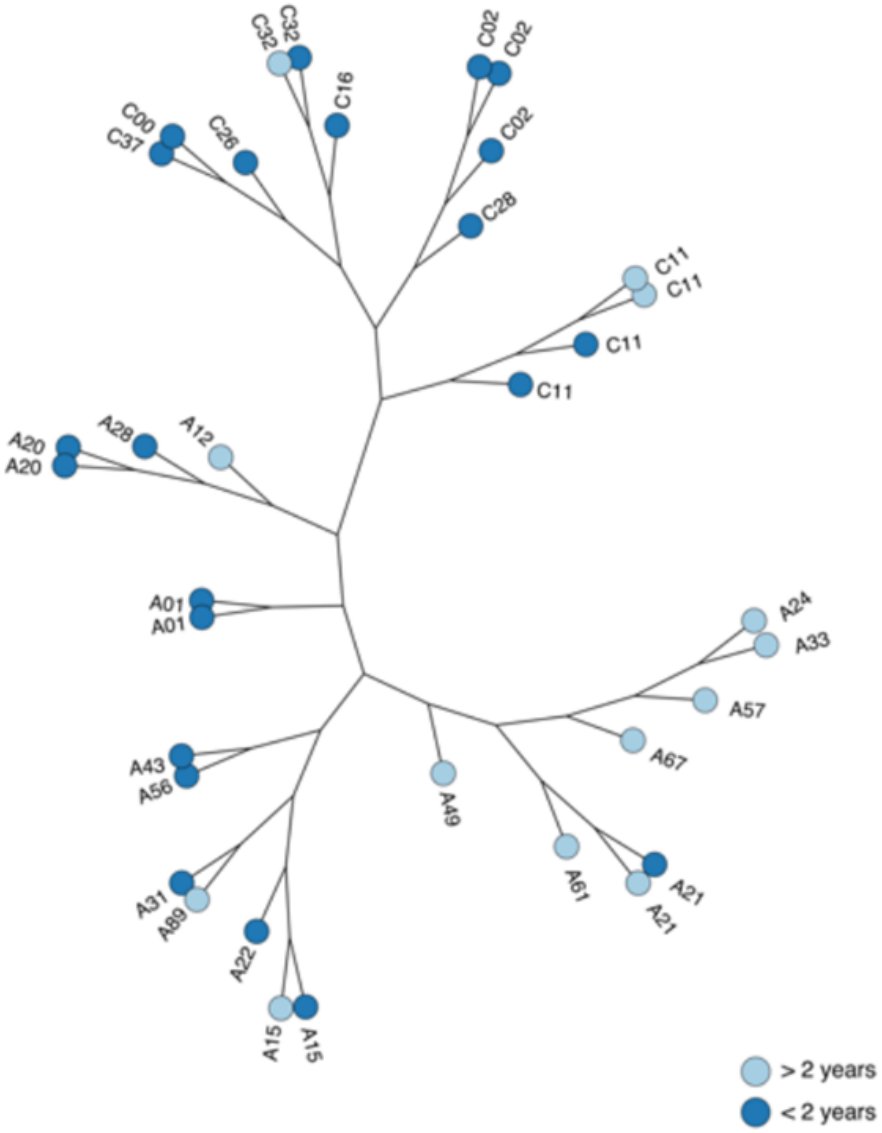


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