Rotavirus A Genome Segments Show Distinct Segregation and Codon Usage Patterns

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Manuscript Source: https://www.biorxiv.org/content/10.1101/2021.03.20.436270v1
Manuscript Authors: Irene Hoxie & John J. Dennehy

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• Depending on the source of the input text, the Sentence Audit may contain occasional html artefacts that are parsed as sentences (E.g. "Download figure. Open in new tab").

• Always consult the original research paper as the true reference source for the text.

Contact Information:

To get a Manuscript Microscope Sentence Audit of any other research paper, simply forward any copy of the text to John.James@OxfordResearchServices.com.

All queries, feedback or suggestions are also very welcome.

Research Paper Sections:

The sections of the research paper input text parsed in this audit.

Section No.	Headings	Sentences
Section: 1	Abstract	12
Section: 2	1. Introduction	15
N/A	--- --- --- --- --- --- ---	0
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The Sentence Audit Of The Research Paper

Title **Rotavirus A Genome Segments Show Distinct Segregation and Codon Usage Patterns**

S1 [001]   Abstract

S1 [002]   Reassortment of the Rotavirus A (RVA) 11-segment dsRNA genome may generate new genome constellations that allow RVA to expand its host range or evade immune responses.

> Reassortment ...
> ... of the Rotavirus A ...
> ... (RVA) ...
> ... 11-segment dsRNA genome ...
> ... may generate new genome constellations ...
> ... that allow RVA ...
> ... to expand its host range ...
> ... or evade immune responses.

S1 [003]   Reassortment may also produce phylogenetic incongruities and weakly linked evolutionary histories across the 11 segments, obscuring reassortant-specific epistasis and changes in substitution rates.

> Reassortment ...
> ... may also produce phylogenetic incongruities ...
> ... and weakly linked evolutionary histories ...
> ... across the 11 segments, ...
> ... obscuring reassortant-specific epistasis ...
> ... and changes ...
> ... in substitution rates.

S1 [004]   To determine the co-segregation patterns of RVA segments, we generated time-scaled phylogenetic trees for each of the 11 segments of 789 complete RVA genomes isolated from mammalian hosts and compared the segments' geodesic distances.

> To determine the co-segregation patterns ...
> ... of RVA segments, ...
> ... we generated time-scaled phylogenetic trees ...
> ... for each ...
> ... of the 11 segments ...
> ... of 789 complete RVA genomes isolated ...
> ... from mammalian hosts ...
> ... and compared the segments' geodesic distances.

S1 [005]   We found that segments 4 (VP4) and 9 (VP7) occupied significantly different treespaces from each other and from the rest of the genome.

> We found ...
> ... that segments 4 ...
> ... (VP4) ...

... and 9 ...

... (VP7) ...

... occupied significantly different treespaces ...

... from each other ...

... and from the rest ...

... of the genome.

S1 [006] By contrast, segments 10 and 11 (NSP4 and NSP5/6) occupied nearly indistinguishable treespaces, suggesting strong co-segregation.

By contrast, ...

... segments 10 ...

... and 11 ...

... (NSP4 ...

... and NSP5/6) ...

... occupied nearly indistinguishable treespaces, ...

... suggesting strong co-segregation.

S1 [007] Host-species barriers appeared to vary by segment, with segment 9 (VP7) presenting the least conservation by host species.

Host-species barriers appeared ...

... to vary ...

... by segment, ...

... with segment 9 ...

... (VP7) ...

... presenting the least conservation ...

... by host species.

S1 [008] Bayesian skyride plots were generated for each segment to compare relative genetic diversity among segments over time.

Bayesian skyride plots were generated ...

... for each segment ...

... to compare relative genetic diversity ...

... among segments ...

... over time.

S1 [009] All segments showed a dramatic decrease in diversity around 2007 coinciding with the introduction of RVA vaccines.

All segments showed a dramatic decrease ...

... in diversity ...

... around 2007 coinciding ...

... with the introduction ...

... of RVA vaccines.

S1 [010] To assess selection pressures, codon adaptation indices and relative codon deoptimization indices were calculated with respect to common host genomes.

To assess selection pressures, ...

... codon adaptation indices ...

... and relative codon deoptimization indices were calculated ...

... with respect ...

... to common host genomes.

S1 [011]   Codon usage varied by segment with segment 11 (NSP5) exhibiting significantly higher adaptation to host genomes.

> Codon usage varied ...
>
> ... by segment ...
>
> ... with segment 11 ...
>
> ... (NSP5) ...
>
> ... exhibiting significantly higher adaptation ...
>
> ... to host genomes.

S1 [012]   Furthermore, RVA codon usage patterns appeared optimized for expression in humans and birds relative to the other hosts examined, suggesting that translational efficiency is not a barrier in RVA zoonosis.

> Furthermore, ...
>
> ... RVA codon usage patterns appeared optimized ...
>
> ... for expression ...
>
> ... in humans ...
>
> ... and birds relative ...
>
> ... to the other hosts examined, ...
>
> ... suggesting ...
>
> ... that translational efficiency is not a barrier ...
>
> ... in RVA zoonosis.

S2 [013]   1. Introduction

S2 [014]   The high mutation rates and large population sizes of RNA viruses allow them to rapidly explore adaptive landscapes, expand host-ranges, and adapt to new environments.

> The high mutation rates ...
>
> ... and large population sizes ...
>
> ... of RNA viruses allow them ...
>
> ... to rapidly explore adaptive landscapes, ...
>
> ... expand host-ranges, ...
>
> ... and adapt ...
>
> ... to new environments.

S2 [015]   Segmented RNA viruses also may undergo 'reassortment' whereby viruses swap entire genome segments during coinfection (1).

> Segmented RNA viruses also ...
>
> ... may undergo 'reassortment' whereby viruses swap entire genome segments ...
>
> ... during coinfection ...
>
> ... (1).

S2 [016]   Reassortment may allow rapid evolution of specific viral traits such as, for example, the acquisition of novel spike glycoproteins during the emergence of H1N1 influenza A in 2009 (2).

> Reassortment ...
>
> ... may allow rapid evolution ...
>
> ... of specific viral traits ...
>
> ... such as, ...
>
> ... for example, ...
>
> ... the acquisition ...
>
> ... of novel spike glycoproteins ...
>
> ... during the emergence ...
>
> ... of H1N1 influenza A ...
>
> ... in 2009 ...
>
> ... (2).

S2 [017]   Similarly, reassortment among segmented dsRNA rotaviruses may have significant implications for human health (3), but it is challenging to determine the prevalence of rotavirus reassortment in nature.

> Similarly, ...
>
> ... reassortment ...
>
> ... among segmented dsRNA rotaviruses ...
>
> ... may have significant implications ...
>
> ... for human health ...
>
> ... (3), ...
>
> ... but it is challenging ...
>
> ... to determine the prevalence ...
>
> ... of rotavirus reassortment ...
>
> ... in nature.

S2 [018]   Our motivation here is to elucidate apparent restrictions (or lack thereof) to RVA genetic exchange in nature by comparing the relative linkage between each of the RVA segments as shown by phylogeny.

> Our motivation here is ...
>
> ... to elucidate apparent restrictions ...
>
> ... (or lack thereof) ...
>
> ... to RVA genetic exchange ...
>
> ... in nature ...
>
> ... by comparing the relative linkage ...
>
> ... between each ...
>
> ... of the RVA segments ...
>
> ... as shown ...
>
> ... by phylogeny.

S2 [019]   In addition, we parse the evolutionary constraints that may contribute to the distinct phylogenies of each segment.

> In addition, ...
>
> ... we parse the evolutionary constraints ...
>
> ... that ...
>
> ... may contribute ...
>
> ... to the distinct phylogenies ...

End of Sample Audit