Human pathogenic RNA viruses establish noncompeting lineages by occupying independent niches.
Thanks To Coauthors

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Monophyletic group (clade) with “good” date-constrained tree

Breaks down trees into groups separated by periods of apparently different substitution rates, likely environmental conditions.
Considered all non-segmented RNA viruses with at least ~200 complete genomes.

Consider events at scale of species diversification.
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First approach: compare lineage coexistence

Real distribution of isolates

Expected distribution of isolates based on root distances

Enterovirus D
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First approach: compare lineage coexistence

Lineages coexist longer than estimated from substitutions alone (no dates)
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Second approach: measure coalescence rate

Build simulated trees according to neutral expectation (Yule-Harding)
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Second approach: measure coalescence rate

2+ lineages, other

All but EVC demonstrates reduced coalescence (competition) relative to neutral expectation between lineages.

All but MMV demonstrates increased coalescence within lineages.
Only tempo, not the mode, of molecular evolution appears to vary substantially intra- vs. inter-lineage.

Comparison of site density of **Multiple Shallow** representing best estimate of adaptive sites

**Multiple Deep**, best estimate of lineage-defining sites

**All Shallow**, unrelated to selection

Site densities are correlated (Pearson). Exception, picornaviruses (RVA/HDV low confidence)
Environmental change: urbanization and climate change may disrupt niches

No cross immunity → Local → Seasonal → Regional

esp. as this relates to vector range
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Thanks For Listening