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Comprehensive Phylogenetic Chronology: Incorporating Dynamic & Co-Evolutionary Information, Illustrated for the Viruses

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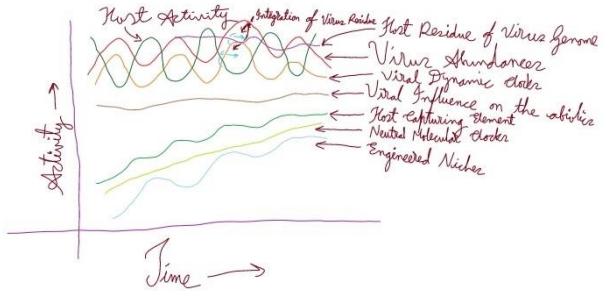
Virus antigenic elements evolve fast in response to the immunity & slow when preserved as particles giving mutation dense & relaxed edges including cross links to varied taxa in the Tree of Life. The immunological history, e.g. series of epidemic bottle necks, incorporated in host evolutionary traits could provide information for anti-parsimonious rapid or relaxed viral element evolution not captured by neutral mutation molecular clocks. Together, they could provide rate of evolution of the viral elements as pace over neutrality. Contemporary forces of evolution like geology, biotic interactions etc. could be required to tease out viral influence on the capturing host elements evolution from the other evolutionary forces.

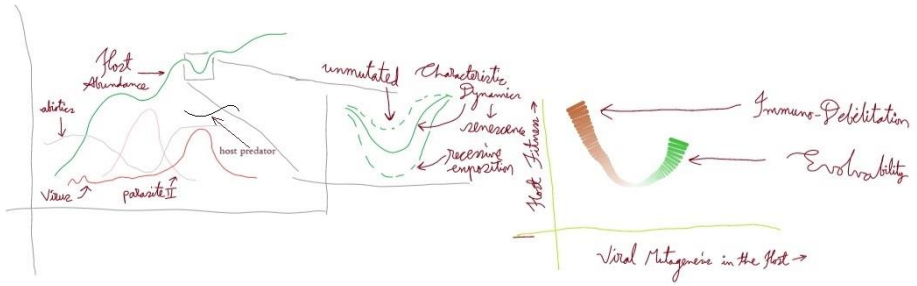
The capturing host elements utilized could be from molecular footprints of the viral evolution that are distributed over the cellular omics especially as rapid non-parsimonious mutations could erase/over-write the history captured in some omic molecules. Similar but external capturing elements could reside in other dynamic co-evolvers e.g. preserved engineered niches or history of influenced interactant species indicating host states evolution; abiotic environment, majorly uninfluenced by the viruses, complementing host-parasite epidemiology suggesting viral influence rather than other abiotically active parasites.

Evolution of immune system due to mutating agents like transposons, viruses etc. could interact with the host-virus co-evolution, the mutating agent virus being of same or different viral taxon. The mutating agent virus & the parasitic virus, if same, would impart knock-out-like advantage to the virus by introducing immune debilitating mutations in the host. This could provide dips in host evolution of possibly characteristic profile differing from other mutation dips (e.g. dips due to regular substitution mutation, another debilitating mutation). Also, rarely, the debilitation & evolvability produced due to mutation could trade-off. The traces of lost lineages of immune systems could remain e.g. in recessivity, in specific senescence, for some generations providing more footprints of the dip & contemporary viral states.

Viral grave-yards or residues in available or inferred host genomes states could also preserve or imply viral evolutionary histories being free from evolution in the virus form. Viral genomes grave yarded or residing in hosts & the vice versa, could be comparable to interspecific trans-nucleation evolutionary experiments & should provide data points otherwise unexplored by cellular & viral genetics, & natural systems in general. We might hypothesize the higher-than-expected affinities of the grave yarded or residing viral elements & host systems in each other indicating closer phylogenetic relations or integrated intrusions of the viruses & hosts among them. These phylogenetic relations or intrusions-integrations would also suggest particular viral evolutionary & co-evolutionary paths.

Systems level properties, especially viral immunity measures or indices e.g. specialized for particular viral phylogenetic niches, could yield another source of capturing systems of virus evolution footprints & products. Quantitative & theoretical characteristics could thus also inform viral evolutionary history inference. Qualitative theoretical formalizations attained exhaustively from the varied approaches, would be especially effective indicators of the evolution of life, including the viruses to attest & elevate their biological nature.





Comprehensive Viral Phylogenetic Chronology
(See text for explanation)

Conquered Viral Phylogenetic Niche

$$(\mathcal{J}^* \geq \mathcal{J}_{mm}(V_i) > 0) \vee Else$$

$$\Updownarrow$$

$$Else \vee \left(V_i \longrightarrow \times\, \mathcal{J}_{mm}(V_i) \ll \mathcal{J}^*\right)$$

$$\mathcal{G} \times \mathcal{E} \Rightarrow \text{Phenotype Information \& Literature}$$

Vivacious Phylogenetic Information

$\Downarrow$

Vivacity

Thus, incorporating varied sources of information of viral evolutionary history from biotic & abiotic viral environment could enable tracing the rapid or relaxed non-parsimonious evolution untraceable by neutral, under or overwritten clocks. Comprehensive analysis - qualitative or quantitative, of co-evolvers – biotic or abiotic, could thus benefit determination of evolutionary history of the involved taxa.