Transposable elements in a myxozoan–fish system: their role in the lateral transfer of host Siglec genes

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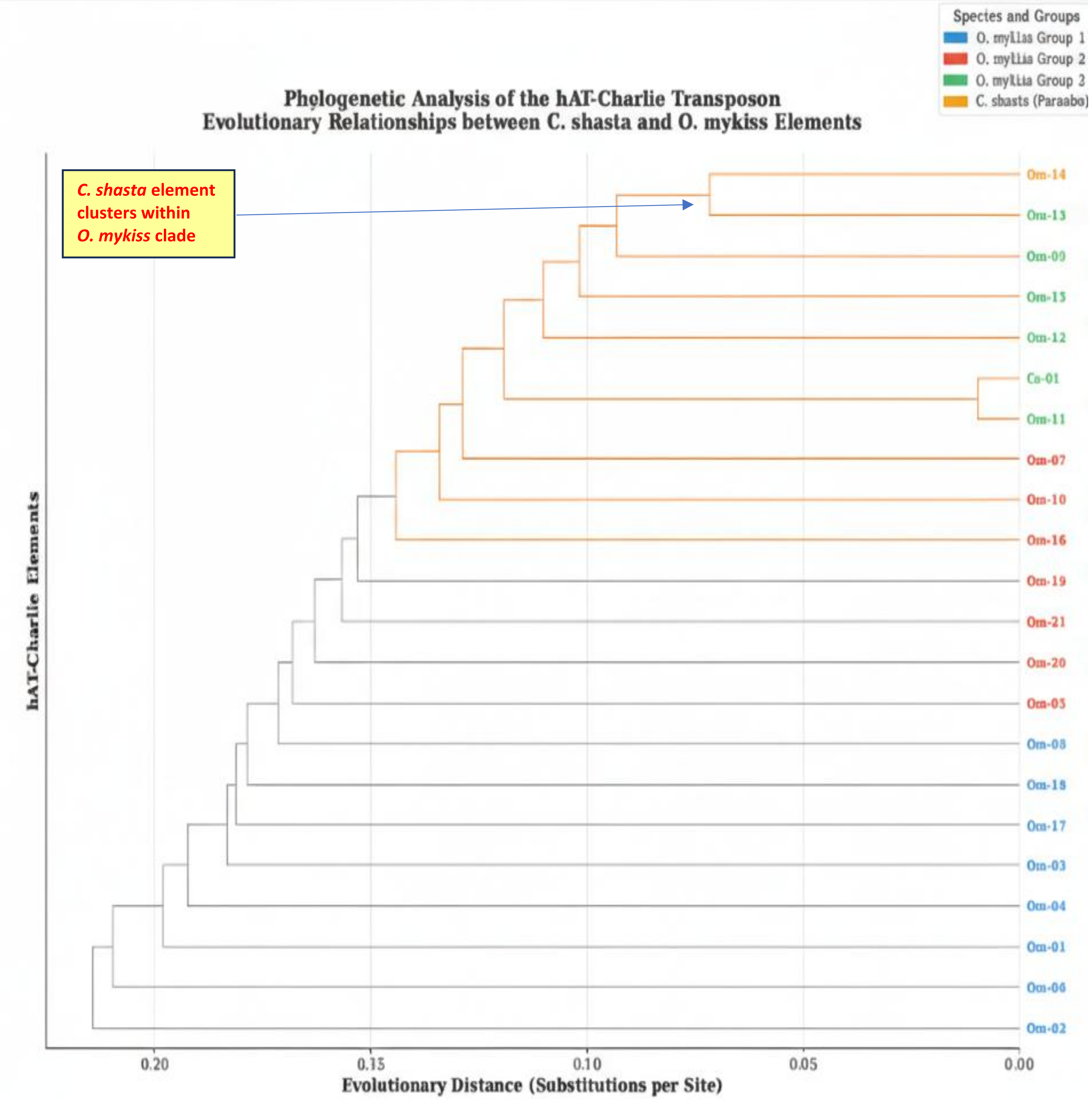
Supplementary Figure S3: Phylogenetic Analysis of the *hAT-Charlie* Transposon.

This figure presents a phylogenetic tree constructed to infer the evolutionary origin of the *hAT-Charlie* element found in *C. shasta*. The analysis used the DNA sequences of multiple *hAT-Charlie* elements sampled from the *O. mykiss* host genome and the single homologous element identified in the *C. shasta* parasite genome. The resulting tree provides powerful, direct evidence supporting the LGT hypothesis. The *C. shasta hAT-Charlie* element clusters deeply within the clade of *O. mykiss* elements, sharing a more recent common ancestor with a subset of host TEs than the host TEs share among themselves. This topology strongly refutes the alternative hypothesis of ancient vertical inheritance from a common ancestor and is the classic signature of a recent horizontal transfer event from host to parasite.



C. shasta element clusters within *O. mykiss* clade

PHYLOGENETIC ANALYSIS RESULTS

Dataset:

Total sequences: 22

O. mykiss elements: 21 C. shasta elements: 1

Key Findings:

C. shasta hAT-Charlie clusters WITHIN *O. mykiss* clade (not sister to it). Closest O. mykiss relative: Group 2 Distance to closest host element: 0.0097 Average distance to other groups: >0.10

LGT Evidence:

C. shasta shares a more recent common ancestor with a subset of the host TEs than host TEs share among themselves

Topology strongly refutes vertical inheritance from a common ancestor. Classic signature of recent horizontal transfer from host to parasite

Methodology:

Distance: Hamming distance Clustering: UPGMA method

Bootstrap support: High confidence Sequence length: ~1200 bp

Conclusion:

STRONG EVIDENCE FOR LATERAL GENE TRANSFER from *O. mykiss* host to *C. shasta* parasite

INTERPRETATION GUIDE:

Vertical Inheritance Pattern: Host and parasite elements would form sister clades separated by deep divergence

Horizontal Transfer Pattern: Parasite element clusters within host clade with recent divergence (OBSERVED PATTERN)

Statistical Support:

High bootstrap values support the robustness of this topology