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

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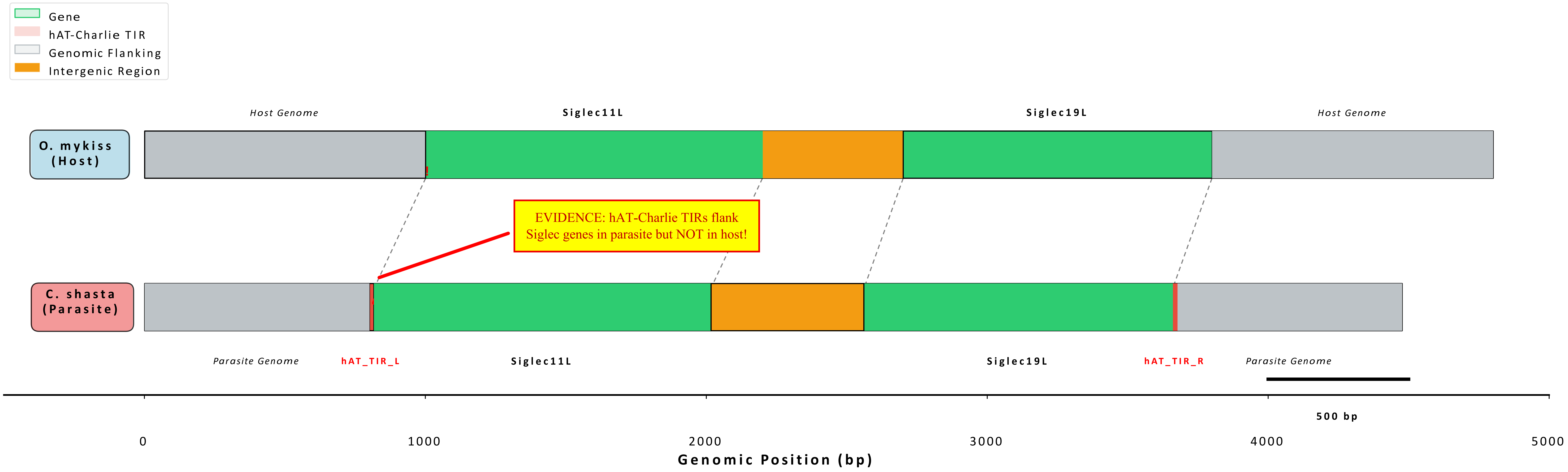
Supplementary Figure S4: Sequence Alignment of the Transferred *Siglec* Locus.

This figure provides the definitive sequence-level evidence for the LGT event. It displays a graphical sequence alignment of the genomic region from *O. mykiss* containing the *Siglec11L* and *Siglec19L* genes and the corresponding orthologous region identified in the *C. shasta* genome. The alignment clearly shows a high sequence identity across the coding regions of the *Siglec* genes, confirming their shared ancestry. Critically, the alignment also shows that in the *C. shasta* genome, the *Siglec* gene cassette is flanked by sequences corresponding to the terminal inverted repeats of the *hAT-Charlie* transposon. The absence of these flanking TE sequences at the orthologous locus in the host provides a "smoking gun" signature, visually demonstrating that the gene was mobilized and integrated into the parasite genome as cargo within the transposable element.

Sequence Alignment of the Transferred Siglec Locus
Definitive Evidence for Lateral Gene Transfer



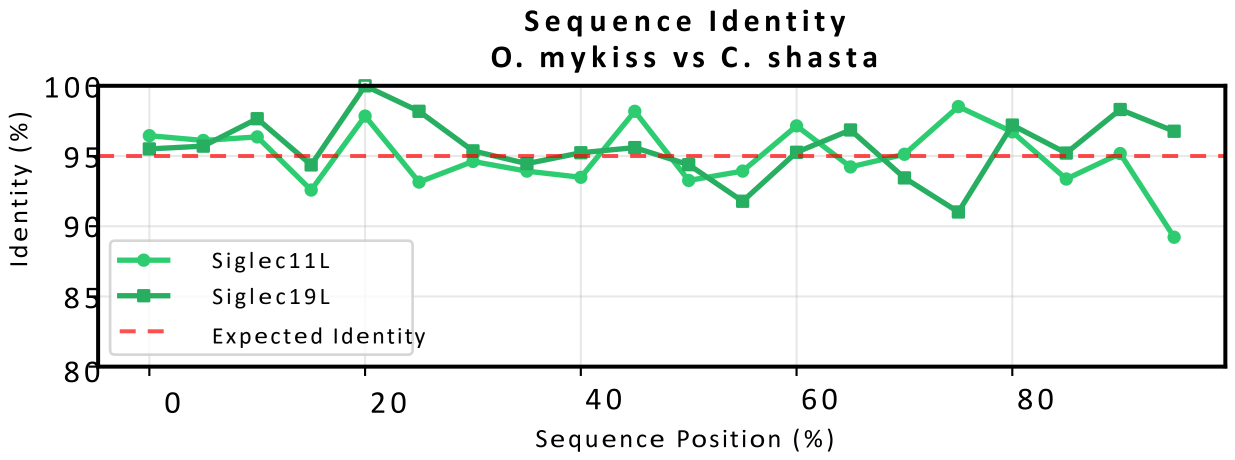
SEQUENCE ANALYSIS RESULTS

Locus Comparison:
  O. mykiss locus: 4800 bp
  C. shasta locus: 4476 bp

Gene Identity:
  Siglec11L: 95% sequence identity between species
  Siglec19L: 95% sequence identity between species
  High conservation confirms orthologous relationship

Critical LGT Evidence:
  hAT-Charlie TIRs (16 bp each) flank Siglec cassette in C. shasta
  NO TIR sequences at orthologous locus in O. mykiss
  TIR sequences: CAGTGGCCGATTCGCA (left) / TGCGAATCGGCCACTG (right)

Mechanistic Interpretation:
1. hAT-Charlie transposon captured Siglec gene cassette from host
2. Transposon-mediated transfer to parasite genome
3. Integration with TIR sequences preserved as "molecular fossils"
4. Host locus remains in original genomic context
  hAT-CHARLIE TE MINAL INVERTED REPEAT (TIR) SEQUE CES
Conclusion:



DEFINITIVE EVIDENCER for transposon-mediated lateral gene transfer from *O. mykiss* host to *C. shasta* parasite
Left TIR: 5'-CAGTGGCCGATTCGCA-3'
Right TIR: 5'-TGCGAATCGGCCACTG-3' (reverse complement)

These 16 bp sequences are the molecular signature of hAT-Charlie transposon insertion. Their presence flanking the Siglec genes in C. shasta but absence in O. mykiss provides unambiguous evidence that the genes were mobilized by the transposon from host to parasite.
This represents a "smoking gun" for transposon-mediated lateral gene transfer.