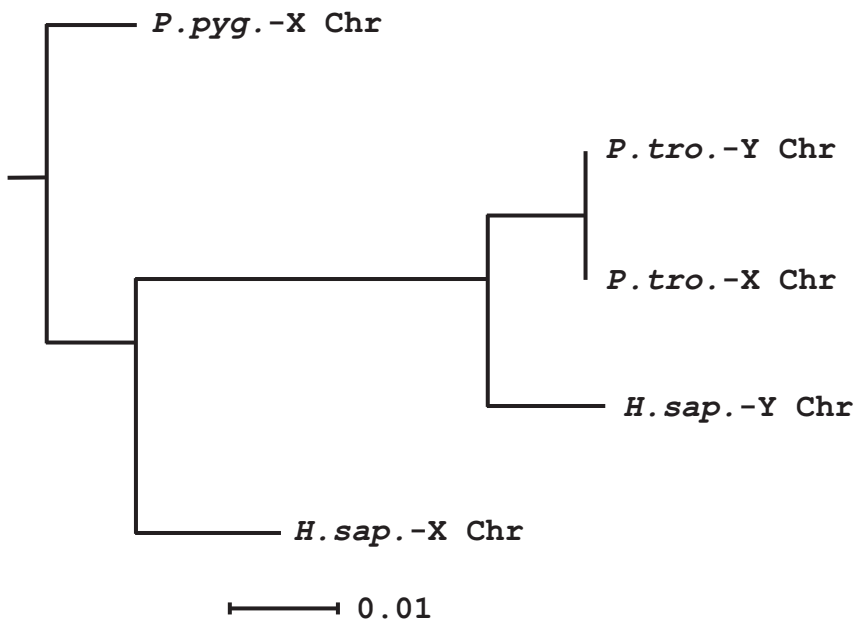
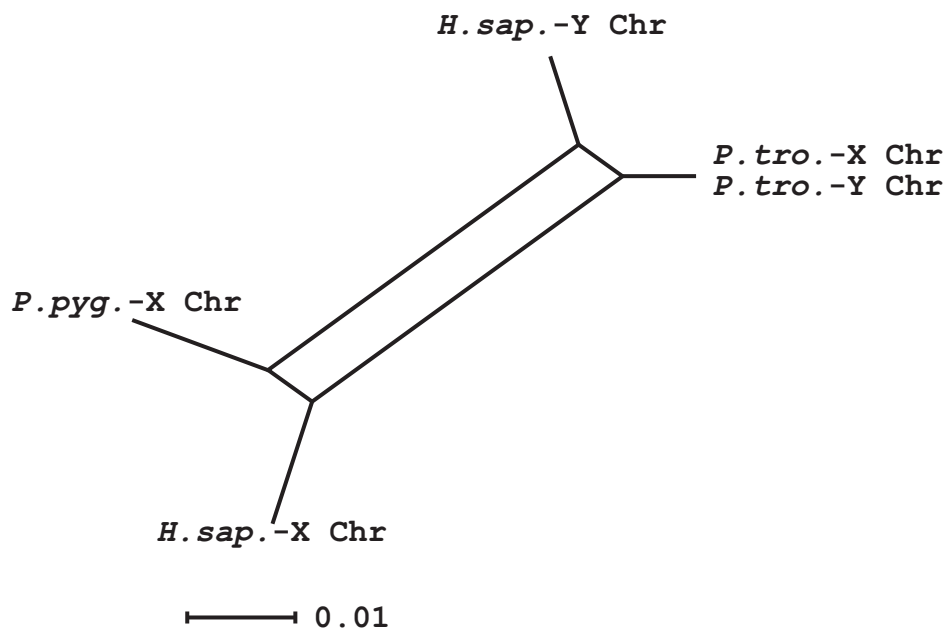


CER 1

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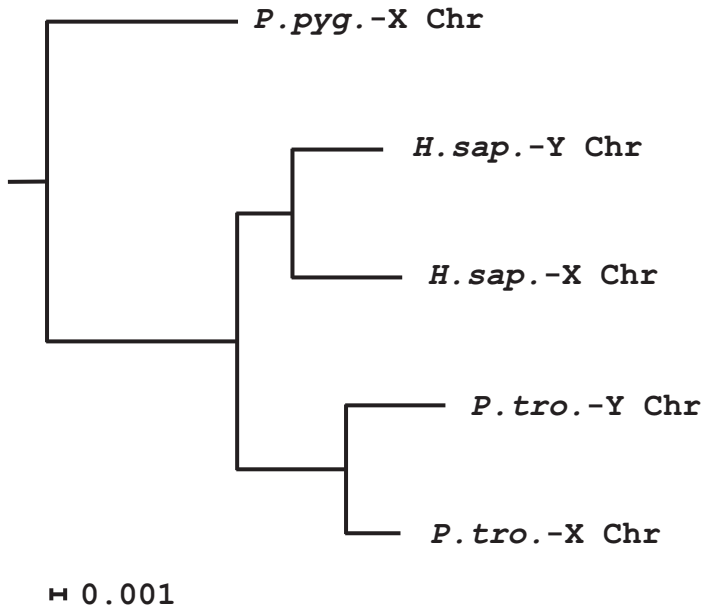


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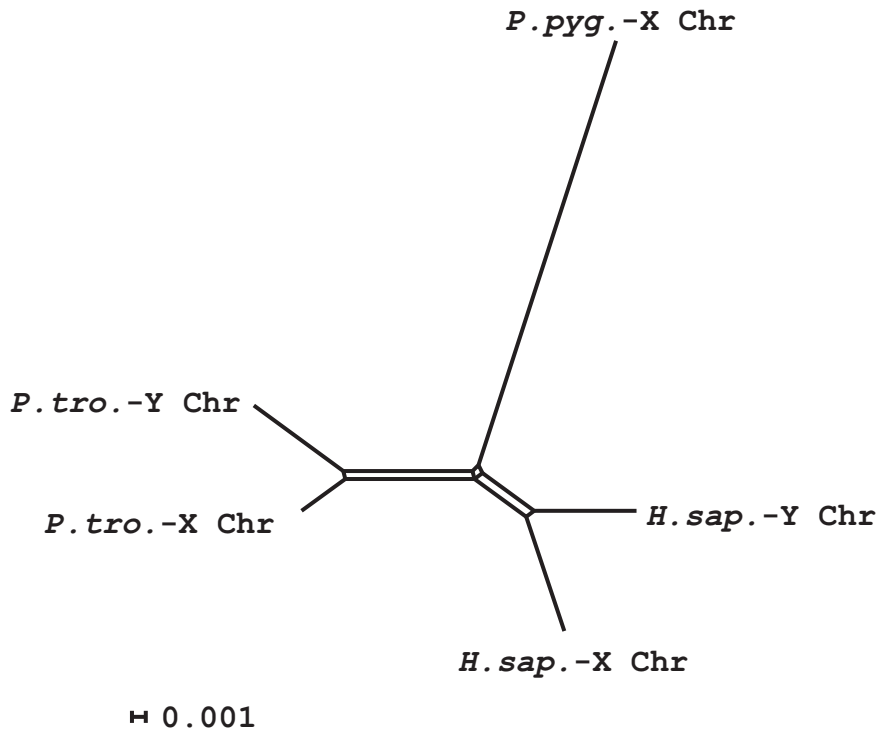


CER 2

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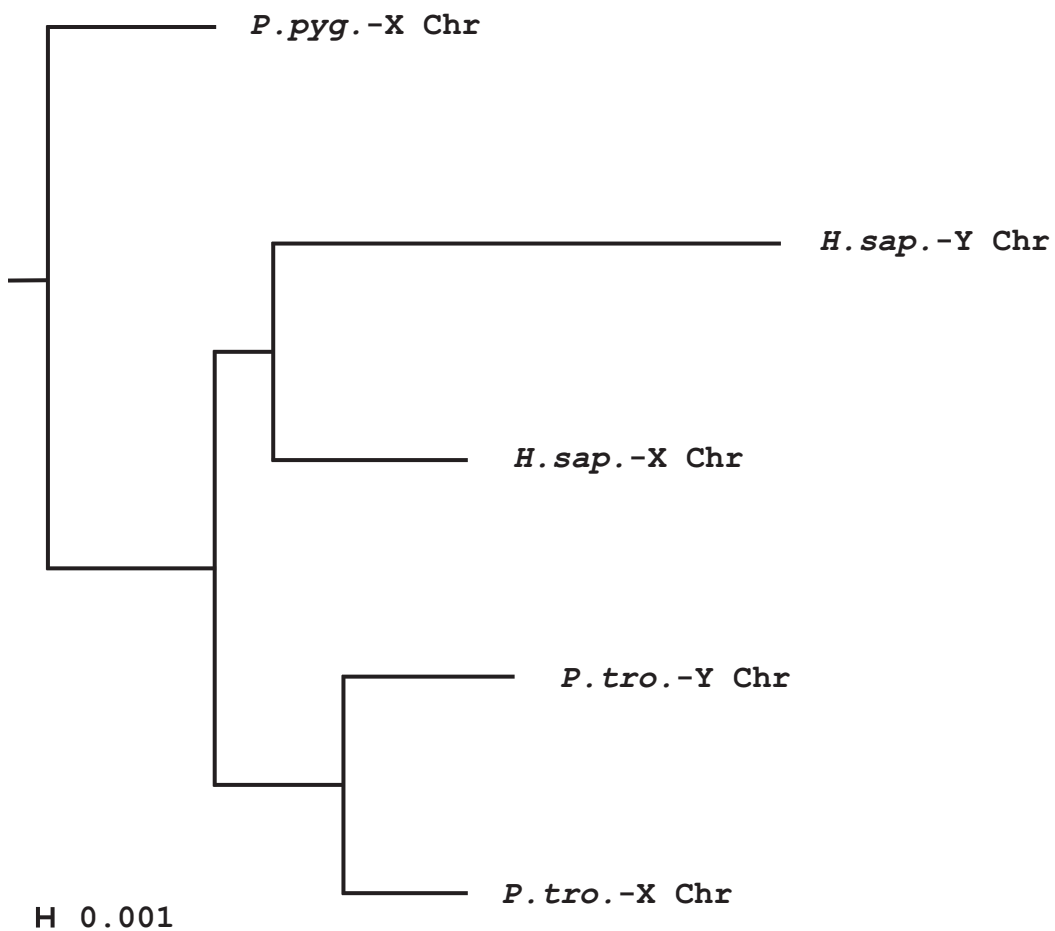


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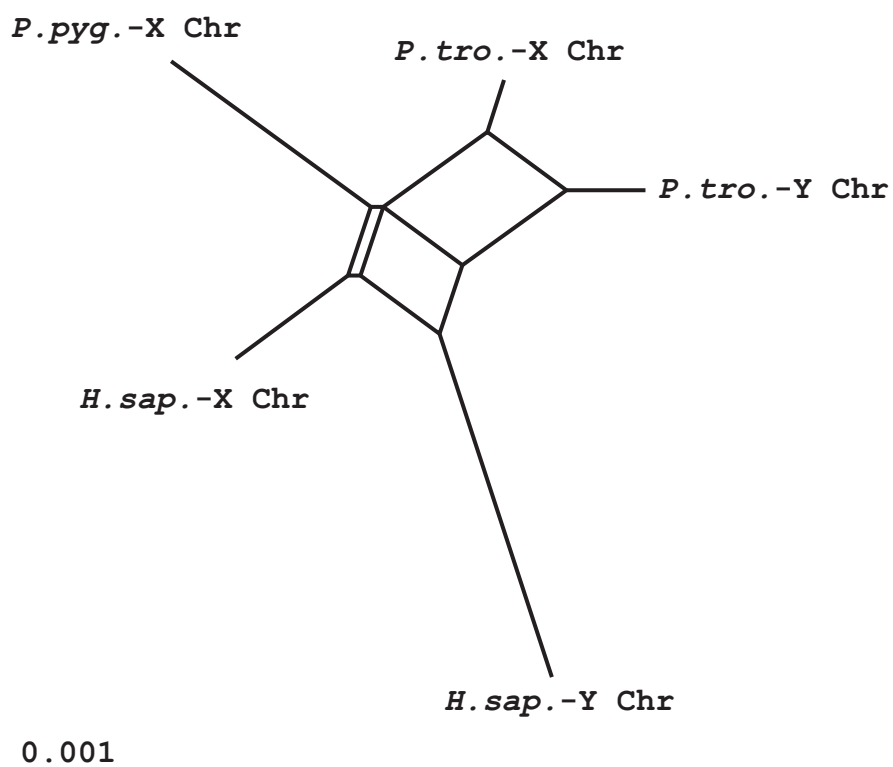


CER 3

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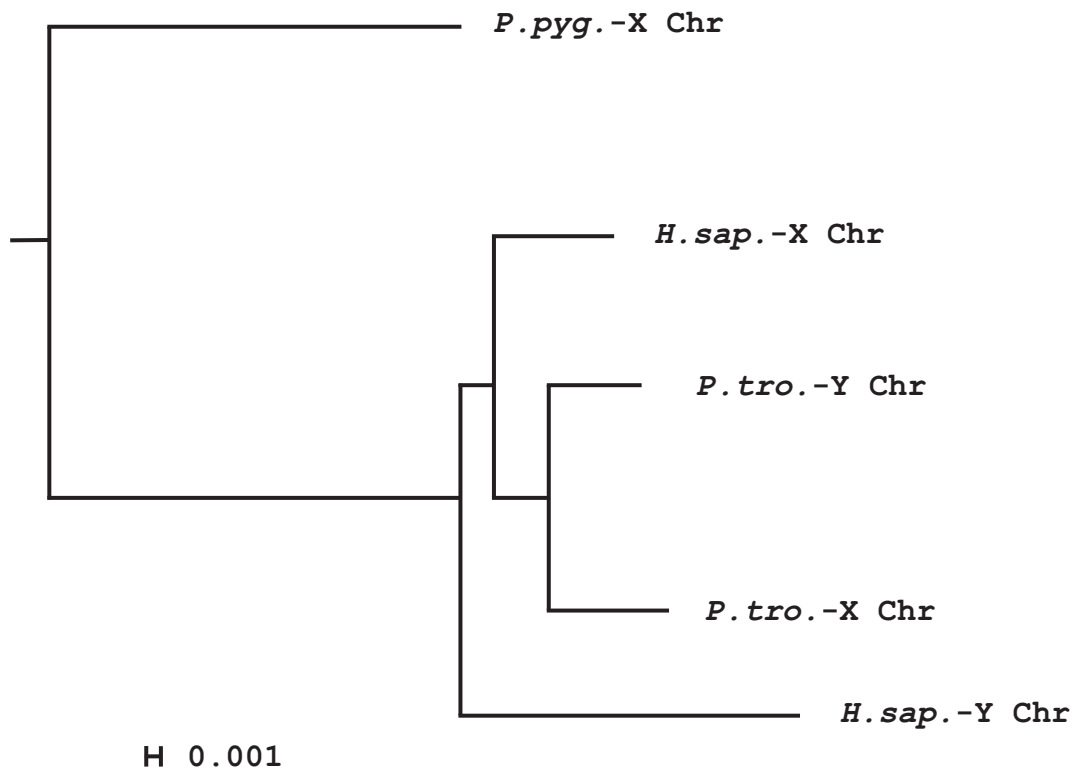


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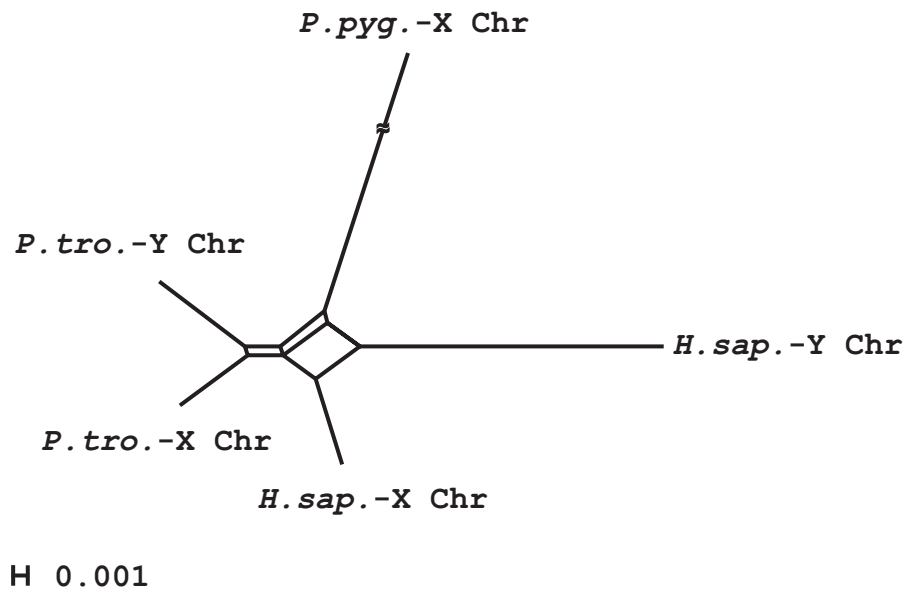


CER 4

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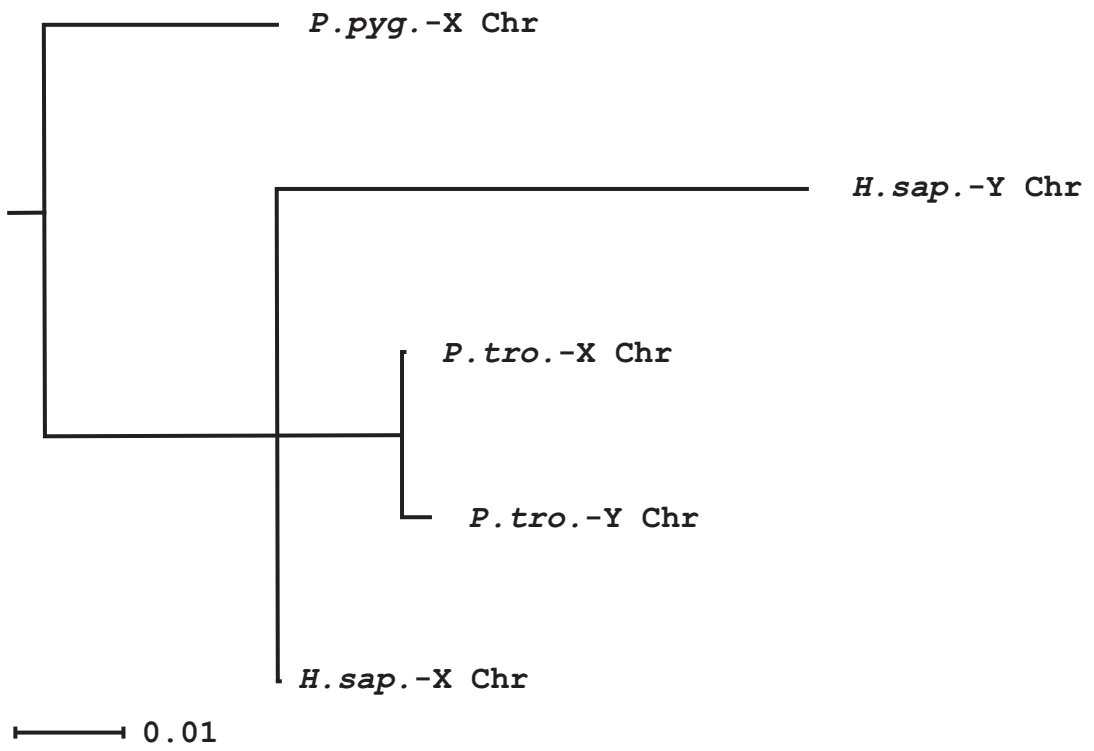


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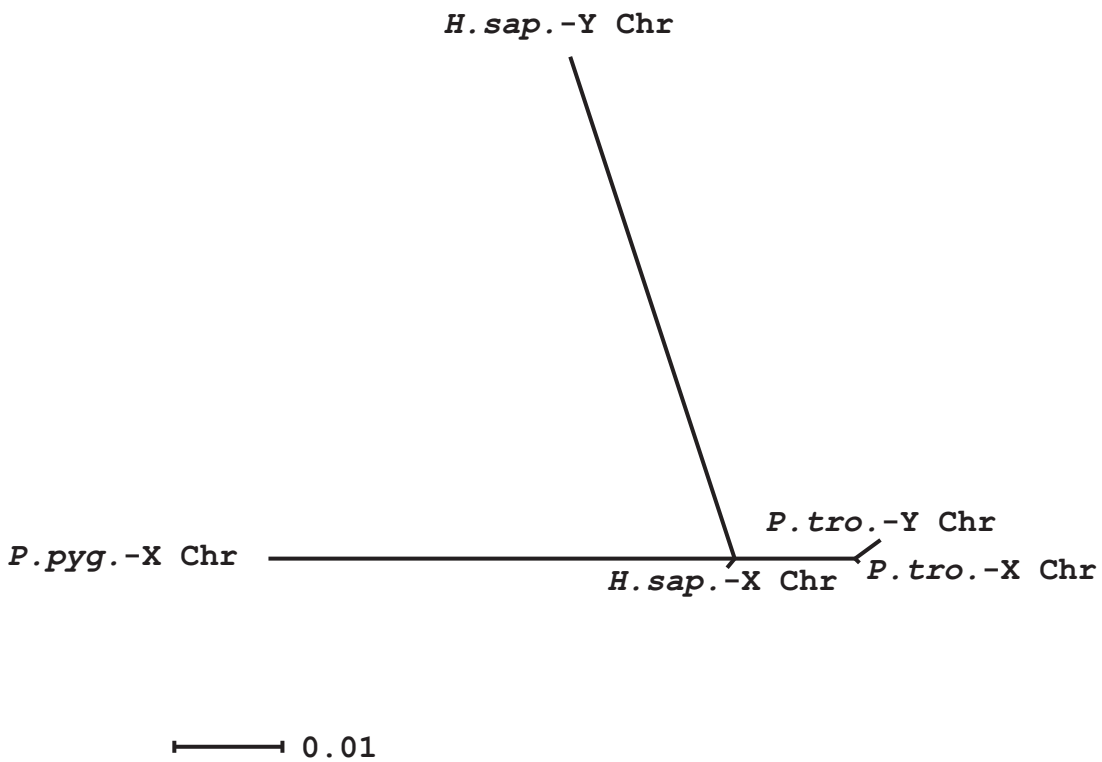


CER 5

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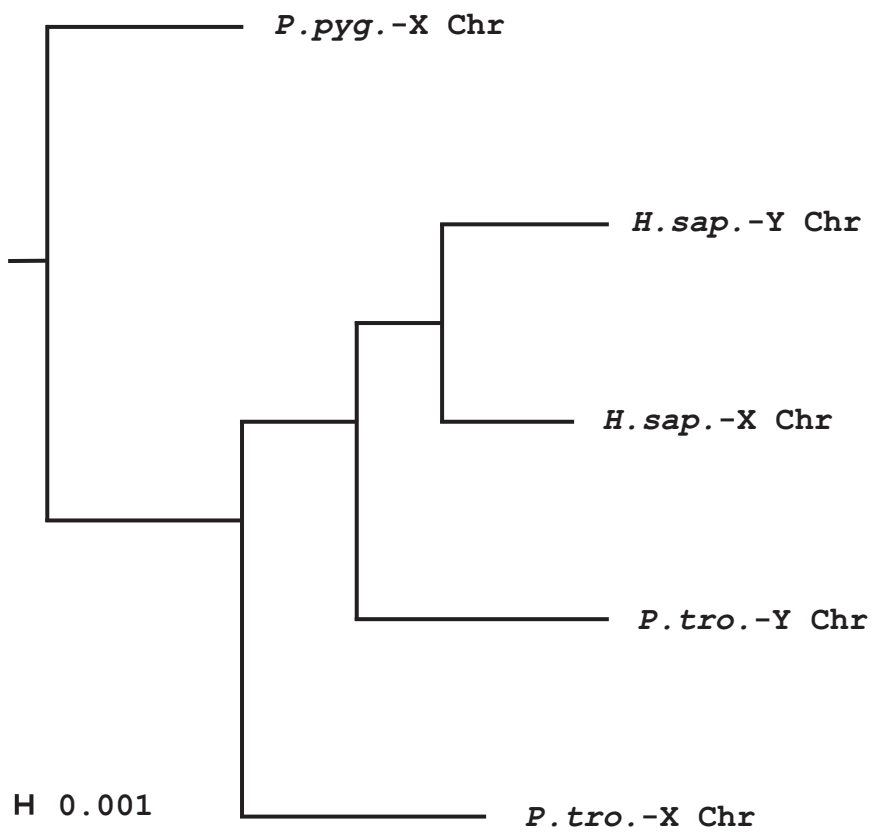


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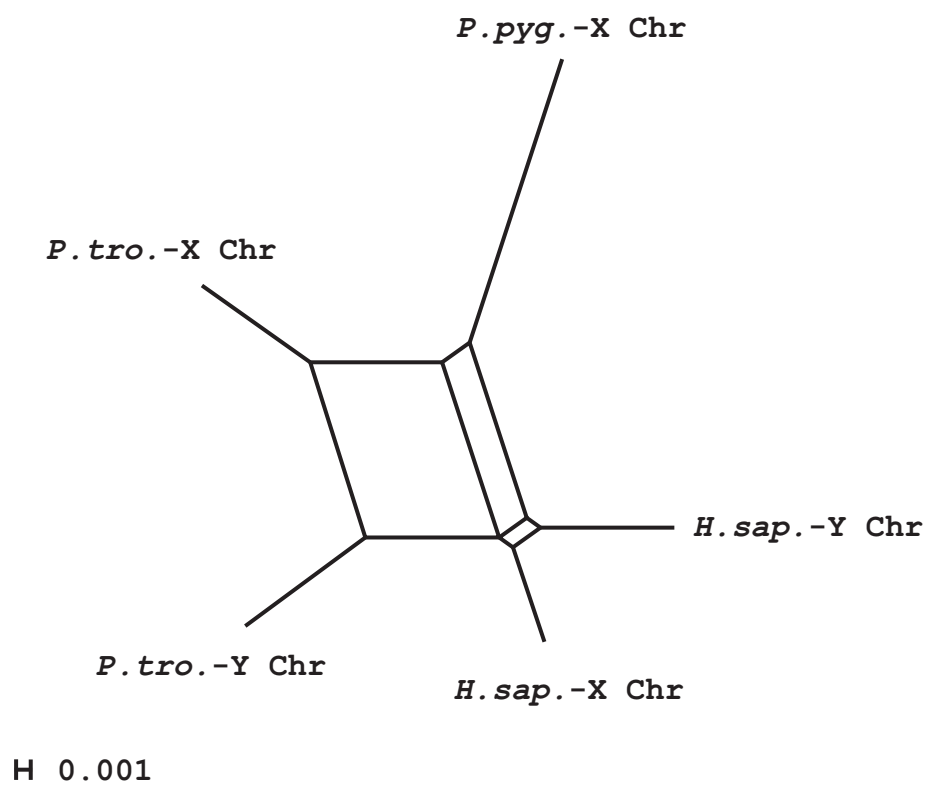


CER 6

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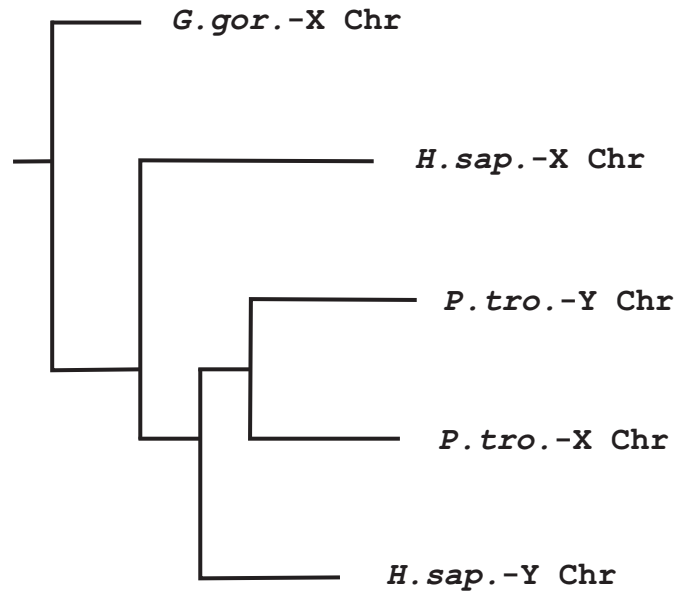


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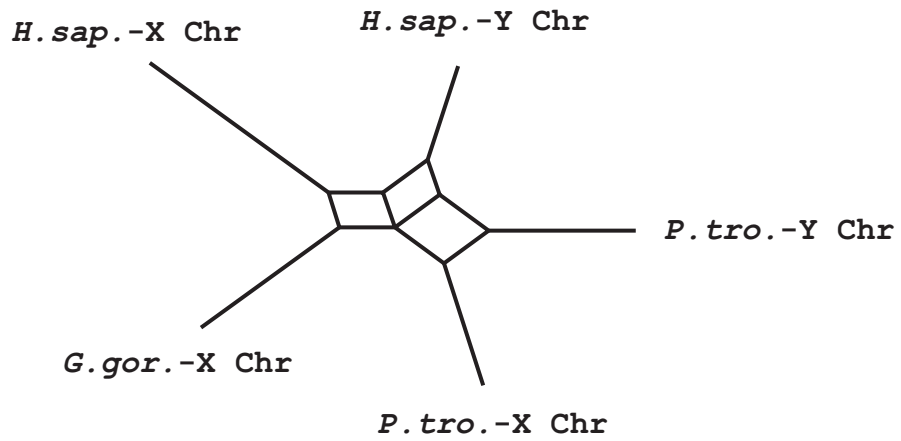
CER 7

A



H 0.001

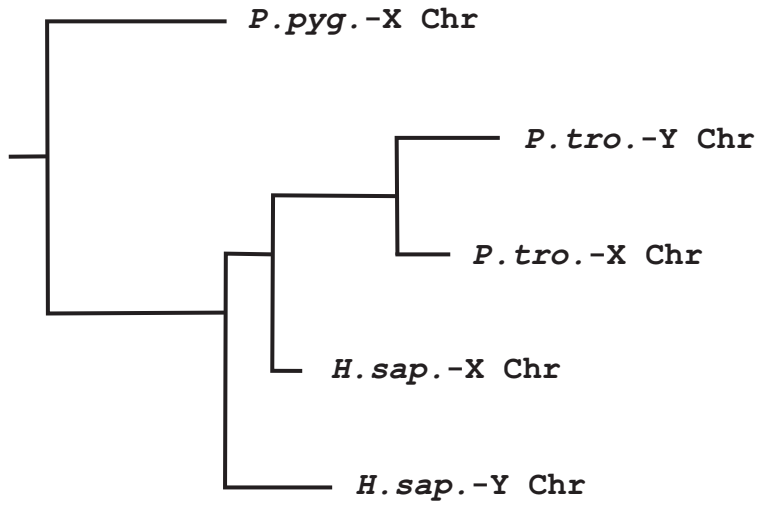
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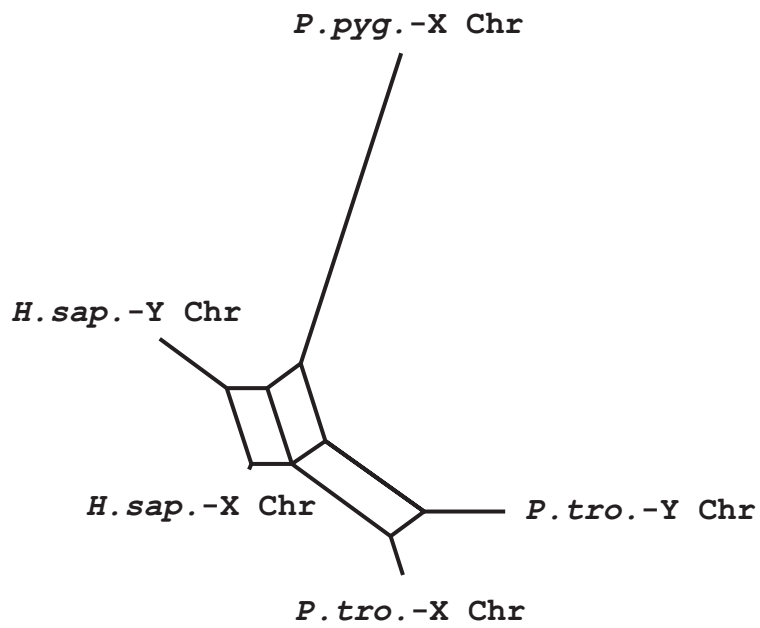
CER 8

A



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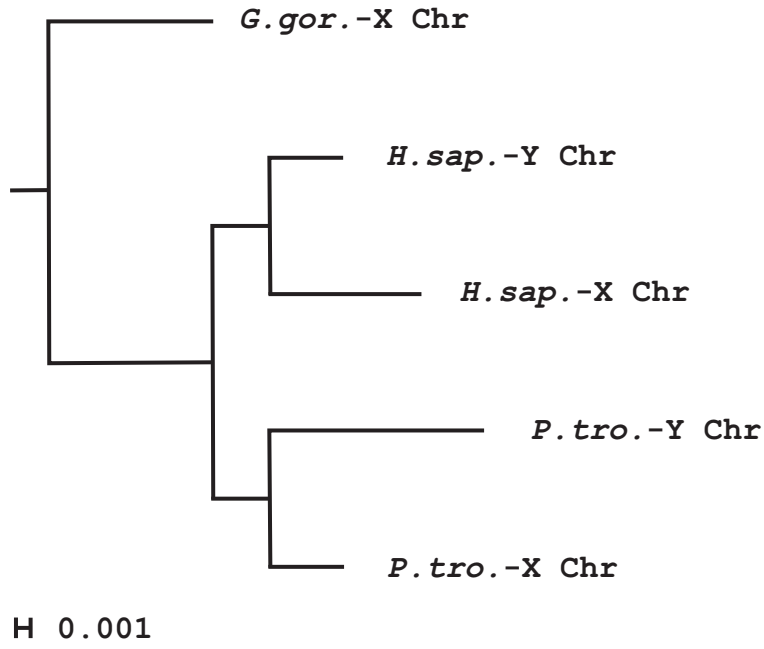
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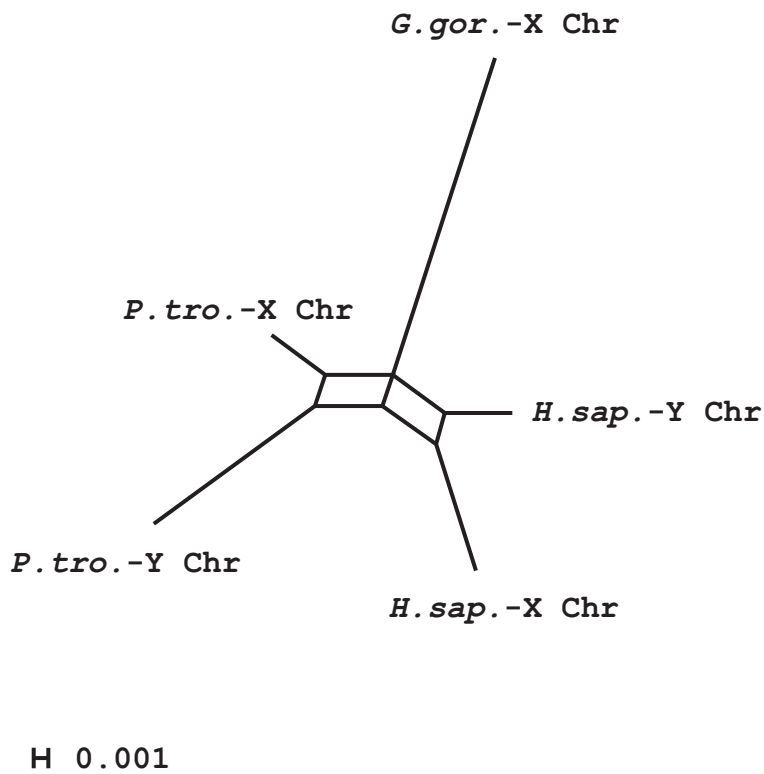
H 0.001

CER 9

A

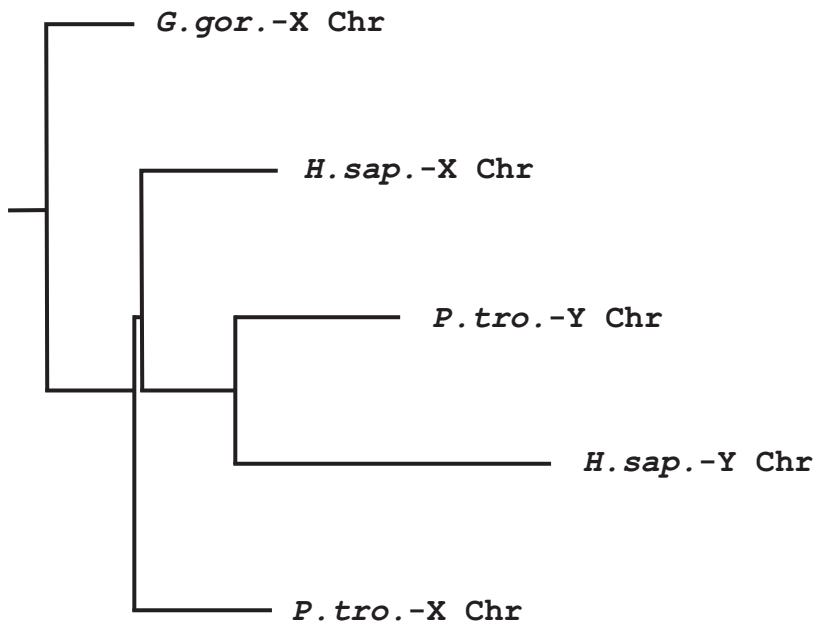


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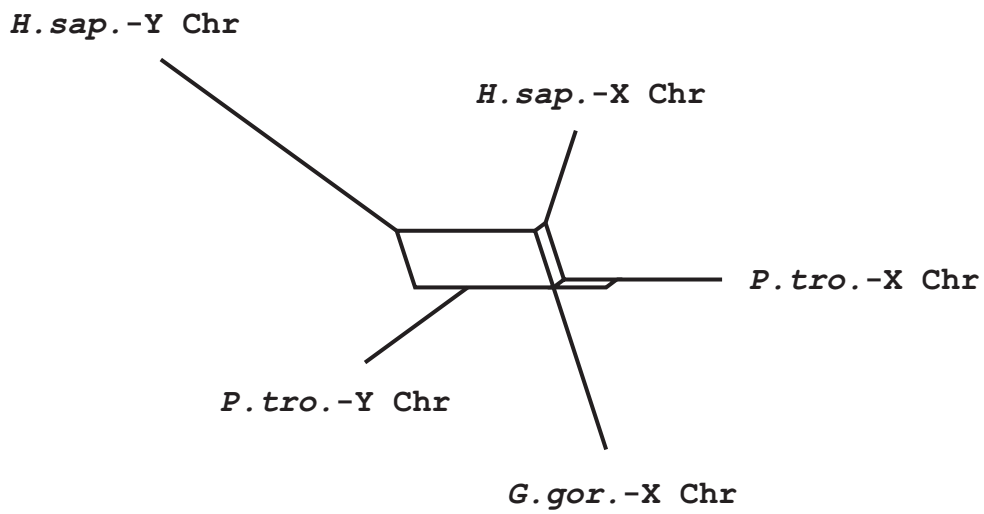
CER 10

A



H 0.001

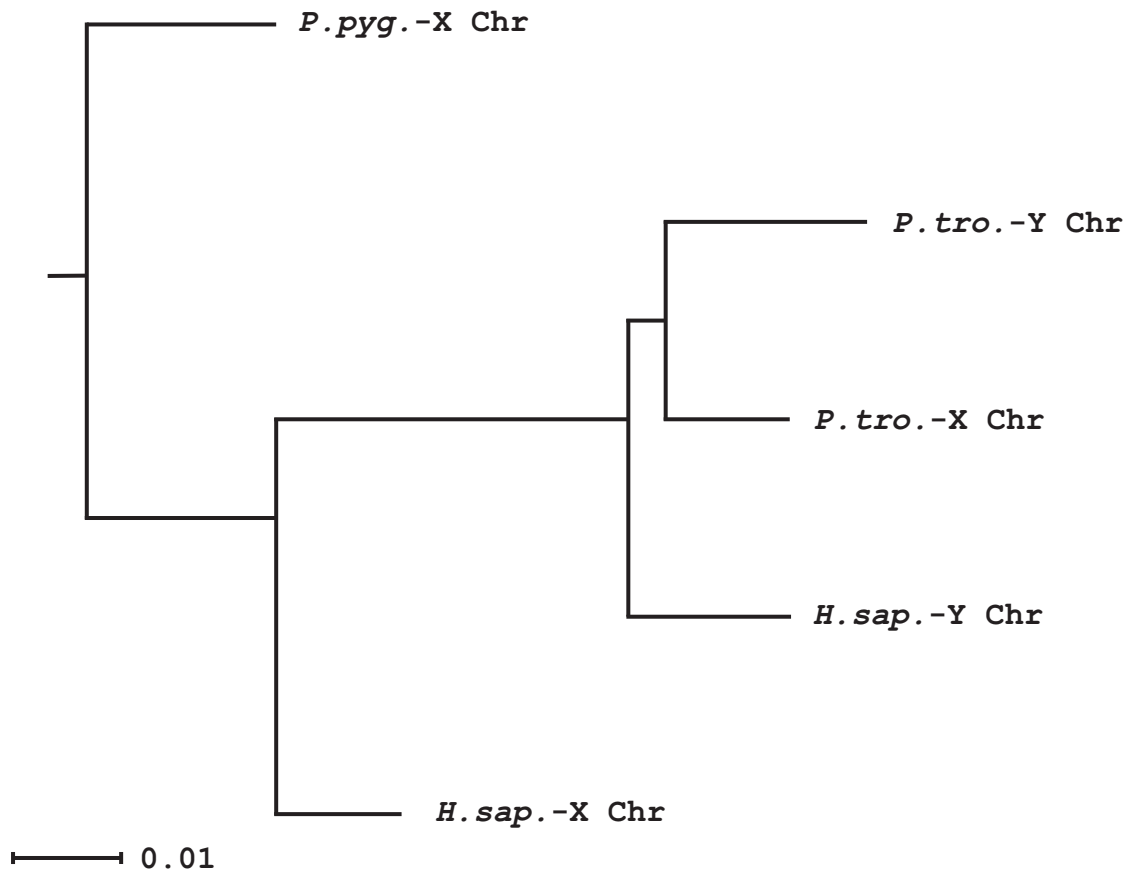
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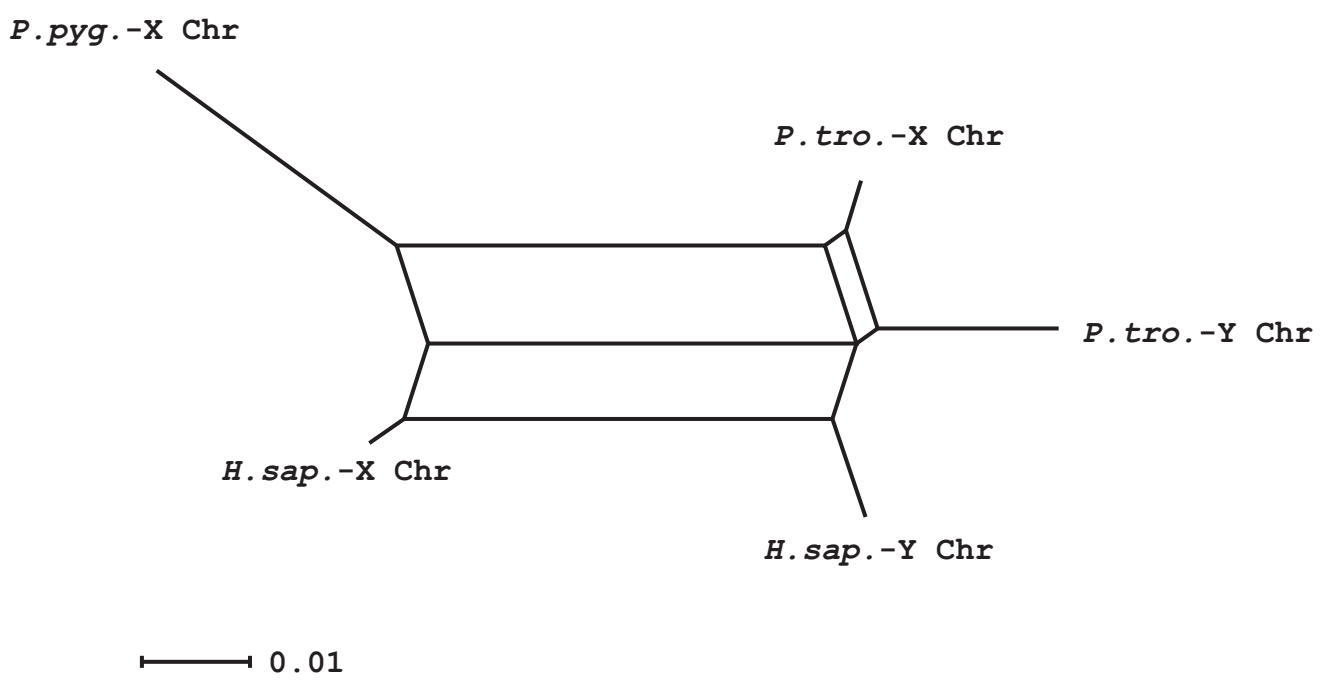
H 0.001

CER 11

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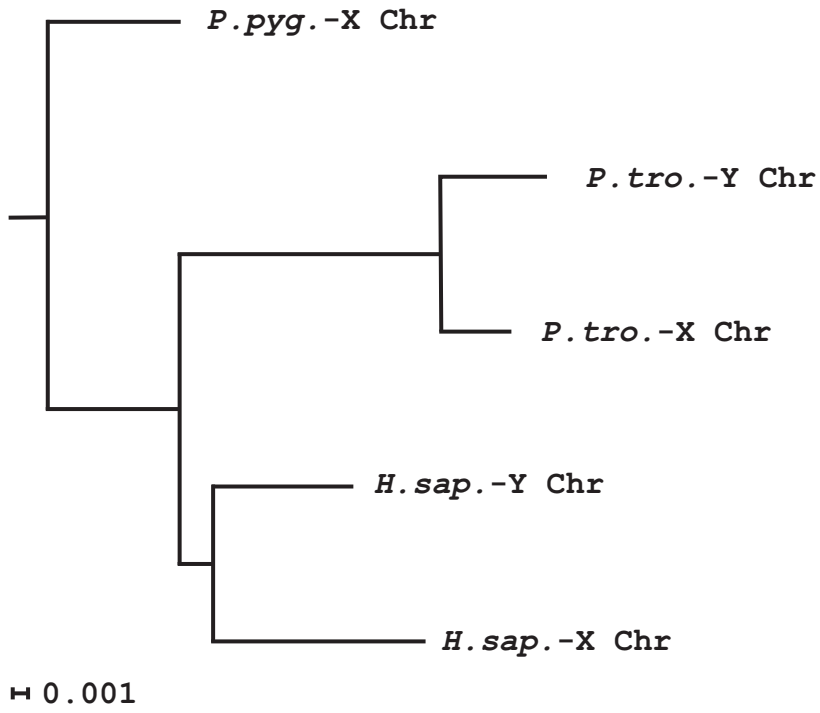


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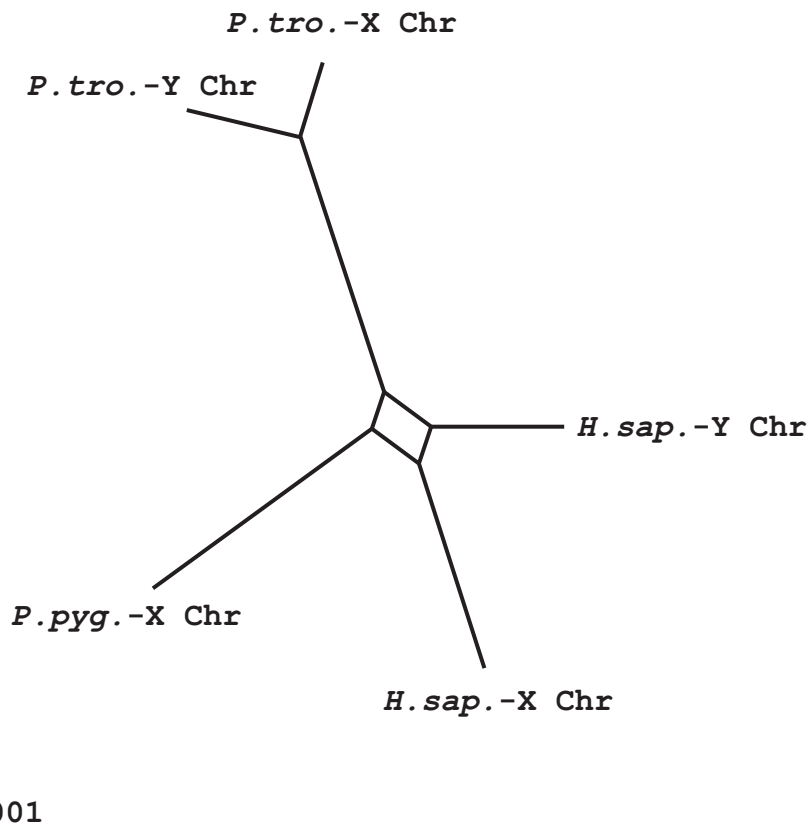


CER 12

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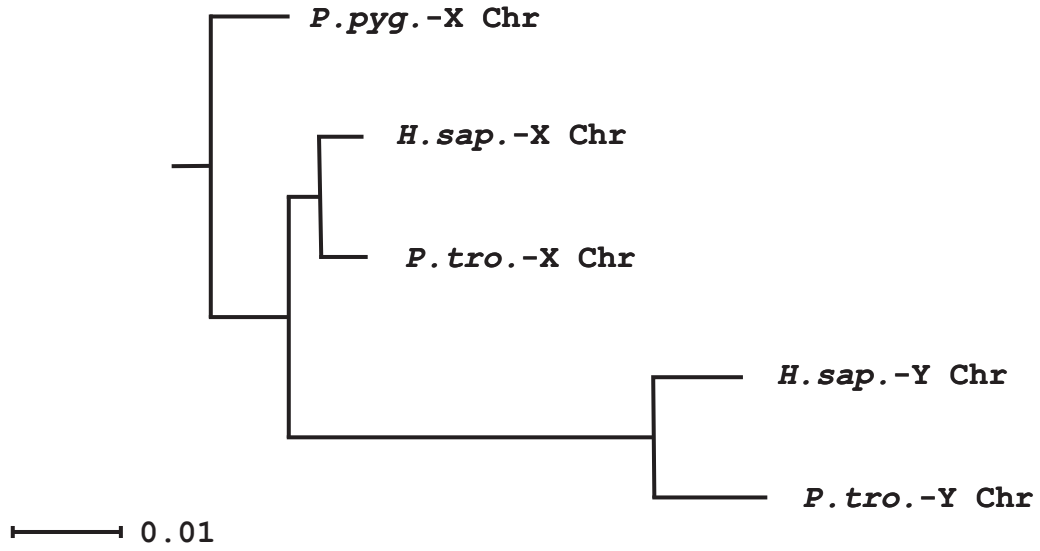


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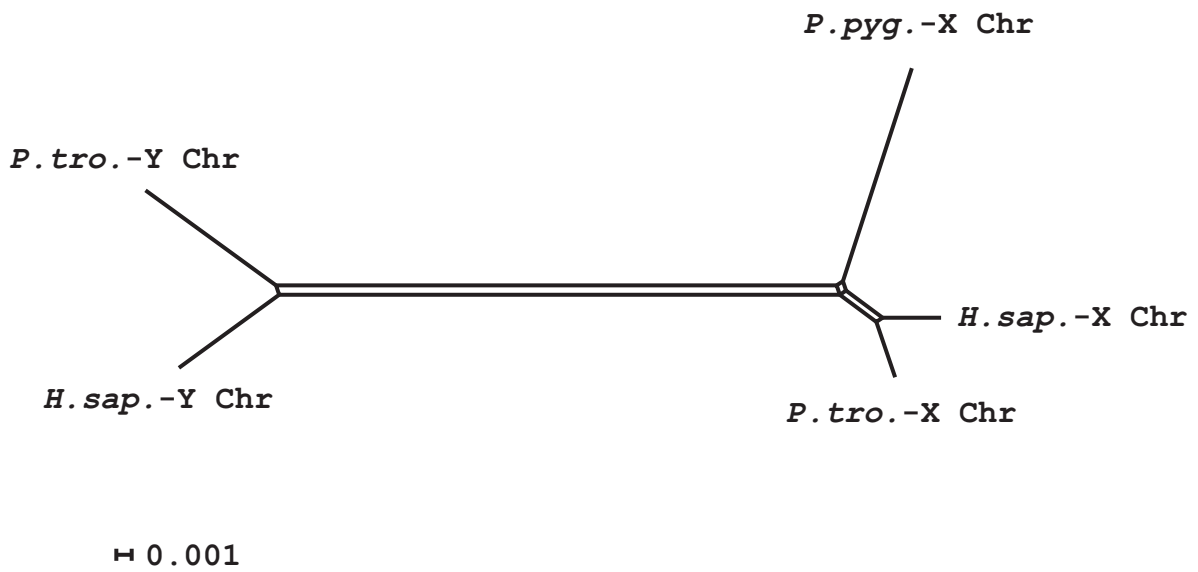


CER 13

A

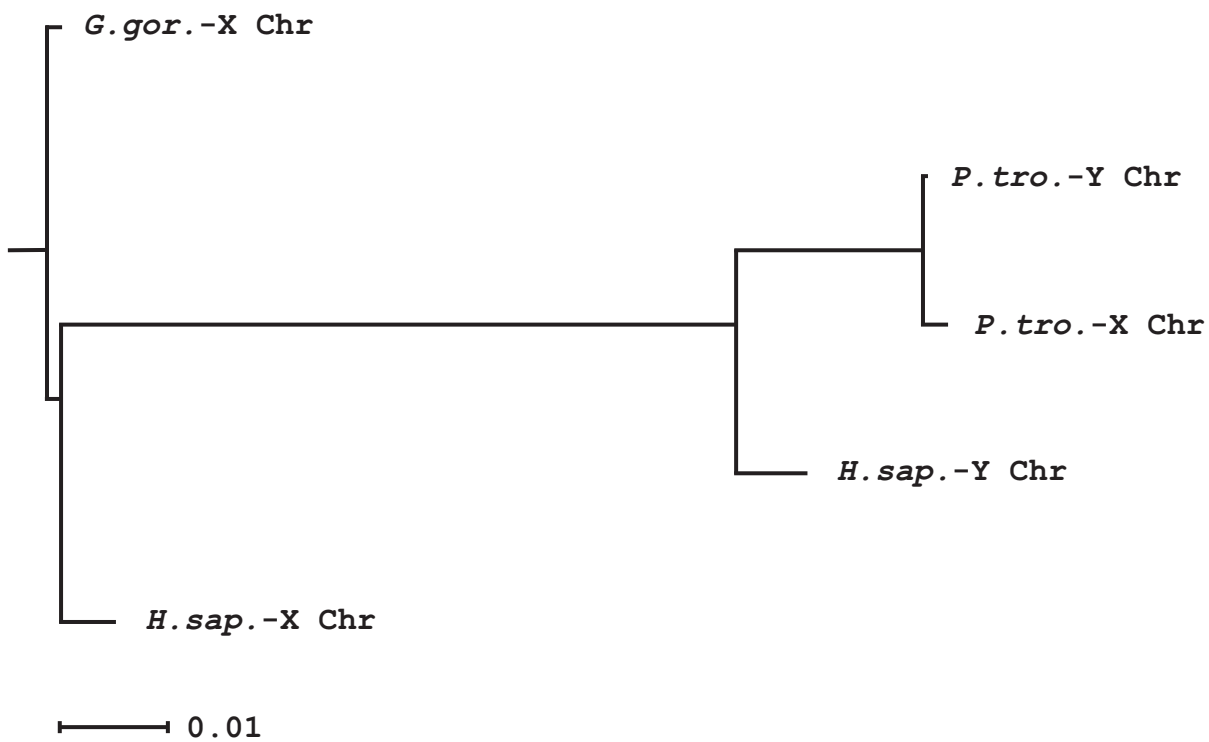


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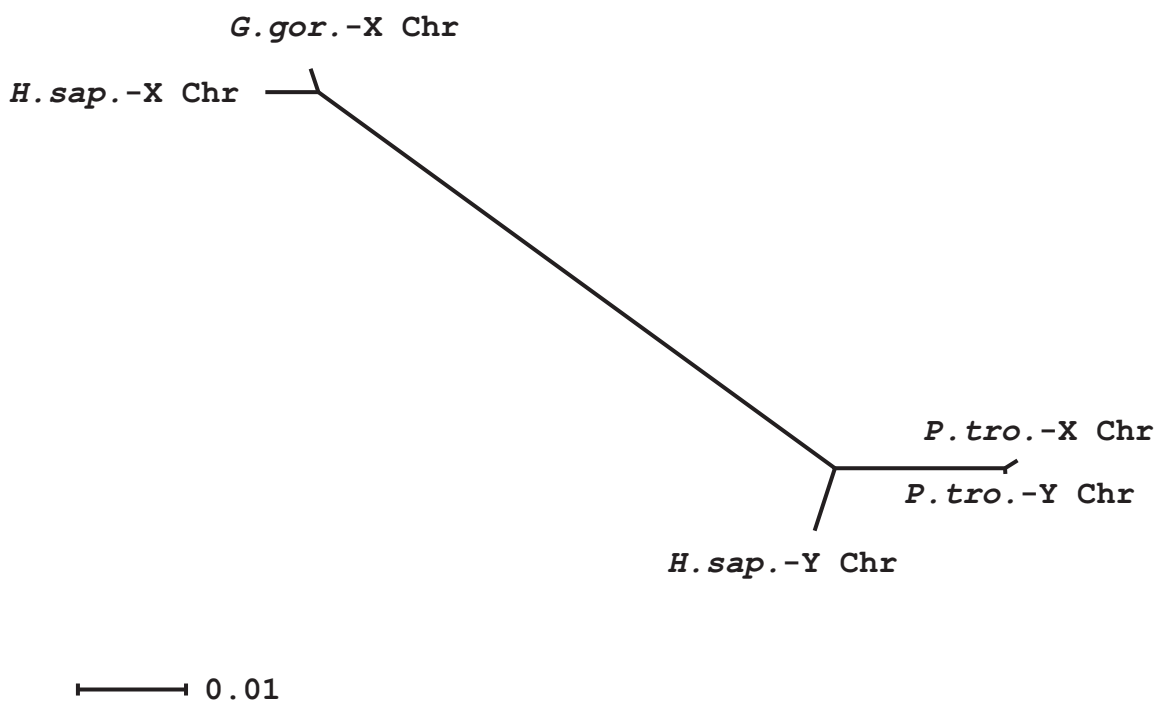


CER 14

A

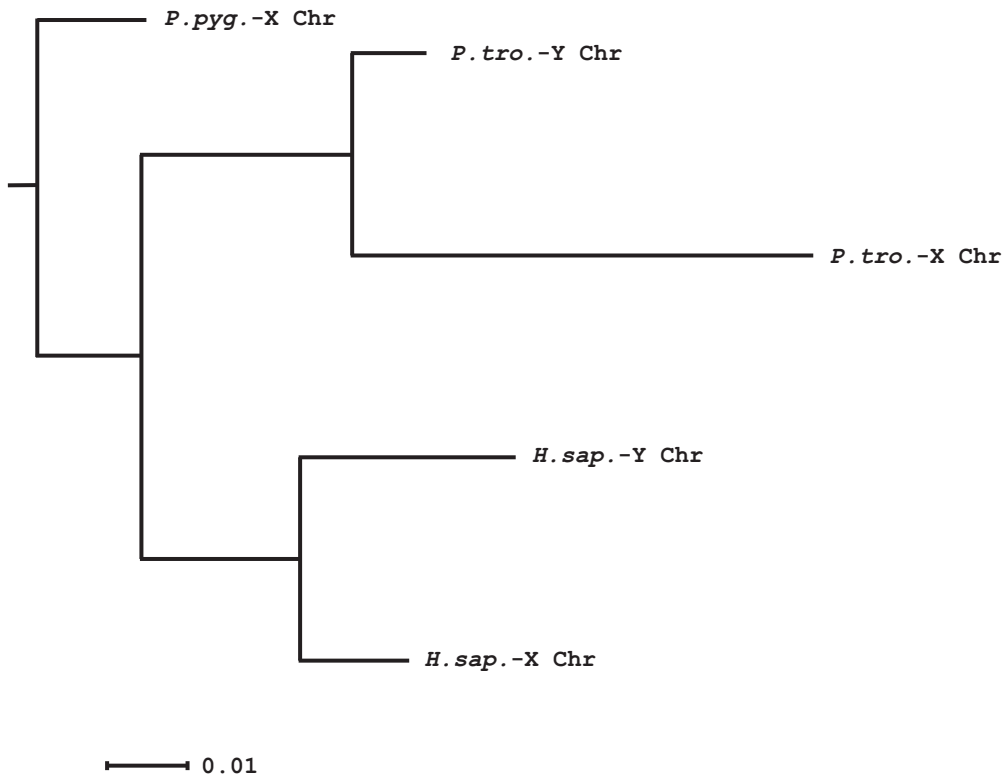


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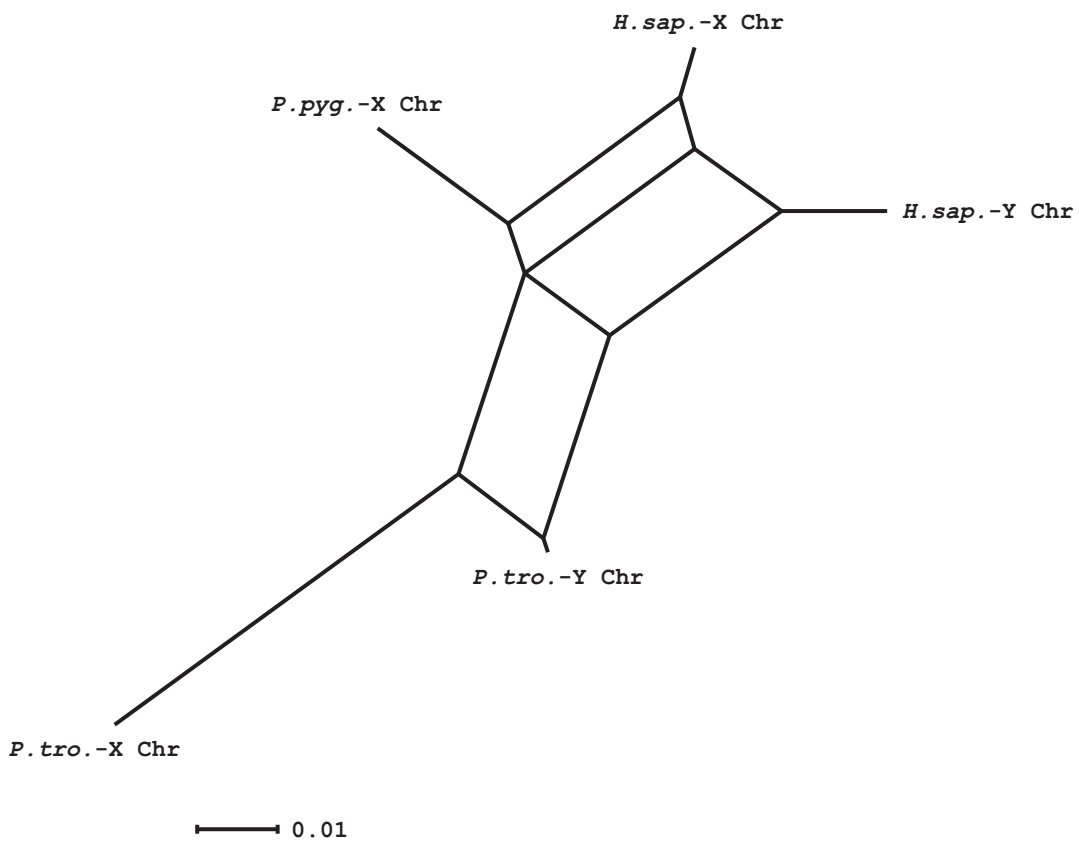


CER 15

A

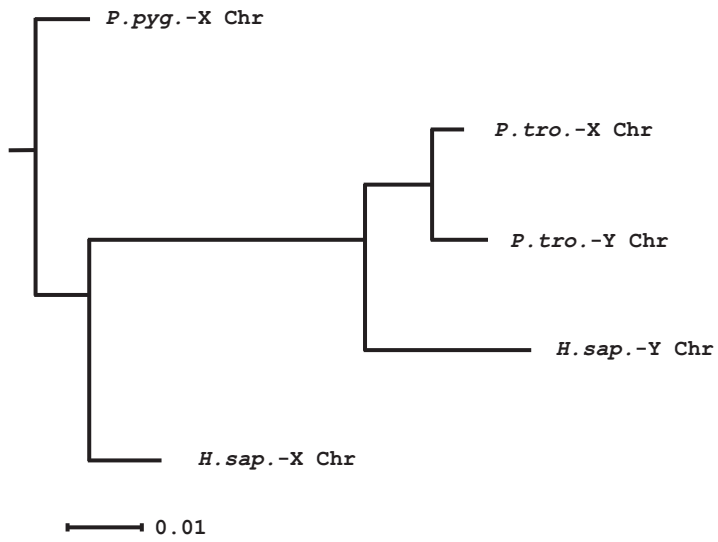


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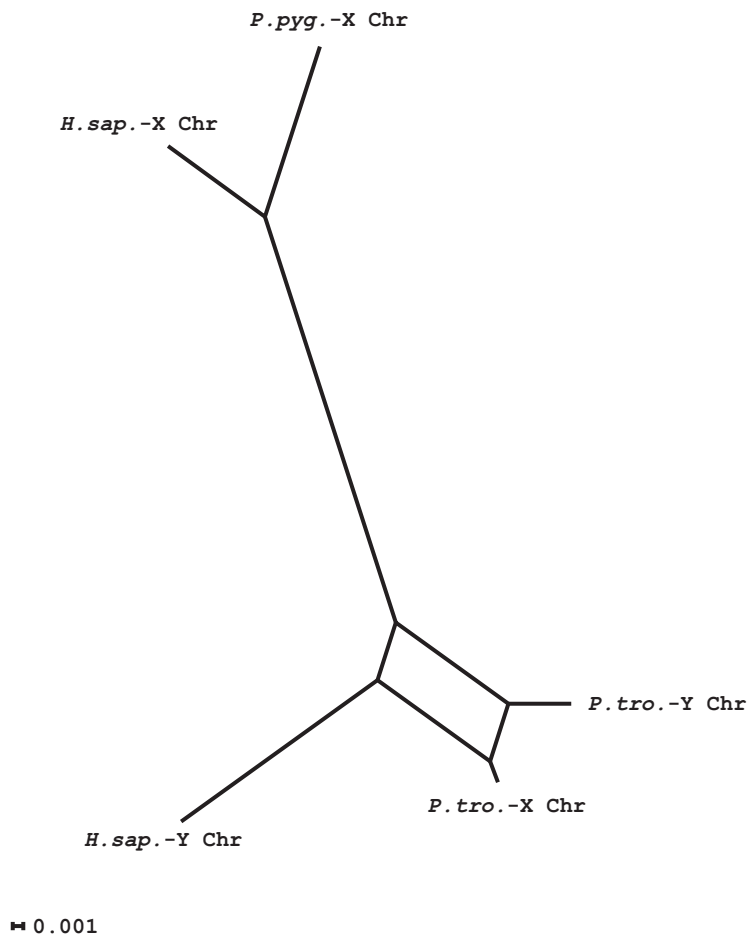


CER 16

A

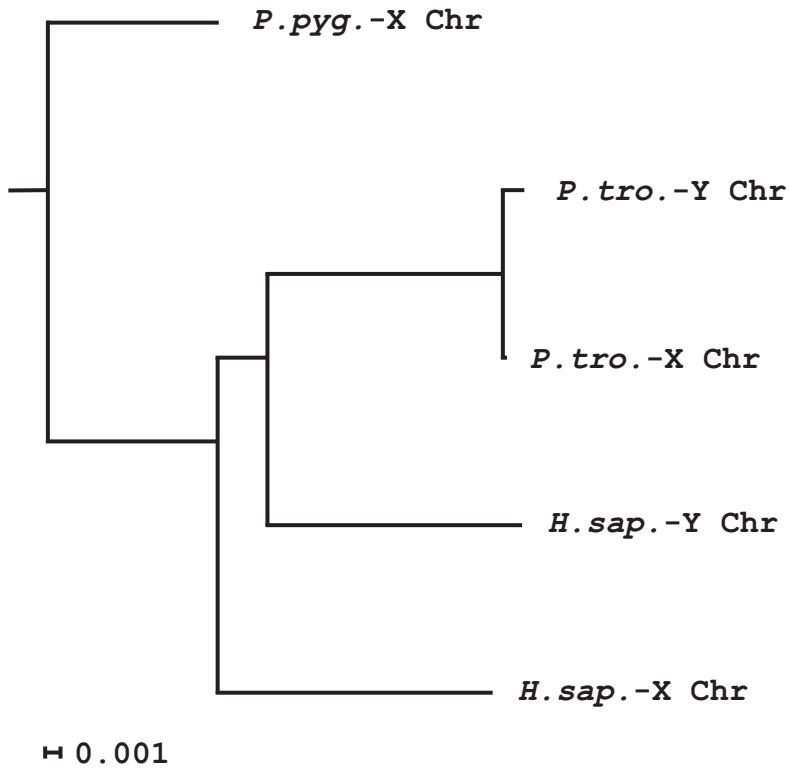


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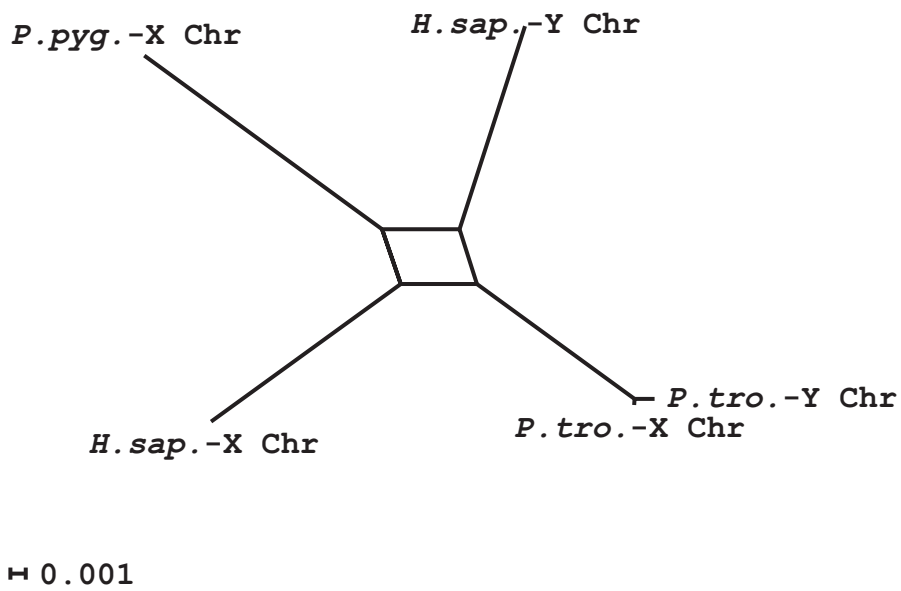


CER 17

A

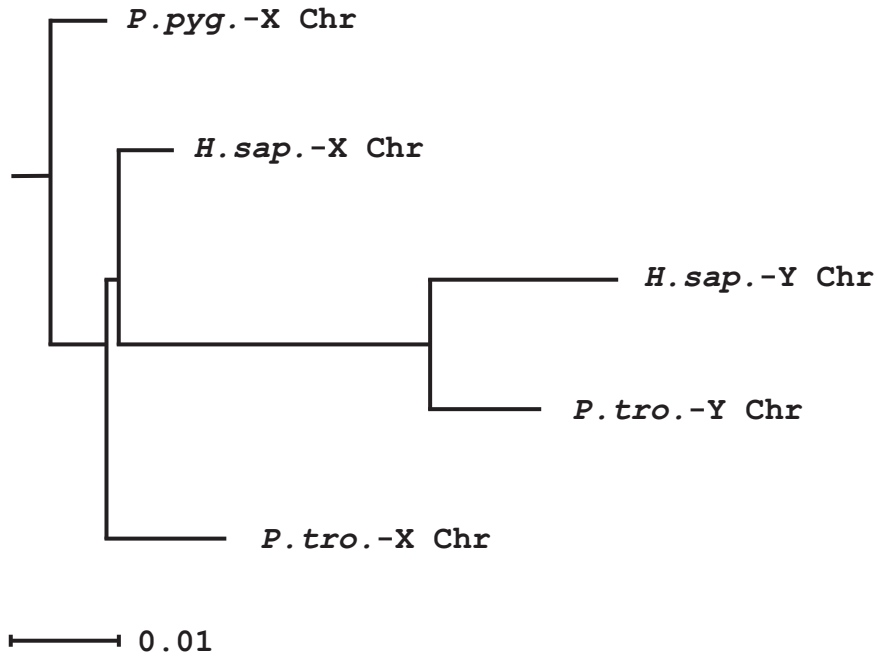


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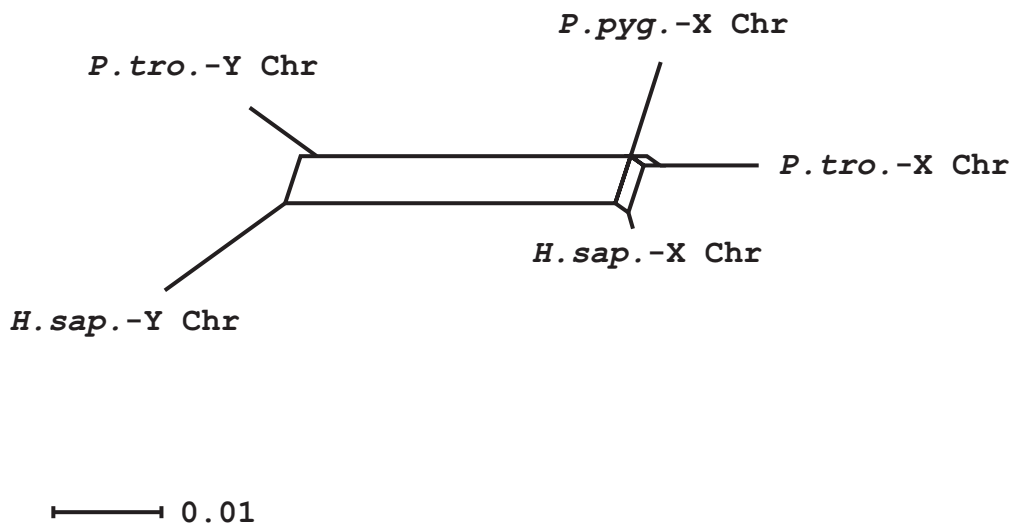


CER 18

A

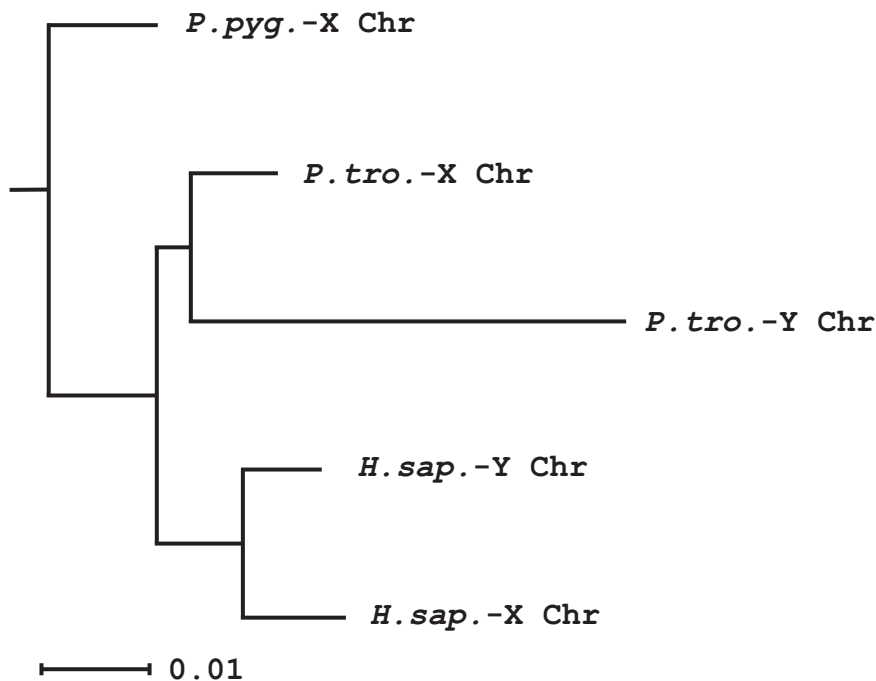


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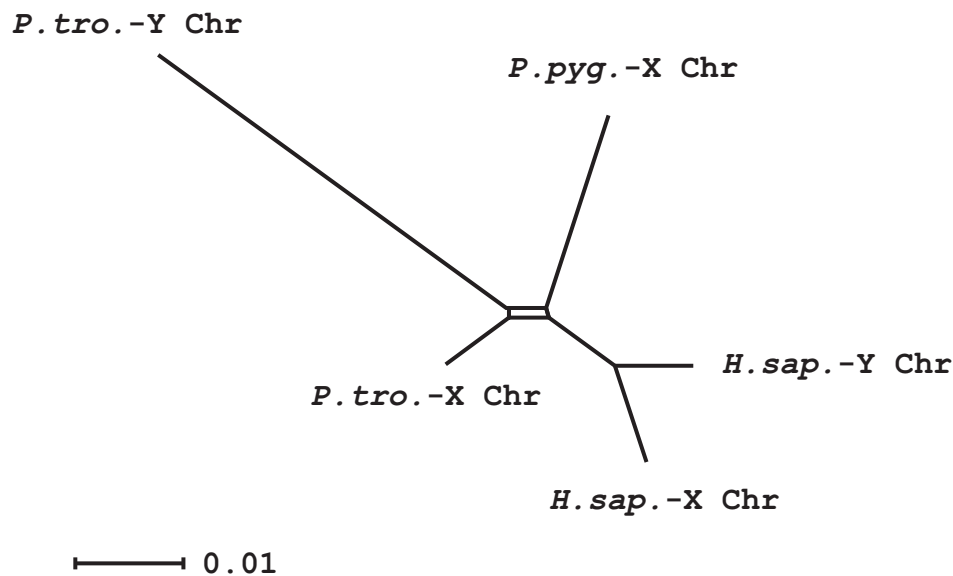


CER 19

A



B



Supplementary figure 3:

Phylogenetic analysis of CERs based on the alignments of supplementary figure 2.

A) Phylogenetic tree obtained with the NJ method.

B) Phylogenetic split decomposition analysis.

Lengths of edges represent the proportion of differences among sequences, as indicated by the scale-bar, using “uncorrected P” distance (note that different scale bare could have been used for NJ and Split Decomposition analyses). Clustering of paralogs and a reticulated structure in the Split Decomposition analysis indicates a history of gene conversion.

Abbreviations are as follow: P.pyg. = *Pongo pygmaeus*; H.sap. = *Homo sapiens*; P.tro. = *Pan troglodytes*; G. go. = *Gorilla gorilla*.