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Figure S2. Equivalency between all Caribbean clade vs *Tolteca*.

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#### Equivalency P. americana Non–Caribbean Pholcophora



Figure S12







Figure S16

#### Niche Overlap Caribbean taxa Papiamenta



#### Niche Overlap Caribbean taxa Tolteca

Figure S17



#### Niche Overlap Mexican Pholcophora Caribbean taxa

Figure S18



#### Niche Overlap Mexican Pholcophora Papiamenta

Figure S19







#### Niche Overlap Non–Caribbean Pholcophora Mexican Pholcophora

Figure S22





### Figure S24 Niche Overlap Non–Caribbean Pholcophora Tolteca







## Figure S27 Niche Overlap P. americana Non–Caribbean Pholcophora



# Figure S28

### Niche Overlap P. americana Papiamenta









Axis 1 = 35.5 % Axis 2 = 18.47 %





Axis 1 = 36.33 % Axis 2 = 25.63 %



Axis 1 = 41.93 % Axis 2 = 18.75 %

Figure S34

PCA correlation circle Mexican Pholcophora x Papiamenta



Axis 1 = 41.38 % Axis 2 = 19.68 %


Axis 1 = 41.69 % Axis 2 = 20.4 %

Figure S36

PCA correlation circle Non-Caribbean Pholcophora x Caribbean taxa



Axis 1 = 41.86 % Axis 2 = 30.01 %

## Figure S37

PCA correlation circle Non-Caribbean Pholcophora x Mexican Pholcopho



Axis 1 = 42.24 % Axis 2 = 30.37 %

Figure S38

PCA correlation circle Non-Caribbean Pholcophora x Papiamenta



Axis 1 = 40.28 % Axis 2 = 31.59 %



Axis 1 = 40.25 % Axis 2 = 32.18 %



Axis 1 = 37.95 % Axis 2 = 33.78 %

Figure S41

PCA correlation circle P. americana x Mexican Pholcophora



Axis 1 = 38.94 % Axis 2 = 33.45 %



Axis 1 = 36.84 % Axis 2 = 35.15 %



Axis 1 = 38.01 % Axis 2 = 33.92 %



Axis 1 = 38.92 % Axis 2 = 33.09 %

## Figure S45



Axis 1 = 36.44 % Axis 2 = 26.85 %
































































**Figure S76. Summary tree of all trees using unpartitioned analysis**. All the trees were constructed from the same gene set but with different multiple-sequence-alignment (MSA) trimming strategies. The ClipKIT\_gappy tree was used as the reference tree, the trees (query trees) from other MSA-trimming strategies were compared to the reference tree, with '+' or '-' indicating that the query trees agree or disagree with the branching events, respectively. Numbers on the branches are SH-aLRT support (%). Best-fit model according to BIC for the reference tree: SYM+I+G4.



**Figure S77. Summary tree of all trees using partitioned analysis.** All the trees were constructed from the same gene set but with different multiple-sequence-alignment (MSA) trimming strategies or the untrimmed MSA. The ClipKIT\_gappy tree was used as the reference tree, the trees (query trees) from other MSA-trimming strategies were compared to the reference tree, with '+' or '-' indicating that the query trees agree or disagree with the branching events, respectively. Numbers on the branches are SH-aLRT support (%).