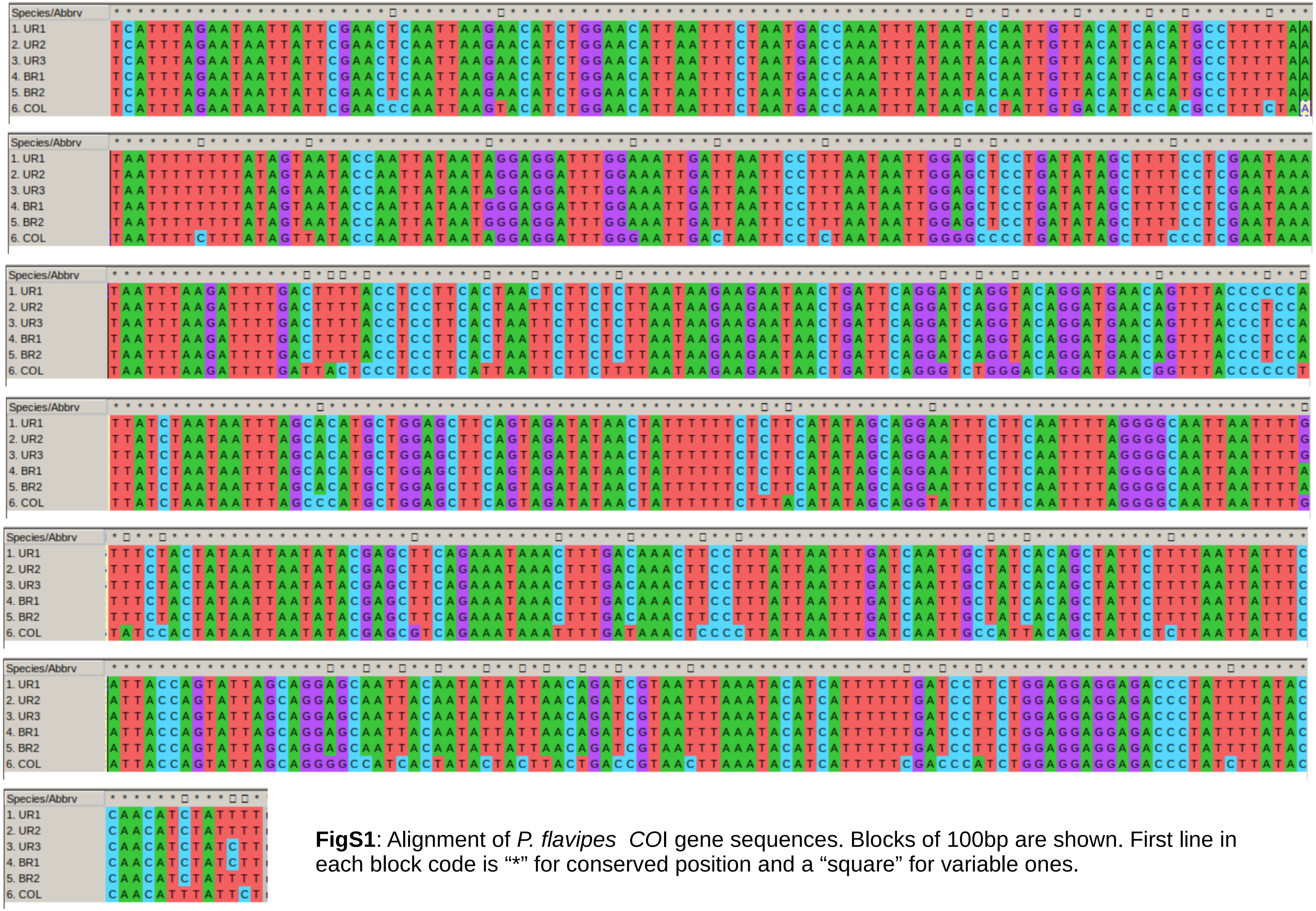
COI Alignment of *P. flavipes* samples (haplotypes)



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Species/Abbrv ***********************□********□**************************************□**□*****□*****□**□******□***
1. UR1        TCATTTAGAATAATTATTCGAACTCAATTAAGAACATCTGGAACATTAATTTCTAATGACCAAATTTATAATACAATTGTTACATCACATGCCTTTTTAA
2. UR2        TCATTTAGAATAATTATTCGAACTCAATTAAGAACATCTGGAACATTAATTTCTAATGACCAAATTTATAATACAATTGTTACATCACATGCCTTTTTAA
3. UR3        TCATTTAGAATAATTATTCGAACTCAATTAAGAACATCTGGAACATTAATTTCTAATGACCAAATTTATAATACAATTGTTACATCACATGCCTTTTTAA
4. BR1        TCATTTAGAATAATTATTCGAACTCAATTAAGAACATCTGGAACATTAATTTCTAATGACCAAATTTATAATACAATTGTTACATCACATGCCTTTTTAA
5. BR2        TCATTTAGAATAATTATTCGAACTCAATTAAGAACATCTGGAACATTAATTTCTAATGACCAAATTTATAATACAATTGTTACATCACATGCCTTTTTAA
6. COL        TCATTTAGAATAATTATTCGAACCCAATTAAGTACATCTGGAACATTAATTTCTAATGACCAAATTTATAACACTATTGTGACATCCCACGCCTTTCTAA

Species/Abbrv *******□********□**************□***********□******□********□**********□**□**************□***********
1. UR1        TAATTTTTTTTATAGTAATACCAATTATAATAGGAGGATTTGGAAATTGATTAATTCCTTTAATAATTGGAGCTCCTGATATAGCTTTTCCTCGAATAAA
2. UR2        TAATTTTTTTTATAGTAATACCAATTATAATAGGAGGATTTGGAAATTGATTAATTCCTTTAATAATTGGAGCTCCTGATATAGCTTTTCCTCGAATAAA
3. UR3        TAATTTTTTTTATAGTAATACCAATTATAATAGGAGGATTTGGAAATTGATTAATTCCTTTAATAATTGGAGCTCCTGATATAGCTTTTCCTCGAATAAA
4. BR1        TAATTTTTTTTATAGTAATACCAATTATAATGGGAGGATTTGGAAATTGATTAATTCCTTTAATAATTGGAGCTCCTGATATAGCTTTTCCTCGAATAAA
5. BR2        TAATTTTTTTTATAGTAATACCAATTATAATGGGAGGATTTGGAAATTGATTAATTCCTTTAATAATTGGAGCTCCTGATATAGCTTTTCCTCGAATAAA
6. COL        TAATTTTCTTTATAGTTATACCAATTATAATAGGAGGATTTGGGAATTGACTAATTCCTCTAATAATTGGGGCCCCTGATATAGCTTTCCCTCGAATAAA

Species/Abbrv ****************□*□□*□*********□***□******□**************************□**□**□***********□********□**□
1. UR1        TAATTTAAGATTTTGACTTTTACCTCCTTCACTAACTCTTCTCTTAATAAGAAGAATAACTGATTCAGGATCAGGTACAGGATGAACAGTTTACCCCCCA
2. UR2        TAATTTAAGATTTTGACTTTTACCTCCTTCACTAATTCTTCTCTTAATAAGAAGAATAACTGATTCAGGATCAGGTACAGGATGAACAGTTTACCCTCCA
3. UR3        TAATTTAAGATTTTGACTTTTACCTCCTTCACTAATTCTTCTCTTAATAAGAAGAATAACTGATTCAGGATCAGGTACAGGATGAACAGTTTACCCTCCA
4. BR1        TAATTTAAGATTTTGACTTTTACCTCCTTCACTAATTCTTCTCTTAATAAGAAGAATAACTGATTCAGGATCAGGTACAGGATGAACAGTTTACCCTCCA
5. BR2        TAATTTAAGATTTTGACTTTTACCTCCTTCACTAATTCTTCTCTTAATAAGAAGAATAACTGATTCAGGATCAGGTACAGGATGAACAGTTTACCCTCCA
6. COL        TAATTTAAGATTTTGATTACTCCCTCCTTCATTAATTCTTCTTTTAATAAGAAGAATAACTGATTCAGGGTCTGGGACAGGATGAACGGTTTACCCCCCT

Species/Abbrv *****************□************************************□*□***********□******************************□
1. UR1        TTATCTAATAATTTAGCACATGCTGGAGCTTCAGTAGATATAACTATTTTTTCTCTTCATATAGCAGGAATTTCTTCAATTTTAGGGGCAATTAATTTTG
2. UR2        TTATCTAATAATTTAGCACATGCTGGAGCTTCAGTAGATATAACTATTTTTTCTCTTCATATAGCAGGAATTTCTTCAATTTTAGGGGCAATTAATTTTG
3. UR3        TTATCTAATAATTTAGCACATGCTGGAGCTTCAGTAGATATAACTATTTTTTCTCTTCATATAGCAGGAATTTCTTCAATTTTAGGGGCAATTAATTTTG
4. BR1        TTATCTAATAATTTAGCACATGCTGGAGCTTCAGTAGATATAACTATTTTTTCTCTTCATATAGCAGGAATTTCTTCAATTTTAGGGGCAATTAATTTTA
5. BR2        TTATCTAATAATTTAGCACATGCTGGAGCTTCAGTAGATATAACTATTTTTTCTCTTCATATAGCAGGAATTTCTTCAATTTTAGGGGCAATTAATTTTA
6. COL        TTATCTAATAATTTAGCCCATGCTGGAGCTTCAGTAGATATAACTATTTTTTCTTTACATATAGCAGGTATTTCTTCAATTTTAGGGGCAATTAATTTTG

Species/Abbrv *□**□********************□***********□*****□*****□**□********************□**□***********□***********
1. UR1        TTTCTACTATAATTAATATACGAGCTTCAGAAATAAACTTTGACAAACTTCCTTTATTAATTTGATCAATTGCTATCACAGCTATTCTTTTAATTATTTC
2. UR2        TTTCTACTATAATTAATATACGAGCTTCAGAAATAAACTTTGACAAACTTCCTTTATTAATTTGATCAATTGCTATCACAGCTATTCTTTTAATTATTTC
3. UR3        TTTCTACTATAATTAATATACGAGCTTCAGAAATAAACTTTGACAAACTTCCTTTATTAATTTGATCAATTGCTATCACAGCTATTCTTTTAATTATTTC
4. BR1        TTTCTACTATAATTAATATACGAGCTTCAGAAATAAACTTTGACAAACTTCCTTTATTAATTTGATCAATTGCTATCACAGCTATTCTTTTAATTATTTC
5. BR2        TTTCTACTATAATTAATATACGAGCTTCAGAAATAAACTTTGACAAACTTCCTTTATTAATTTGATCAATTGCTATCACAGCTATTCTTTTAATTATTTC
6. COL        TATCCACTATAATTAATATACGAGCGTCAGAAATAAATTTTGATAAACTCCCCTTATTAATTTGATCAATTGCCATTACAGCTATTCTCTTAATTATTTC

Species/Abbrv ******************□**□**□**□***□**□*□**□**□*****□*****************□**□**□********************□******
1. UR1        ATTACCAGTATTAGCAGGAGCAATTACAATATTATTAACAGATCGTAATTTAAATACATCATTTTTTGATCCTTCTGGAGGAGGAGACCCTATTTTATAC
2. UR2        ATTACCAGTATTAGCAGGAGCAATTACAATATTATTAACAGATCGTAATTTAAATACATCATTTTTTGATCCTTCTGGAGGAGGAGACCCTATTTTATAC
3. UR3        ATTACCAGTATTAGCAGGAGCAATTACAATATTATTAACAGATCGTAATTTAAATACATCATTTTTTGATCCTTCTGGAGGAGGAGACCCTATTTTATAC
4. BR1        ATTACCAGTATTAGCAGGAGCAATTACAATATTATTAACAGATCGTAATTTAAATACATCATTTTTTGATCCTTCTGGAGGAGGAGACCCTATTTTATAC
5. BR2        ATTACCAGTATTAGCAGGAGCAATTACAATATTATTAACAGATCGTAATTTAAATACATCATTTTTTGATCCTTCTGGAGGAGGAGACCCTATTTTATAC
6. COL        ATTACCAGTATTAGCAGGGGCCATCACTATACTACTTACTGACCGTAACTTAAATACATCATTTTTCGACCCATCTGGAGGAGGAGACCCTATCTTATAC

Species/Abbrv ******□***□□*
1. UR1        CAACATCTATTTT
2. UR2        CAACATCTATTTT
3. UR3        CAACATCTATCTT
4. BR1        CAACATCTATCTT
5. BR2        CAACATCTATTTT
6. COL        CAACATTTATTCT
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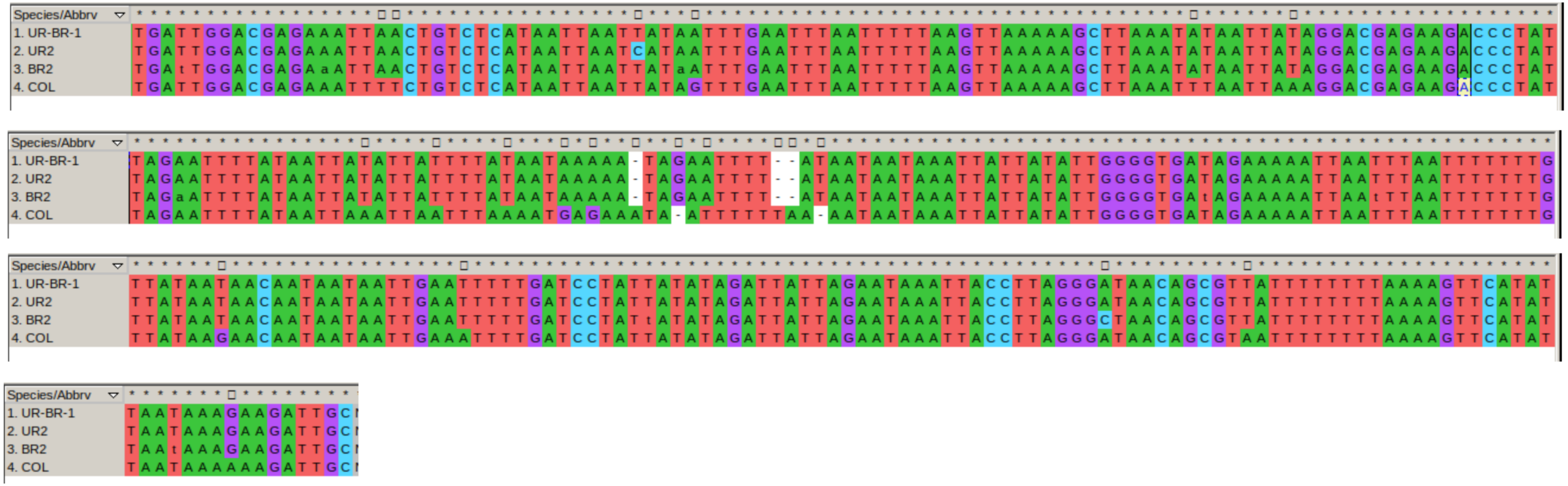
FigS1: Alignment of *P. flavipes* COI gene sequences. Blocks of 100bp are shown. First line in each block code is "*" for conserved position and a "square" for variable ones.

16S Alignment of *P. flavipes* samples (haplotypes)



Species/Abbrv	*****************□□****************□***□**********************************□******□******************
1. UR-BR-1	TGATTGGACGAGAAATTAACTGTCTCATAATTAATTATAATTTGAATTTAATTTTTAAGTTAAAAAGCTTAAATATAATTATAGGACGAGAAGACCCTAT
2. UR2	TGATTGGACGAGAAATTAACTGTCTCATAATTAATCATAATTTGAATTTAATTTTTAAGTTAAAAAGCTTAAATATAATTATAGGACGAGAAGACCCTAT
3. BR2	TGAtTGGACGAGAaATTAACTGTCTCATAATTAATTATaATTTGAATTTAATTTTTAAGTTAAAAAGCTTAAATATAATTATAGGACGAGAAGACCCTAT
4. COL	TGATTGGACGAGAAATTTTCTGTCTCATAATTAATTATAGTTTGAATTTAATTTTTAAGTTAAAAAGCTTAAATTTAATTAAAGGACGAGAAGACCCTAT

Species/Abbrv	****************□****□****□***□*□**□**□*□****□□*□***
1. UR-BR-1	TAGAATTTTATAATTATATTATTTTATAATAAAAA-TAGAATTTT--ATAATAATAAATTATTATATTGGGGTGATAGAAAAATTAATTTAATTTTTTTG
2. UR2	TAGAATTTTATAATTATATTATTTTATAATAAAAA-TAGAATTTT--ATAATAATAAATTATTATATTGGGGTGATAGAAAAATTAATTTAATTTTTTTG
3. BR2	TAGaATTTTATAATTATATTATTTTATAATAAAAA-TAGAATTTT--ATAATAATAAATTATTATATTGGGGTGAtAGAAAAATTAAtTTAATTTTTTTG
4. COL	TAGAATTTTATAATTAAATTAATTTAAAATGAGAAATA-ATTTTTTAA-AATAATAAATTATTATATTGGGGTGATAGAAAAATTAATTTAATTTTTTTG

Species/Abbrv	******□****************□**□*********□*********************
1. UR-BR-1	TTATAATAACAATAATAATTGAATTTTTGATCCTATTATATAGATTATTAGAATAAATTACCTTAGGGATAACAGCGTTATTTTTTTTAAAAGTTCATAT
2. UR2	TTATAATAACAATAATAATTGAATTTTTGATCCTATTATATAGATTATTAGAATAAATTACCTTAGGGATAACAGCGTTATTTTTTTTAAAAGTTCATAT
3. BR2	TTATAATAACAATAATAATTGAATTTTTGATCCTATtATATAGATTATTAGAATAAATTACCTTAGGGCTAACAGCGTTATTTTTTTTAAAAGTTCATAT
4. COL	TTATAAGAACAATAATAATTGAAATTTTGATCCTATTATATAGATTATTAGAATAAATTACCTTAGGGATAACAGCGTAATTTTTTTTAAAAGTTCATAT

Species/Abbrv	*******□********
1. UR-BR-1	TAATAAAGAAGATTGC
2. UR2	TAATAAAGAAGATTGC
3. BR2	TAAtAAAGAAGATTGC
4. COL	TAATAAAAAAGATTGC

FigS2: Alignment of *P. flavipes* *16S* gene sequences. Blocks of 100bp are shown. First line in each block code is “*” for conserved position and a “square” for variable ones.

28S Alignment of *P. flavipes* samples (haplotypes)

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Species/Abbrv ***************▯▯***********************************************************************************
1. UR-BR-1    ATGTCGCGTACCTCT--CGGGGTACGGGGCACGCGGTCGCGTCGCGTTATGTCCGGCGACGTGGGCGTGCACTTCTCCCCCGGTAGAACGTCGCGACCCG
2. COL        ATGTCGCGTACCTCTCGCGGGGTACGGGGCACGCGGTCGCGTCGCGTTATGTCCGGCGACGTGGGCGTGCACTTCTCCCCCGGTAGAACGTCGCGACCCG

Species/Abbrv *********************▯************************▯***▯*************************************************
1. UR-BR-1    TTGGGCGTCGGCATAAGGCCCGCACGGCACAGACTGTCCCGGCGTT-AAC-GCGCCCGGGGCAGACCGTCGCGGTTCGCCCGGCCGGCTGCCCGACGGTA
2. COL        TTGGGCGTCGGCATAAGGCCCACACGGCACAGACTGTCCCGGCGTTTAACCGCGCCCGGGGCAGACCGTCGCGGTTCGCCCGGCCGGCTGCCCGACGGTA

Species/Abbrv ****************************************************************************************************
1. UR-BR-1    CACGCACGGTATTTGGCCGCATCGAACGTG--CGCCCGGCCCGCCGCAAGCGCGGCCAGCGATTCCCGGTGGTCGGACCTAGCGCCGTCCCCGGGCCTGG
2. COL        CACGCACGGTATTTGGCCGCATCGAACGTG--CGCCCGGCCCGCCGCAAGCGCGGCCAGCGATTCCCGGTGGTCGGACCTAGCGCCGTCCCCGGGCCTGG

Species/Abbrv ***********************************************▯***************
1. UR-BR-1    TCAGCTGTTGGCGCGCGGTGTCCTCGGGCTGGCCAATCGAATTTACACAGAAATACCGGTCGG
2. COL        TCAGCTGTTGGCGCGCGGTGTCCTCGGGCTGGCCAATCGAATTTACAAAGAAATACCGGTCGG
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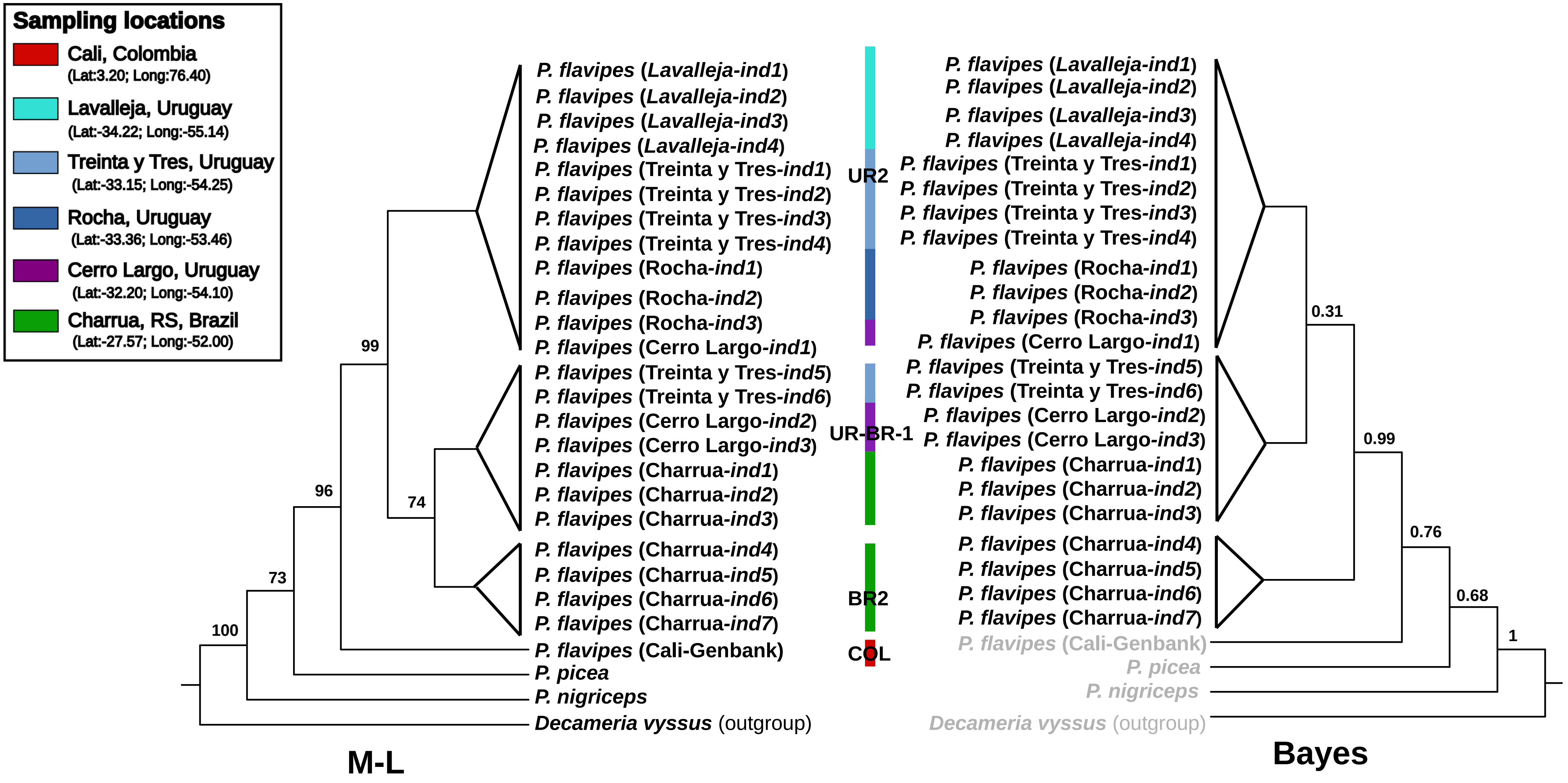
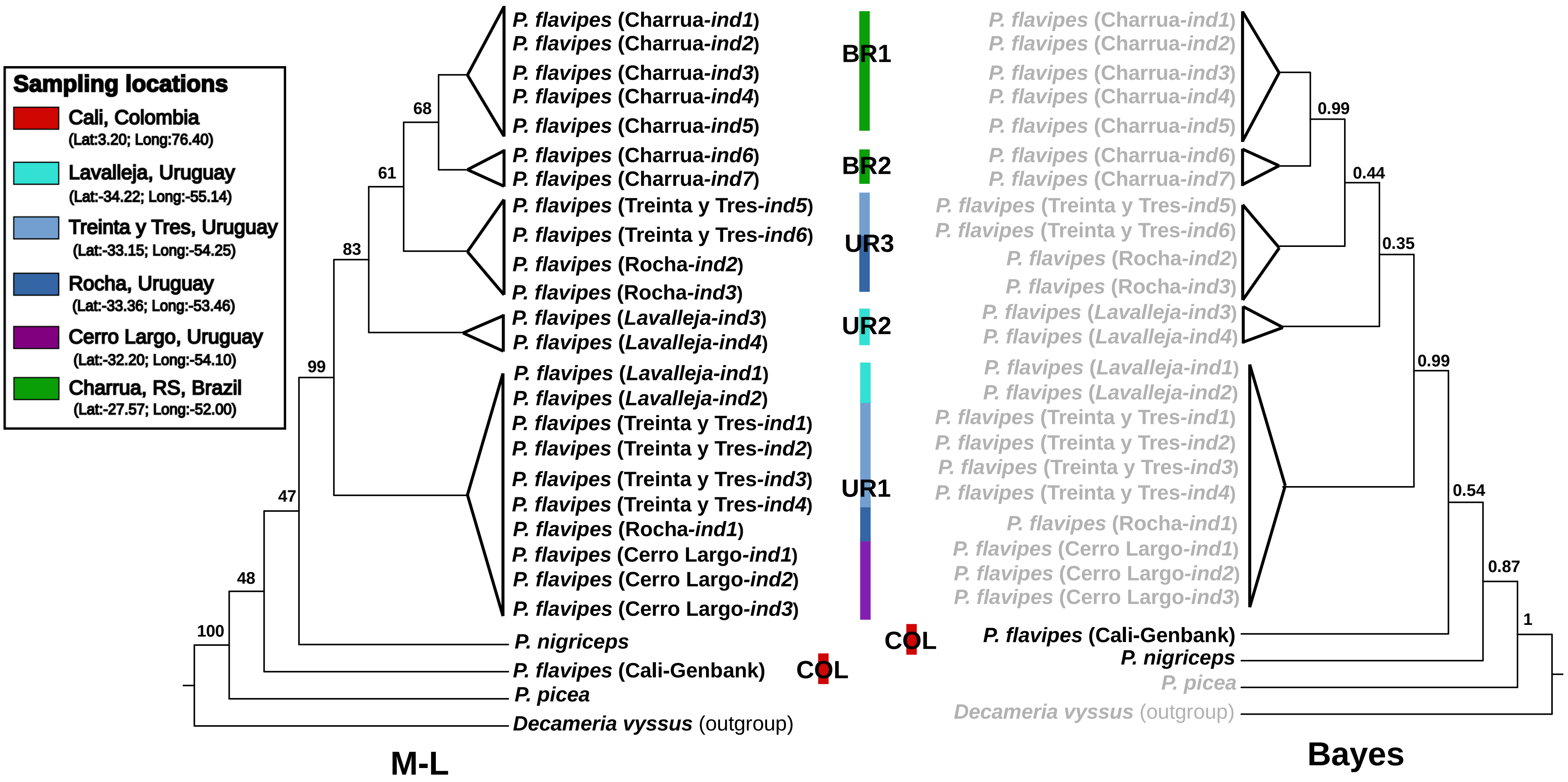
FigS3: Alignment of *P. flavipes* *28S* gene sequences. Blocks of 100bp are shown. First line in each block code is “*” for conserved position and a “square” for variable ones.

16S phylogeny



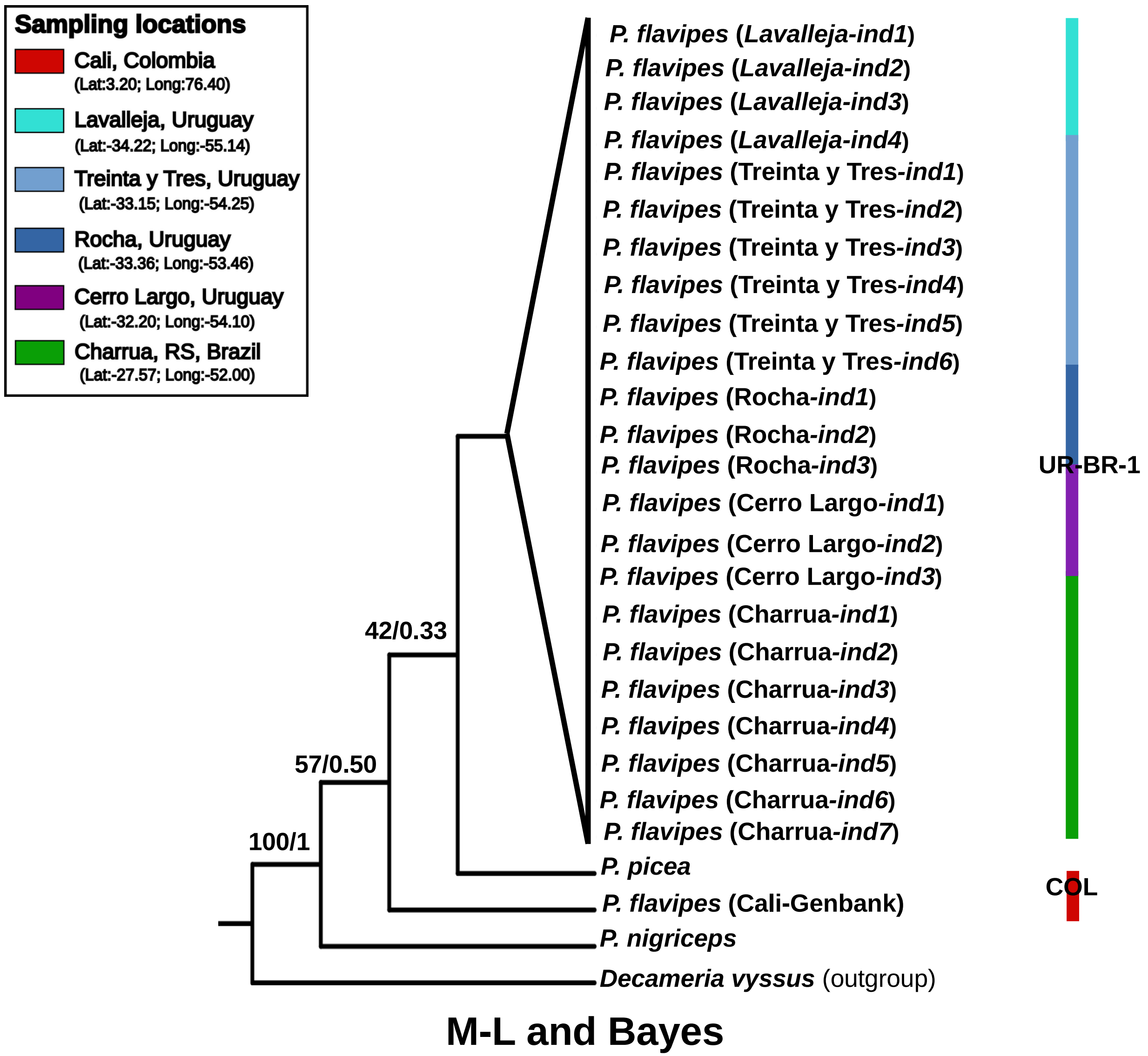
FigS4: *16S* gene; For Maximum likelihood (left, M-L) and Bayesian (right, Bayes) trees, bootstrap values and Bayesian posterior probability are shown at each node, respectively. Conserved relationships between methods presented in gray color and changes are in black at Bayes tree. Central lines color coded the geographical distribution and haplotype assigned name.

COI phylogeny



FigS5: *COI* gene; For Maximum likelihood (left, M-L) and Bayesian (right, Bayes) trees, bootstrap values and Bayesian posterior probability are shown at each node, respectively. Conserved relationships between methods presented in gray color and changes are in black at Bayes tree. Central lines color coded the geographical distribution and haplotype assigned name.

28S phylogeny



FigS6: *28S* gene; Phylogenetic tree, identical topology for Maximum likelihood (ML) and Bayesian methods. Values from Bootstrap (ML) and posterior probability (Bayesian) in each node. Individual name in each terminal node. Color code for geographical distribution and haplotype assigned name.