

Analyses of plumage coloration and genetic variation confirm the hybridization of *Pipra fasciicauda* and *Pipra aureola* in the Brazilian Amazon basin

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1 **Abstract**

2 The present study aimed to confirm the occurrence of a hybridization event between the Band-tailed Manakin
3 (*Pipra fasciicauda*) and the Crimson-hooded Manakin (*Pipra aureola*), based on the existence of a specimen
4 that presents morphological traits of both taxa. We analyzed 297 taxidermized skins of adult males of the two
5 species, including the potential hybrid. We also analyzed the mitochondrial (ND2, ND3 e COI) and nuclear
6 (FGB-I5, MB-I2 e GAPDH-I3) genes of 12 adult specimens of the two taxa, diagnosed phenotypically, in
7 addition to the potential hybrid. The analyses of the plumage indicated that the potential hybrid has an
8 intermediate pattern of white banding on the tail that is less extensive than that found in *Pipra fasciicauda*, but
9 that its other phenotypic traits are characteristic of *Pipra aureola*. The molecular topologies revealed two clades,
10 one that groups *P. aureola* together with the potential hybrid, and the other, that corresponds to *P. fasciicauda*.
11 These findings allowed us to confirm the occurrence of a process of hybridization and potential introgression
12 through secondary events in the *P. aureola* lineage.

13

14 Key words: Hybrids; intrageneric hybridization; introgression; manakins; Pipridae; secondary contact

15 **Introduction**

16 Hybridization and introgression events are common in birds, especially in closely-related species (De
17 Kort et al. 2002). These events have been interpreted as the result of many different processes, including the
18 influence of natural stimuli, the lack of potential mates of the same species or errors in conspecific recognition.
19 Grant and Grant (1992) concluded that hybridization events are extremely common in birds, occurring in
20 approximately one in every ten species, a process that may support the formation of new species (Toews
21 et al. 2018). In a recent study, Weir et al. (2015) concluded that hybridization in Amazonian birds may be a
22 consequence of the slow evolution of reproductive isolation, given that even taxa known to have diverged at
23 least four million years ago may hybridize when they come into contact.

24 The species of the family Pipridae, known as manakins, are a group of small Neotropical birds with an
25 ample distribution in the Amazon basin. There is a number of reported cases of hybridization in piprids,
26 including intra- and inter-generic matings, confirmed by both morphological traits and genetic analyses
27 (Brumfield et al. 2001). Both types of hybridization have been recorded in the genus *Pipra*, with intergeneric
28 matings between the Wire-tailed Manakin (*Pipra filicauda*) and White-crowned Manakin (*Pseudopipra pipra*)
29 (Graves 1993), Crimson-hooded Manakin (*Pipra aureola*) and Flame-crested Manakin (*Heterocercus linteatus*)
30 (Parkes 1961), and an intrageneric case between *P. aureola* and *P. filicauda*, a hybrid that was initially identified
31 as *Pipra heterocerca* (Haffer 1970).

32 Although no evidence of hybridization involving the Band-tailed Manakin (*Pipra fasciicauda*) has been
33 reported previously, an enigmatic specimen from the municipality of Acará, in the northern Brazilian state of
34 Pará, raised the possibility of hybridization in this species. In the present study, we investigated the probable
35 process of intrageneric hybridization/introgression between the sister species *P. fasciicauda* and *P. aureola*,
36 based on the analysis of plumage traits and molecular data.

37

38 **Material and Methods**

39 During an expedition to survey *Pipra fasciicauda* in the area of Acará, a known locality for the
40 occurrence of this species (Novaes and Lima 2009), PVC detected several individuals with plumage slightly
41 different from that of a typical *P. fasciicauda* and more similar to *P. aureola*. The plumage of these individuals
42 was more reddish in general than that of *P. fasciicauda*, and lacked the white band on the tail. Given these
43 characters, one specimen was collected for a more systematic evaluation, based on plumage patterns and

44 molecular data, in addition to a specimen with typical *P. fasciicauda* plumage. Specimen collection was
45 authorized by the Chico Mendes Institute of Biodiversity-ICMBio, through protocol number 44560-3. The
46 presence of *P. aureola* in this region was never well documented, but there are some recent reports from this
47 region, and the habitat in the study area appears to be favorable to the contact of the two species, given that it
48 represents a transition between ‘terra firme’ forest and ‘várzea’ (swamp) forests with *Heliconia* sp.

49 We analyzed the plumage patterns in 297 taxidermized skins of male manakins deposited in the
50 ornithological collection of the Emílio Goeldi Museum (MPEG: Museu Paraense Emílio Goeldi), in Belém.
51 These specimens included 190 *Pipra fasciicauda*, 106 *Pipra aureola*, and one individual with an intermediate
52 phenotype (the putative hybrid) between *P. fasciicauda* and *P. aureola*. We classified the plumage of the head,
53 throat, breast, and flanks, using Smithe’s (1975) color catalog, and determined the presence and configuration of
54 the white band in the tail to summarize the phenotypic differences between the study species.

55 We complemented this analysis of the plumage with genetic analyses of 13 samples of muscle tissue,
56 including nine *P. fasciicauda*, three *P. aureola*, and the putative hybrid. These specimens were collected from
57 six localities within the geographic ranges of the respective species (Fig 1), and were provided by the Emílio
58 Goeldi Museum (Online Resource 1). We extracted total genomic DNA using the Wizard Genomic DNA
59 Purification kit (Promega Corporation), following the protocol provided by the manufacturer. We used
60 Polymerase Chain Reaction (PCR) to amplify three mitochondrial markers (NADH dehydrogenase subunit 2
61 (ND2), NADH dehydrogenase subunit 3 (ND3), Cytochrome oxidase subunit I, COI), and three nuclear regions,
62 intron 5 of the Beta-fibrinogen gene (FGB-I5), intron 2 of the Myoglobin (MB-I2), and Glyceraldehyde 3-
63 phosphate dehydrogenase (GAPDH-I3). We determined the nucleotide sequences in an ABI 3500 automatic
64 sequencer (Applied Biosystems). We provide information on the primers and amplification conditions of each
65 gene or region analyzed in the present study in the Electronic Supplementary Material (Online Resource 2).

66 We edited the sequences in the FASTA format, corrected them in BioEdit version 7.1.3 (Hall 1999),
67 and aligned them automatically in CLUSTAL-W (Thompson et al 1994), an option from the above-mentioned
68 software. We codified the double peaks observed in the nuclear markers, which were confirmed as heterozygous
69 sites, based on the IUPAC nucleotide nomenclature. We concatenated the genes in Sequence Matrix version
70 1.7.8 (Vaidya et al. 2011). We further selected the optimum nucleotide substitution model in PartitionFinder,
71 version 1.1.1 (Lanfear et al. 2012), and identified the best partition of these data for the construction of the
72 Bayesian Inference topology, based on the Akaike Information Criterion, in MrBayes 3.2.0 (Huelsenbeck and

73 Ronquist 2001). We rooted the phylogenetic tree (multilocus and mitochondrial) at *P. filicauda* (N = 4), using
74 samples provided by the National Institute for Amazonian Research (INPA).

75

76 **Results**

77 Our morphological data indicate that the specimen collected in the region of Acará shares some
78 plumage traits with the males of both *Pipra fasciicauda* and *Pipra aureola*, but shows more similarities to the
79 latter species (Table 1). In the ventral view of the tail of the potential hybrid, the specimen presents the
80 continuous white band typical of *Pipra fasciicauda*, while in the dorsal view, only the three outer rectrices have
81 white marks, and no white coloration is exhibited when the bird is perched in a natural position. The flanks of
82 the potential hybrid have more black than *P. fasciicauda*, and the undertail coverts are almost entirely black, as
83 in *P. aureola*, also masking the white band of the rectrices when the bird is perched naturally, while in *Pipra*
84 *fasciicauda*, only a small distal portion is black, displaying the diagnostic white band of this species. More subtle
85 traits, such as the plumage of the head, throat, breast, the rudimentary blackish flanks, and the presence of a
86 partial white band indicate that *Pipra aureola* and *Pipra fasciicauda* are the parental species (Fig 2, Table 1).

87 The mitochondrial markers had a total of 2085 base pairs (bps), 901 bps for the ND2 gene (17 variable
88 sites), 385 bps for ND3 (13 variable sites), and 799 bps for COI (07 variable sites). We found no
89 insertion/deletions (indels), stop codons or ambiguous peaks in the electropherograms of these markers,
90 confirming their mitochondrial origin. The nuclear markers generated a database of 1566 bps, with 390 bps for
91 the GAPDH-I3, 537 bps for the FGB-I5, and 639 bps for the MB-I2. Overall, we found two polymorphisms sites
92 in the GAPDH-I3 fragment and seven in the FGB-I5 sequence, although we found no polymorphic sites in the
93 MB-I2. The concatenated genes were arranged in the following order: FGB-I5, COI, GAPDH-I3, MB-I2, ND2
94 and ND3, and the program indicated that the codons provided the best arrangement for the understanding of
95 partitioning the data. We identified the GTR+I+G model as the optimum evolutionary model for the FGB-I5
96 sequences, the HKY+I+G model for the COI gene (codon 1), the K80+I for COI (codon 2), and the F81 model
97 for COI (codon 3). We also identified the F81+I model as the optimum for the GAPDH-I3 sequences, the F81
98 model for MB-I2, the HKY+I model for ND2 (codon 1), the F81 model for ND2 (codon 2), and the HKY for the
99 ND2 (codon 3) sequence, as well as the HKY for the ND3 sequence (codons 1 and 2) and the K80 model for
100 ND2 (codon 3).

101 The topologies produced by the mitochondrial (Online Resource 3) and multilocus (Fig 1) datasets are

102 congruent, with two main clades, one that groups the *P. aureola* specimens and the hybrid (Pfa40), and the other
103 that includes the *P. fasciicauda* specimens. The topology based on the nuclear data alone (not shown) did not
104 provide a clear phylogenetic interpretation of the two species, given that the intrageneric variation in the nuclear
105 genes did not differentiate *P. fasciicauda* from *P. aureola*. Given this, the potential hybrid did not present
106 heterozygous sites that allowed the contribution of the parental ancestors to be interpreted. This precludes the
107 confirmation of *P. fasciicauda* as the paternal lineage, based on the genetic data. All the sequences generated in
108 the present study were deposited in GenBank (www.ncbi.nlm.nih.gov) under access numbers MN128472
109 through MN128514 for mitochondrial genes and MN166326 through MN166360 for nuclear genes (Online
110 Resource 1).

111

112 Discussion

113 Based on the integrated analysis of morphological, molecular, and zoogeographic data, we conclude
114 that the hybrid specimen was the product of a process of hybridization between *Pipra fasciicauda* and *Pipra*
115 *aureola*, with a subsequent introgression event involving the *P. aureola* lineage, given that the specimen in
116 question presents more morphological similarities with *P. aureola*. This indicates the possible existence of a
117 sympatric zone between the two taxa, given that a specimen of *P. fasciicauda* (Pfa41) was collected at the same
118 site as the potential hybrid (Fig 1), which was previously considered to be part of the geographic distribution of
119 only *P. fasciicauda*. Sympatry between closely-related piprids has been reported previously in the Amazonian
120 basin. In particular, this species is distributed in the region of the mouth of the Tapajós River (Haffer 1970,
121 1997), and the lower Xingu and Tocantins rivers (Ridgely and Tudor 1994), which is the region where the
122 potential hybrid analyzed in the present study was collected. However, no integrated analysis of the
123 morphological and molecular data had been applied previously to specimens from this region to confirm the
124 possible existence of interspecific hybrids. Haffer (1970) concluded that an ample hybrid zone between *P.*
125 *aureola* and *P. fasciicauda* certainly did not exist, but that the occurrence of isolated hybrids in contact zones
126 may eventually be detected. The results of the present study corroborate this hypothesis.

127 Interspecific hybridization in the genus *Pipra* was confirmed by Haffer (1970), who concluded that the
128 morphological description of a hybrid, denominated *P. heterocerca*, was in fact the result of a cross between *P.*
129 *aureola* and *P. filicauda*. The hybrid described in the present study, which appears to be the result of the
130 crossing of *P. fasciicauda* and *P. aureola*, provides additional evidence that this type of hybridization is not

131 unusual in this genus. Some authors have discussed the circumstances that may promote heterospecific mating.
132 Aspects of the behavior and evolution of *P. fasciicauda* and *P. aureola* may have facilitated hybridization, in
133 particular, the similarities of their prenuptial rituals, which include the formation of leks and the elaborate
134 courtship behavior, together with the morphological similarities of the different forms. Analyzing vocal
135 repertoires, Curé et al. (2010) found that closely-related species may interact and respond to each other, despite
136 their other differences. As sister taxa, it seems likely that *P. fasciicauda* and *P. aureola* will have similar
137 vocalizations (Sick 1997), and PVC conducted tests (unpublished data) of song recognition in these two manakin
138 species (*P. fasciicauda* and *P. aureola*) and in hybrids from the Acará area, and obtained high rates of response
139 from hybrids to the songs and calls of both parent species, as well as positive responses using records of *P.*
140 *fasciicauda* and *P. aureola* to attract each other. Alatalo et al. (1990) also highlighted a combination of plumage
141 and vocal traits that contribute to hybridization, by causing errors in the recognition of conspecific males.

142 Our analysis on the morphology of the hybrid indicates a plumage pattern shared by *P. aureola* and *P.*
143 *fasciicauda*, with more characters being similar to *P. aureola*. The genetic data also indicated that this species
144 represented the maternal lineage. This suggests that, following hybridization, a process of introgression
145 occurred through secondary crosses with the *P. aureola* lineage. It thus seems likely that the hybrid is not the
146 product of a first generation cross, given that the only trait it shares with *P. fasciicauda* is the white band on the
147 tail, which is never observed in *P. aureola*. Introgression events have been reported in manakins (Dias et al.
148 2018; Weir et al. 2015), which indicates that phylogenetic proximity and recent divergence times facilitate the
149 maintenance of the fertility of the hybrids, and the subsequent occurrence of introgression events.

150 We emphasize the importance of understanding how the efficacy of interspecific sexual interactions
151 influences the evolution of a hybrid zone, especially given that the potential backcrossing of hybrids with either
152 parent species may eventually lead to introgression (Rezende et al. 2013). In this case, hybridization and
153 introgression are mechanisms that may have a direct influence on the evolution of this bird group and,
154 depending on the effectiveness of pre- and post-zygotic barriers, may also affect genetic variation and speciation,
155 creating fundamental difficulties for the delimitation of taxa and the interpretation of their phylogenetic
156 relationships (Toews et al. 2018, Dias et al. 2018).

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202 **Figure Caption**

203

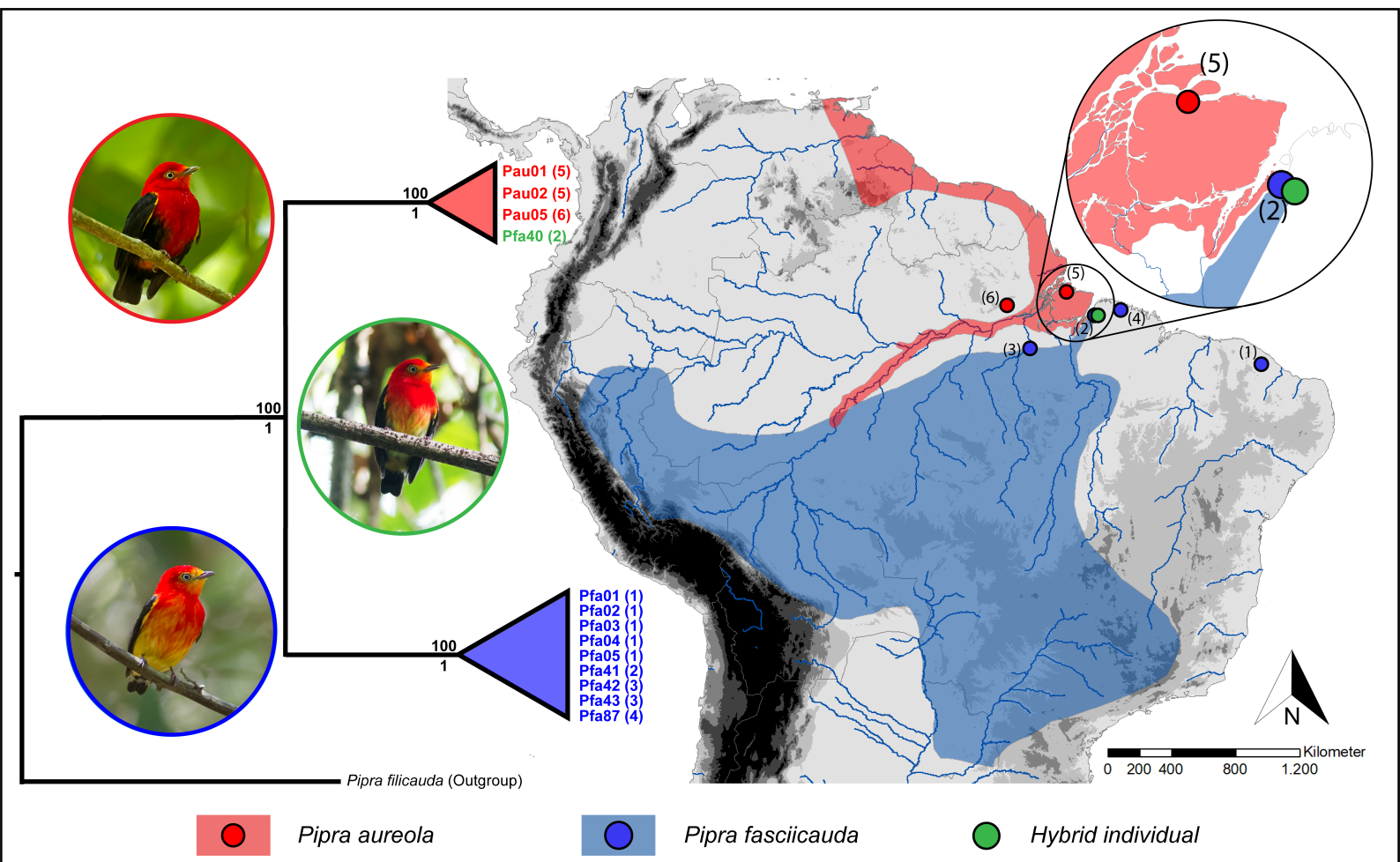
204 **Fig 1** Geographic distribution of *Pipra fasciicauda* (blue) and *Pipra aureola* (red), showing the collecting sites
 205 of the genetic data analyzed in the present study (Online Resource 1) and the topology of the Maximum
 206 Likelihood and Bayesian Inference analyses of *Pipra fasciicauda*, *Pipra aureola* and the potential hybrid, based
 207 on the multilocus data (ND2, ND3, COI, FGB-I5, MB-I2, GAPDH-I3) with *Pipra filicauda* as the outgroup. The
 208 numbers within parentheses correspond to those of the collecting sites identified in the Online Resource section,
 209 and the inset in the upper right portion of the map is a closeup of the region of Acará, where the specimens of the
 210 potential hybrid and typical *P. fasciicauda* were collected. Photographs are provided in the phylogenetic tree to
 211 show the parental species and the potential hybrid, *Pipra aureola*, outlined in red (credit: Ciro Albano), *Pipra*
 212 *fasciicauda*, outlined in blue, and the potential hybrid from the Acará region, outlined in green (credit: Pablo
 213 Vieira Cerqueira). The numbers above and below the branches correspond to the nonparametric bootstrap and
 214 posterior probabilities, respectively. The species distribution shape files were adapted from BirdLife
 215 International-Data Zone

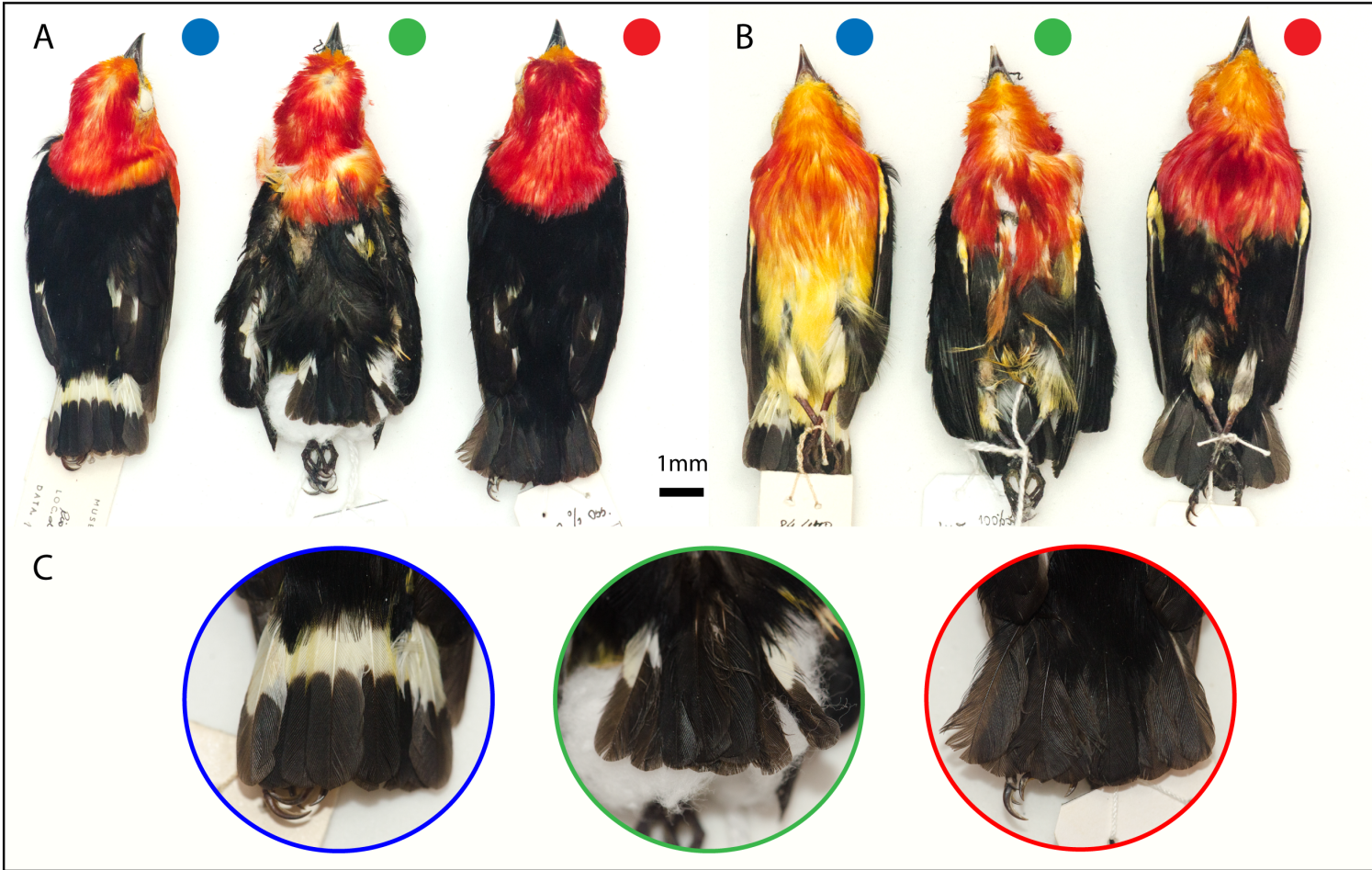
216

217 **Fig 2** Specimens showing plumage characters of each parental species, with the red and blue colors representing
 218 *Pipra aureola* and *Pipra fasciicauda*, respectively, and the potential hybrid in green. A) Dorsal view, B) Ventral
 219 view, and C) Closeups of the dorsal portion of the tail, showing the pattern of the white band: *P. fasciicauda*
 220 presents a complete white band, *P. aureola* lacks the band, and the potential hybrid presents an incomplete band
 221 with white marks on only the three outer rectrices. Voucher numbers: *Pipra fasciicauda* (MPEG 35883), Hybrid
 222 individual (MPEG 82869) and *Pipra aureola* (MPEG 47486)

Table 1 Comparison of the plumage coloration of *Pipra fasciicauda*, *Pipra aureola*, and the potential hybrid, including the crown, throat, breast, flanks, and the presence of the white band on the tail.

		<i>Pipra fasciicauda</i>	Hybrid	<i>Pipra aureola</i>
Crown		Geranium (#12) and Orange Yellow (#18)	Geranium (#12)	Geranium (#12)
Throat		Orange Yellow (#18) finely tinged of Flame Scarlet (#15)	Flame Scarlet (#15)	Flame Scarlet (#15)
Breast		Flame Scarlet (#15)	Geranium (#12)	Geranium (#12)
Flanks		Orange Yellow (#18)	Jet Black (#89) Less extensive than in <i>P. aureola</i>	Jet Black (#89)
Presence of white tail bands	Dorsal view	Yes	No (Only in the three outer rectrices)	No
	Ventral view	Yes	Yes	No





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Online Resource 1. The *Pipra aureola* and *Pipra fasciicauda* specimens analyzed in the present study and *Pipra filicauda* used as out-group, with information on the identification of the specimens and the markers sequenced with their respective GenBank access codes. The markers not sequenced in each individual are indicated by a minus (-) sign. The specimens were obtained from the ornithological collections of the Goeldi Museum (Museu Paraense Emílio Goeldi: MPEG*) in Belém and the National Institute for Amazonian Research (INPA) in Manaus, Brazil.

Collect point (Map)	Taxon	Laboratory code	Tombo	Collection	Locality	Geographical coordinates	ND2	ND3	COI	FGB-I5	MB-I2	GAPDH-I3
01	<i>P. fasciicauda</i>	Pfa01		MPEG*	Brasil, Ceará, Guaramiranga, Serra de Baturité, Parque das Trilhas	04° 16' 06" S; 38° 56' 14" W	MN128 475	MN128 506	MN1 2849 1	MN166 352	MN166 326	MN166340
01	<i>P. fasciicauda</i>	Pfa02		MPEG*	Brasil, Ceará, Guaramiranga, Serra de Baturité, Parque das Trilhas	04° 16' 06" S; 38° 56' 14" W	MN128 476	MN128 507	MN1 2849 2	MN166 353	MN166 327	MN166341
01	<i>P. fasciicauda</i>	Pfa03		MPEG*	Brasil, Ceará, Guaramiranga, Serra de Baturité, Parque das Trilhas	04° 16' 06" S; 38° 56' 14" W	MN128 477	MN128 508	MN1 2849 3	MN166 354	MN166 328	MN166342
01	<i>P. fasciicauda</i>	Pfa04		MPEG*	Brasil, Ceará, Guaramiranga, Serra de Baturité, Parque das Trilhas	04° 16' 06" S; 38° 56' 14" W	MN128 478	MN128 509	MN1 2849 4	MN166 355	MN166 329	MN166343
01	<i>P. fasciicauda</i>	Pfa05		MPEG*	Brasil, Ceará, Guaramiranga, Serra de Baturité, Parque das Trilhas	04° 16' 06" S; 38° 56' 14" W	MN128 479	MN128 510	MN1 2849	MN166 356	MN166 330	MN166344
02	Ambiguous individual	Pfa40		MPEG*	Brasil, Pará, Acará, Comunidade Menino Jesus	01°29'14" S; 48°18' 57" W	MN128 480	MN128 511	MN1 2849 6	MN166 357	MN166 331	MN166345
02	<i>P. fasciicauda</i>	Pfa41		MPEG*	Brasil, Pará, Acará, Comunidade Menino Jesus	01°29'14" S; 48°18' 57" W	-	MN128 512	MN1 2849 7	MN166 358	MN166 332	MN166346

03	<i>P. fasciicauda</i>	Pfa42	55524	MPEG*	Rio Xingu, Altamira, Ilha da Taboca, UHE Belo Monte	3°22'63"S, 51°57'57"W	MN128 481	MN128 513	MN1 2849 8	MN166 359	MN166 333	MN166347
03	<i>P. fasciicauda</i>	Pfa43	55525	MPEG*	Rio Xingu, Altamira, Ilha da Taboca UHE Belo Monte	3°22'83"S, 51°57'15"W	MN128 482	MN128 514	MN1 2849 9	MN166 360	MN166 334	MN166348
04	<i>P. fasciicauda</i>	Pfa87		MPEG*	Primavera, Pará		MN128 483	-	MN1 2850 0	-	-	-
05	<i>P. aureola</i>	Pau01	A8491	MPEG*	Brasil, Pará, Ilha do Marajó, Município de Chaves, Fazenda Anjos	00°11'18,6"S; 49°53'11,3"W	MN128 472	-	MN1 2848 8	MN166 349	MN166 335	MN166337
05	<i>P. aureola</i>	Pau02	58085	MPEG*	Brasil, Pará, Ilha do Marajó, Município de Chaves, Fazenda Anjos	00°11'18,6"S; 49°53'11,3"W	MN128 473	-	MN1 2848 9	MN166 350	-	MN166338
06	<i>P. aureola</i>	Pau05	66561	MPEG*	Brasil, Pará, Almeirim, FLOTA do Paru	00°56'S; 53°14'W	MN128 474	MN128 505	MN1 2849 0	MN166 351	MN166 336	MN166339
	<i>P. filicauda</i>	Pfi12	INPA A 611	INPA	ESEC Juami-Japurá; boca do Rio Juami; margem direita do Rio Japurá, ca 70 km WNW Japurá		MN128 484	-	MN1 2850 1	-	-	-
	<i>P. filicauda</i>	Pfi13	INPA A 962	INPA	Ilha do Barbado, Rio Solimões, ca 60 km E de Tefé		MN128 485	-	MN1 2850 2	-	-	-
	<i>P. filicauda</i>	Pfi15	INPA A 1052	INPA	Parque Nacional Viruá, margem direita do Rio Anauá, localidade "Campinho"		MN128 486	-	MN1 2850 3	-	-	-

P. filicauda

Pfi16

INPA A
2095

Caracaraí; Vista Alegre;
margem esquerda do Rio
Branco; ca 26 Km W da
base do Parque Nacional do
Vuruá

MN128
487

-

MN1
2850

-

-

-

Analyses of plumage coloration and genetic variation confirm the hybridization of *Pipra fasciicauda* and *Pipra aureola* in the Brazilian Amazon basin

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Online Resource 2 Genes analyzed in the present study, with their respective primers and nucleotide sequences

Gene	Primer	Sequence	Reference
ND3	L10755	5' GACTTCCAATCTTTAAAATCTGG 3'	Chesser 1999.
	H11151	5' GATTTGTTGAGCCGAAATCAAC 3'	Chesser 1999.
ND2	L5216	5' GGCCCATACCCGRAAAT 3'	Hackett 1996.
	H6313	5' CTCTTATTTAAGGCTTTGAAGGC 3'	Hackett 1996.
COI	FISHF1	5' TCAACCAACCACAAAGACATTGGCAC 3'	Ward et al. 2005.
	COIA	5' AGTATAAGCGTCTGGGTAGTC 3'	Palumbi and Benzie 1991.
FGB-I5	FIB5	5' CGCCATACAGAGTATACTGTGACA 3'	Driskell and Cristidis 2004.
	FIB6	5' GCCATCCTGGCGATTCTGAA 3'	Driskell and Cristidis 2004.
MB-I2	MYO2	5' GCCACCAAGCACAAAGATCCC 3'	Heslewood et al. 1998.
	MYO3F	5' GCAAGGACCTTGATAATGACTT 3'	Slade et al. 1993.
GAPDH-I3	G3PDH13b	5' TCCACCTTTGATGCGGGTGCTGGCAT 3'	Fjeldsa et al. 2003.
	G3PDH14b	5' AAGTCCACAACACGGTTGCTGTA 3'	Fjeldsa et al. 2003.

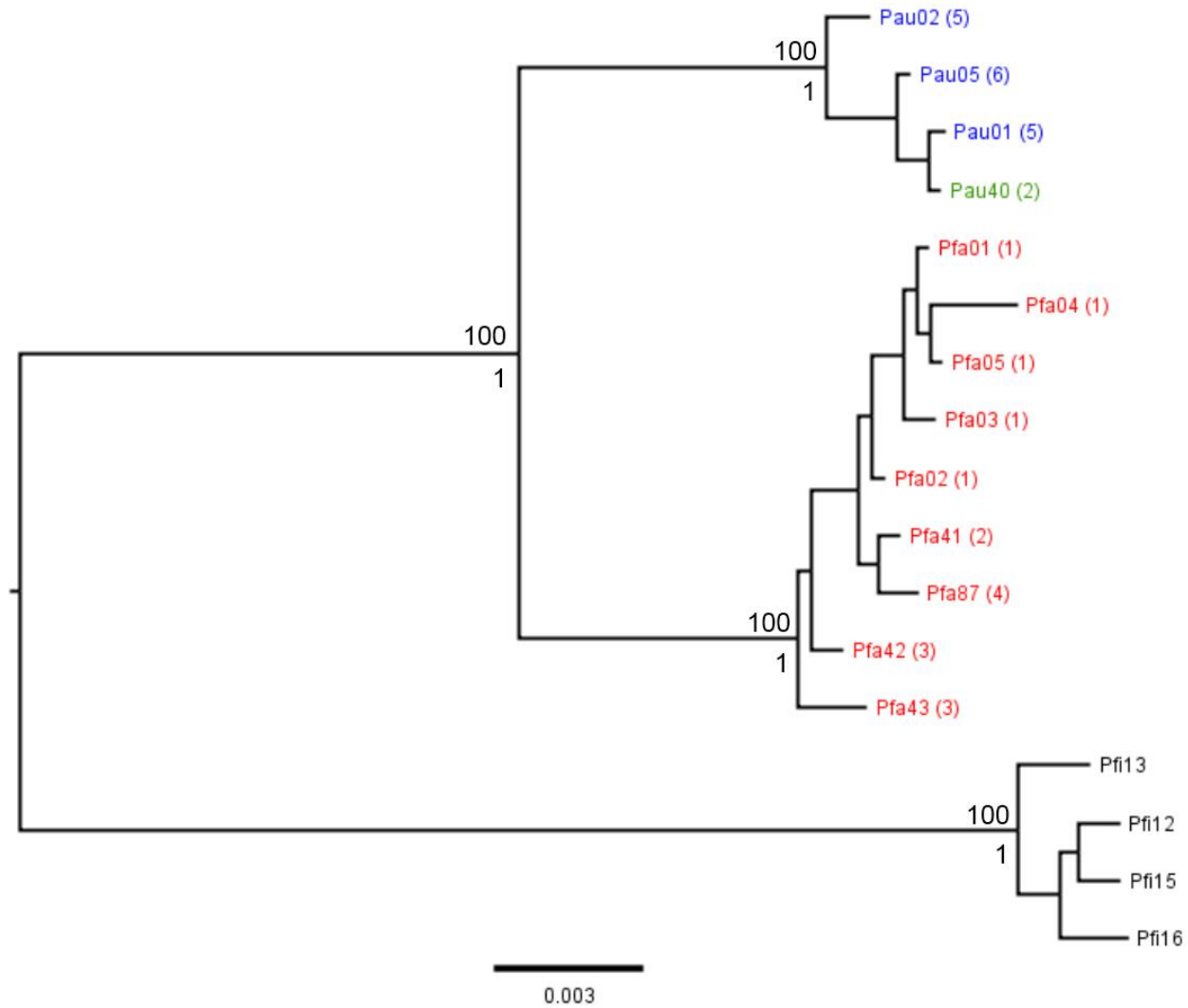
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Online Resource 3 Bayesian inference topology of *Pipra fasciicauda* (Pfa) and *Pipra aureola* (Pau), with *a posteriori* values below the branches and bootstrap values above.

The topology was rooted by *Pipra filicauda* (Pfi)