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# Deceiving colors: recognition of color morphs as separate species in orchid bees is not supported by molecular evidence

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**Abstract** – The orchid bees includes many species whose integument color is predominantly metallic, in particular those from the genus *Euglossa*. In the Atlantic Forest, some species exhibit color variation that seems to be linked with their distribution, with warmer colors (green, with coppery and reddish tones) in lower latitudes and cooler colors (blue, with purple shades) in higher latitudes. Contrasting taxonomic interpretations of this color variation lead to the recognition of distinct species for the different color morphs. In all three case studies investigated in this work (*Euglossa iopocila*, *Euglossa stellfeldi*, and *Euglossa townsendi*), the different forms were sampled throughout their distribution. Thirty samples from 16 different localities were used, which had their DNA extracted, amplified, and sequenced for fragments of the genes cytochrome b (cytb) and cytochrome C oxidase subunit 1 (CO1). A concatenated data matrix, totaling 1,089 bp, was submitted for Bayesian and maximum likelihood analyses. The resulting phylogenetic trees, together with the estimated genetic distances between samples, led to the conclusion that the different color morphs in all the three case studies do not represent separate species, but only integumental color variations of their respective species.

## Atlantic Forest / Euglossini / mtDNA / molecular taxonomy

### 1. INTRODUCTION

Orchid bees are a charismatic insect group in the Neotropical fauna, being widely known for their close association with flowers, most notably from Orchidaceae, that offer floral volatiles as reward. Many orchid bee species are also recognized for their brilliant metallic integumental coloration. In species of *Euglossa*, greenish coloration predominates, with variable tones and nuances ranging from copper (as in *Euglossa pleosticta* Dressler) to bluish (as in *Euglossa viridis* Perty). Many species, however, have their dominant integument color deep blue,

even sometimes verging on purple tones, as in *Euglossa iopyrrha* Dressler (Dressler 1982a, b).

Characters of integumental coloration have been used frequently by taxonomists within the genus *Euglossa*. These generally involve color of specific structures, such as the clypeus (Rebêlo and Moure 1996) and terminal terga (Dressler 1982a). Faria and Melo (2007) were the first to document the variation of general integumental color among individuals from the same species. According to them, *Euglossa iopocila* Dressler, 1982, and *Euglossa stellfeldi* Moure, 1947, include both blue and green specimens throughout their distribution. In the same study, they also discuss *Euglossa anodorhynchi* Nemésio, 2006, a species proposed for its predominantly blue integument color, but which is very similar structurally to *Euglossa townsendi* Cockerell.

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Faria and Melo (2007) also remarked that this kind of variation follows a latitudinal pattern, with green individuals occurring in the northern portions of their distribution and blue individuals occurring farther south along the Atlantic Forest, in eastern Brazil. Furthermore, specimens of *E. iopoecila* and *E. stellfeldi* with intermediate coloration (greenish-blue color) were documented at the middle of the species distribution (northeastern coast of São Paulo and southeastern coast of Rio de Janeiro), possibly revealing the existence of hybridization zones.

Nemésio (2009), in a review of orchid bees of the Atlantic Forest, stated that coloration is genetically defined and should be given the same weight as other morphological characters already used in the group. He proposed that integument color should be recognized as a valid taxonomic character, strong enough to sustain the proposal of new species. Furthermore, he discussed the noticeable influence of humidity on coloration, which can be seen while drying and humidifying pinned specimens in collections. While drying, individuals tend to become more reddish and, after humidifying, they shift to more bluish tones. Although humidity's influence was recognized, Nemésio rejected the notion that latitudinal humidity variation could be responsible for color variation within species. Based in these arguments, Nemésio (2009) proposed new species, some morphologically similar to those species cited by Faria and Melo (2007), basing taxonomic decisions mainly on color characters. The details involving the three case studies here discussed are summarized below.

*E. iopoecila* case study Nemésio (2009) did not agree with the interpretation of Faria and Melo (2007) for *E. iopoecila* and argued that the northern green morph should be treated as a separate species, proposing for it the name *Euglossa roubiki* Nemésio, 2009. Under his view, the name *E. iopoecila* would apply only to the southern blue morph.

*E. stellfeldi* case study Nemésio (2009) misapplied the name *E. stellfeldi*, using it for the species known as *Euglossa annectans* Dressler, 1982. For *E. stellfeldi* proper (sensu Faria &

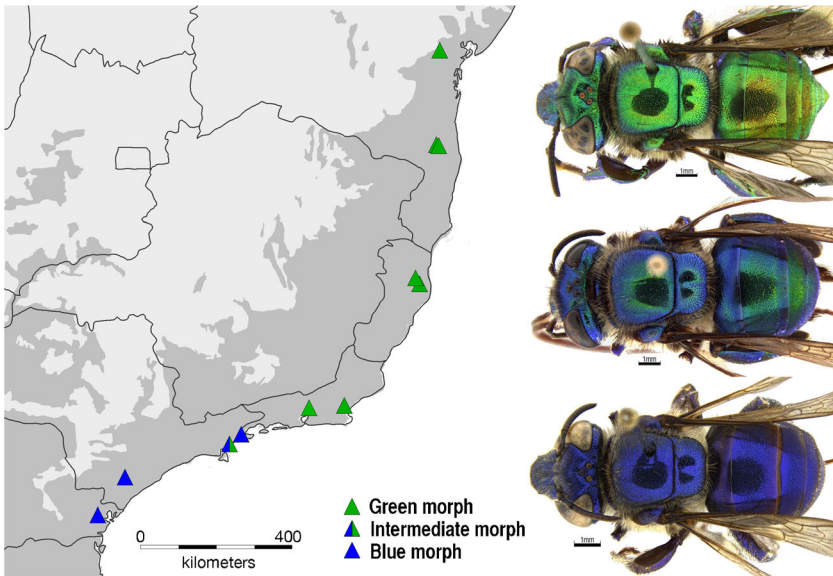
Melo), he used two different names, *Euglossa solangeae* Nemésio, 2007, for the greenish blue morph found at the southern portion of the distribution, and reinstated the name *Euglossa carinilabris* Dressler, 1982, for the northern green morph. This latter name had been synonymized under *E. stellfeldi* by Faria and Melo (2007).

*E. townsendi* case study Rebêlo and Moure (1996) interpreted *E. townsendi*, a species described originally from Mexico, as having a very wide distribution, ranging from Mexico to Argentina. Nemésio (2009), upon comparing the holotype of *E. townsendi* with similar females from southeastern Brazil, reached the conclusion that they could not be conspecific and proposed the name *Euglossa aratingae* for the latter population. Additionally, another recently described species, *E. anodorhynchi* Nemésio, 2006, ranging from coastal areas of Santa Catarina to southern São Paulo, presents an identical morphology to *E. townsendi*, except for its strong blue integument color, leading Faria and Melo (2007) to suggest that *E. anodorhynchi* could “represent only a color variation within a more widely distributed taxon.”

Considering the opposing taxonomic views, we conducted a study in which sequence data from two mitochondrial gene fragments were used to explore the boundaries between the color morphs of these three *Euglossa* cases in order to elucidate the identity of the biological units involved.

## 2. MATERIALS AND METHODS

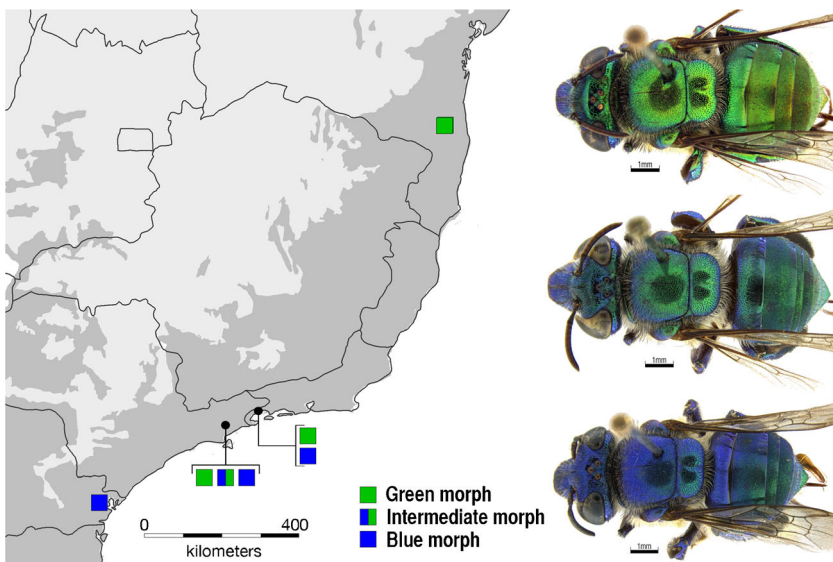
For extraction of molecular data, 41 recently collected males (maximum age of 4 years after collection) and one female from 18 localities in Brazil and Mexico were used. Different color specimens were used for each case, including blue, green, and, when available, intermediate color individuals (Figures 1, 2, and 3). The specimens were attracted using the protocols of Dodson et al. (1969), where artificial



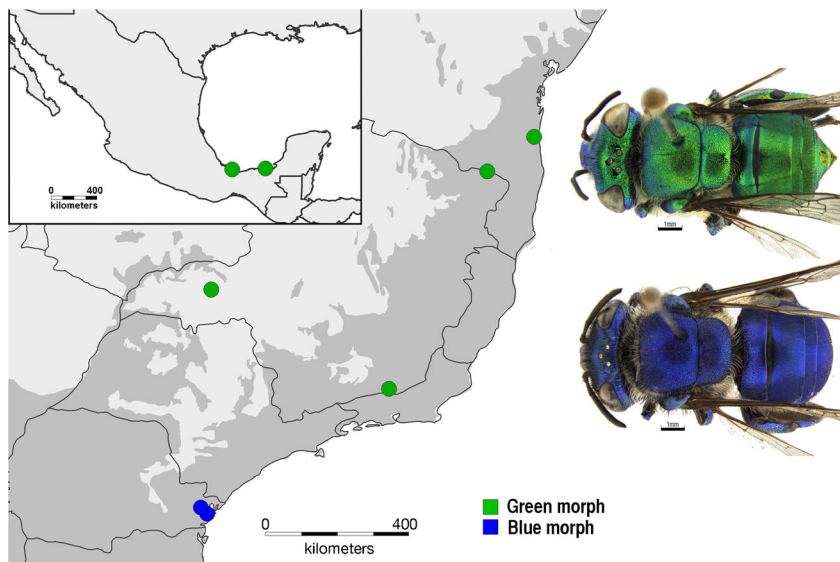
**Figure 1.** Map of eastern Brazil showing the geographic origin of the specimens of *Euglossa iopoeila* used in the present study. Original distribution of the Atlantic forest is indicated in *darker gray*. Different color morphs are illustrated at the *right*.

scents are used to attract euglossine males that are captured with entomological nets. Specimen data

for the samples that were successfully amplified and sequenced are presented in Table I.



**Figure 2.** Map of eastern Brazil showing the geographic origin of the specimens of *Euglossa stellfeldi* used in the present study. Original distribution of the Atlantic forest is indicated in *darker gray*. Different color morphs are illustrated at the *right*.



**Figure 3.** Maps showing the geographic origin of the specimens of *Euglossa townsendi* used in the present study. Original distribution of the Atlantic forest in eastern Brazil is indicated in *darker gray*. Different color morphs are illustrated at the *right*.

Maps showing the geographic origin of the sequenced specimens (Figures 1, 2, and 3) and the known distribution of *E. townsendi* (including the taxa described as *E. anodorhynchi* and *E. aratingae*), based on specimens deposited in the entomological collection of the Universidade Federal do Paraná (Figure 4), were prepared in Diva-Gis 7.5.0.

The genetic material was extracted from mesosomal muscular tissue (with four exceptions, BFt02, BFt03, BFt07, and BFt08, where genetic material was extracted from leg maceration) with the EZ-DNA Extraction Kit (Biosystems®, Brazil). For polymerase chain reactions (PCRs), we used Mastercycler Personal and Mastercycler Gradient thermocyclers (Eppendorf) and the following reagents: 2–5  $\mu$ L of DNA sample, 2.5  $\mu$ L of 10 $\times$  PCR buffer (Invitrogen), 2.5  $\mu$ L of MgCl<sub>2</sub> (25 mM), 0.4  $\mu$ L of dNTPs (25 mM), 1  $\mu$ L of each primer (25 mM), 0.2  $\mu$ L of Platinum® Taq DNA Polymerase (Invitrogen), and with the final volume of 25  $\mu$ L obtained by addition of Milli-Q autoclaved water.

Two gene fragments were amplified: cytochrome c oxidase subunit 1 (CO1) and cytochrome b (cytb) with the usage of the universal primers HCO and LCO (CO1; Folmer et al. 1994) and mtD-26 and

mtD-28 (cytb; Simon et al. 1994). These fragment positions were referenced with the complete mitochondrion genome of *Apis mellifera* Linnaeus (Crozier and Crozier 1993), to identify CO1 (1837-2494, 657 bp) and cytb (11428-11860, 432 bp). The successful amplified samples were sent to Macrogen in South Korea for purification and sequencing with an ABI 3730xl DNA Analyzer (Applied Biosystems) sequencer.

Sequence data from additional species of Euglossina and of other subtribes in Apini were included in the analyses in order to provide topological structuring for the resulting phylograms and to allow for simultaneous analysis of the three cases here investigated. These sequences were taken from GenBank, and their data are detailed in Table II. All the sequences were edited using Geneious R6 (Biomatters Ltd., 2005–2013) and aligned in the same software by using the MAFFT multiple aligner v 1.3 plugin (Katoh et al. 2002) to produce a concatenated matrix with both genes. From this matrix, genetic pairwise *p* distances were calculated using MEGA v5.2 (Tamura et al. 2011).

The Bayesian phylogenetic reconstruction was performed through CIPRES Science Gateway online

**Table 1.** List of specimens of *Euglossa* included in this study, separated by taxonomic case, with their respective voucher code, color morph, collecting data, and GenBank accession numbers

Case study	Code	Color morph	Specimen data	GenBank accession no.	
				COI	cytb
<i>E. townsendi</i>	BFt01	Green	Brazil, Bahia Ilhéus, UESC, 14.798° S, 39.172° W, 15 January 2010, G. Melo	–	KF443111
	BFt02	Green	Brazil, Bahia Ilhéus, UESC, 14.798° S, 39.172° W, 15 January 2010, G. Melo	KF443089	–
	BFt03	Green	Brazil, Rio de Janeiro, Com. Levy Gasparian, 21.995° S, 43.325° W, 28 October 2010, C.M. Maia & L.M. Santos	–	KF443115
	BFt07	Green	Mexico, Veracruz, Los Tuxtlas, 18.5° N, 95.016° W, June 2009, D. Schonkopf	–	KF443113
	BFt08	Green	Mexico, Campeche, Atastia, 18.55° S, 92.166° W, June 2009, T. Eltz	KF443088	KF443112
	BFt09	Green	Brazil, Minas Gerais, Uberlândia, Faz. Água Limpa, 19.166° S, 48.4° W, 19 July 2008, T.M.S. Mesquita	–	KF443114
	BFt11	Green	Brazil, Minas Gerais, Bandeira, Res. Biodiversitas, 15.783° S, 40.516° W, 19 January 2011, G. Melo	KF443087	KF443110
	BFa01	Blue	Brazil, Paraná, Paranaguá, F.E. Palmito, 25.566° S, 48.516° W, 9 December 2009, L.P. Amaral Neto	KF443085	KF443108
	BFa02	Blue	Brazil, Paraná, Antonina, RPPN Rio Cachoeira, 25.378° S, 48.696° W, 1 February 2007, A.J.C. Aguiar	KF443086	KF443109
	<i>E. iopoecila</i>	BFi01	Green	Brazil, Bahia, Santa Teresinha, Serra Jiboia, 12.853° S, 39.475° W, 8 June 2007, J.A. Rafael & F.F. Xavier	–
BFi02		Green	Brazil, Espírito Santo, Sooretama, Res. Vale, 19.152° S, 40.019° W, 6 January 2011, B.R. Ferrari & E. Ferrari	KF443098	KF443124
BFi03		Green	Brazil, Bahia, Camaçã, Serra Bonita, 15.393° S, 39.564° W, 21 January 2011, G. Melo	KF443099	KF443125
BFi04		Green	Brazil, Espírito Santo, Sooretama, Rebio Sooretama, 18.992° S, 40.129° W, 7 January 2011, B.F. Ferrari & E. Ferrari	KF443103	KF443129
BFi05		Green	Brazil, Rio de Janeiro, Rio das Ostras, Rebio União, 22.427° S, 42.043° W, 12 January 2011, B.R. Ferrari & E. Ferrari	KF443100	KF443126
BFi06		Blue	Brazil, Rio de Janeiro, Paraty, PN Serra da Bocaina, 23.208° S, 44.822° W, 17 January 2011, B.R. Ferrari & E. Ferrari	KF443105	KF443131
BFi07		Intermediate	Brazil, São Paulo, Ubatuba, Estrada Rio Escuro, 23.475° S, 45.140° W, 19 January 2011, B.R. Ferrari & E. Ferrari	KF443101	KF443127

Table 1 (continued)

Case study	Code	Color morph	Specimen data	GenBank accession no.	
				COI	cytb
	BFi08	Green	Brazil, São Paulo, Ubatuba, Estrada Rio Escuro, 23.475° S, 45.140° W, 19 January 2011, B.R. Ferrari & E. Ferrari	KF443106	KF443132
	BFi09	Green	Brazil, Rio de Janeiro, Guapimirim, PN Serra dos Órgãos, 22.493° S, 42.998° W, 13 January 2011, B.R. Ferrari & E. Ferrari	KF443102	KF443128
	BFi10	Green	Brazil, Bahia, Camacã, Faz. Paris, 15.425° S, 39.497° W, 22 January 2011, G. Melo	KF443104	KF443130
	BFi12	Blue	Brazil, São Paulo, Sete Barras, Faz. Morro do Capim, 22.366° S, 47.966° W, 13 January 2009, Mattozo & Thomaz	–	KF443135
	BFi13	Blue	Brazil, Paraná, Antonina, RPPN Rio Cachoeira, 25.378° S, 48.696° W, 23 June 2007, Faria Jr, Weiss & Mattozo	–	KF443134
	BFi14	Blue	Brazil, Paraná, Antonina, RPPN Rio Cachoeira, 25.378° S, 48.696° W, 24 November 2007, Faria Jr, Weiss & Mattozo	–	KF443133
<i>E. stellfeldti</i>	BFs01	Green	Brazil, Bahia, Camacã, Faz. Santa Bárbara, 15.383° S, 39.533° W, 14 January 2007, G. Melo & Carvalho	KF443090	KF443116
	BFs04	Blue	Brazil, Paraná, Antonina, RPPN Rio Cachoeira, 25.378° S, 48.696° W, 27 October 2007, Faria Jr, Weiss & Mattozo	KF443097	KF443123
	BFs05a	Blue	Brazil, São Paulo, Ubatuba, Estrada Rio Escuro, 23.475° S, 45.140° W, 19 January 2011, B.R. Ferrari & E. Ferrari	KF443091	KF443117
	BFs05av	Intermediate	Brazil, São Paulo, Ubatuba, Estrada Rio Escuro, 23.475° S, 45.140° W, 19 January 2011, B.R. Ferrari & E. Ferrari	KF443092	KF443118
	BFs05v	Green	Brazil, São Paulo, Ubatuba, Estrada Rio Escuro, 23.475° S, 45.140° W, 19 January 2011, B.R. Ferrari & E. Ferrari	KF443093	KF443119
	BFs06a	Blue	Brazil, Rio de Janeiro, Paraty, APA Cairuçu, 23.269° S, 44.667° W, 18 January 2011, B.R. Ferrari & E. Ferrari	KF443096	KF443122
	BFs06v	Green	Brazil, Rio de Janeiro, Paraty, APA Cairuçu, 23.269° S, 44.667° W, 18 January 2011, B.R. Ferrari & E. Ferrari	KF443094	KF443120
	BFs07	Green	Brazil, Bahia, Camacã, Serra Bonita, 15.393° S, 39.564° W, 21 January 2011, G. Melo	KF443095	KF443121



**Figure 4.** Map showing the known distribution of *Euglossa townsendi* (including the taxa described as *E. anodorhynchi* and *E. aratingae*) based on specimens deposited in the entomological collection of the Universidade Federal do Paraná.

servers (Miller et al. 2010) with MrBayes 3.2.1 (Ronquist et al. 2012) from a six-partition data set, divided by gene and codons, with the selection of a mixed evolutionary model instead of an a priori model (Ronquist and Huelsenbeck 2003). A Markov Chain Monte Carlo (MCMC) was randomly run with an initial number of  $6 \times 10^6$  generations. After the analysis, 25 % of the trees were discarded, producing a consensus tree with posterior probabilities as a branch support.

The maximum likelihood and bootstrap analyses were also conducted through CIPRES servers, with the option of automatic bootstrap stop, from the same sequence alignment used in the Bayesian analysis, by RAxML BlackBox (Stamatakis et al. 2008).

### 3. RESULTS

From the initial 42 specimens, 30 were successfully amplified for the CO1 fragment

and 37 for the cytb fragment, providing 22 samples with both genes amplified and 8 with only one gene amplified (seven for cytb and one for CO1). Three samples (BFt10, BFi12, and BFs03) could not be amplified for any of the genes, possibly due to poor specimen preservation. Three amplifications (BFi11/CO1, BFi11/cytb, and BFi03/CO1) were contaminated by fungus, as checked using a basic local alignment search tool (BLAST; Altschul et al. 1997). Additionally, ten other samples were compromised by the occurrence of pseudogenes, even after re-amplification and sequencing. Pseudogenes were detected by the presence of stop codons along the sequence, using the Geneious R6 translation tool. Therefore, from the 42 initial samples, 30 were successfully sequenced and used in the analysis (Table I).



**Table II.** List of additional species of Apini included in this study, with respective published reference and GenBank accession numbers

Taxa	Reference	COI	cytb
<i>Apis mellifera</i> Linnaeus	Crozier and Crozier (1993)	NP008083	NP008093
<i>Apis cerana</i> Fabricius	Tan et al. (2011)	YP0037355170	YP003735180
<i>Melipona bicolor</i> Lepeletier	Silvestre et al. (2008)	NP775708	NP775718
<i>Bombus hypocrita</i> Perez	Hong et al. (2008)	YP003519421	YP002519431
<i>Bombus ignitus</i> Smith	Cha et al. (2007)	YP001974606	YP001974616
<i>Euglossa amazonica</i> Dressler	Ramirez et al. (2010)	EU421466	–
<i>Euglossa heterosticta</i> Moure	Ramirez et al. (2010), Darveau et al. (2005)	EU421500	AY916102
<i>Euglossa truncata</i> Rebêlo & Moure	Ramirez et al. (2010)	EU421486	–
<i>Euglossa bursigera</i> Moure	Ramirez et al. (2010), Darveau et al. (2005)	EU421573	AY916113
<i>Euglossa laevicincta</i> Dressler	Ramirez et al. (2010)	EU421527	–
<i>Euglossa annectans</i> Dressler	Ramirez et al. (2010)	EU421488	–
<i>Euglossa chalybeata</i> Friese	Darveau et al. (2005)	–	AY916115
<i>Euglossa ignita</i> Smith	Darveau et al. (2005)	–	AY916114
<i>Euglossa imperialis</i> Cockerell	Ramirez et al. (2010), Koulianos et al. (1999)	EU421537	AF002730
<i>Exaerete frontalis</i> (Guérin)	Ramirez et al. (2010), Darveau et al. (2005)	EU421478	EU421478
<i>Eulaema meriana</i> (Olivier)	Ramirez et al. (2010), Cameron and Mardulyn (2001)	EU421512	AF181614
<i>Aglae caerulea</i> Lepeletier & Serville	Ramirez et al. (2010)	EU421542	–
<i>Eufriesea ornata</i> (Mocsáry)	Ramirez et al. (2010), Darveau et al. (2005)	EU421518	AY916093

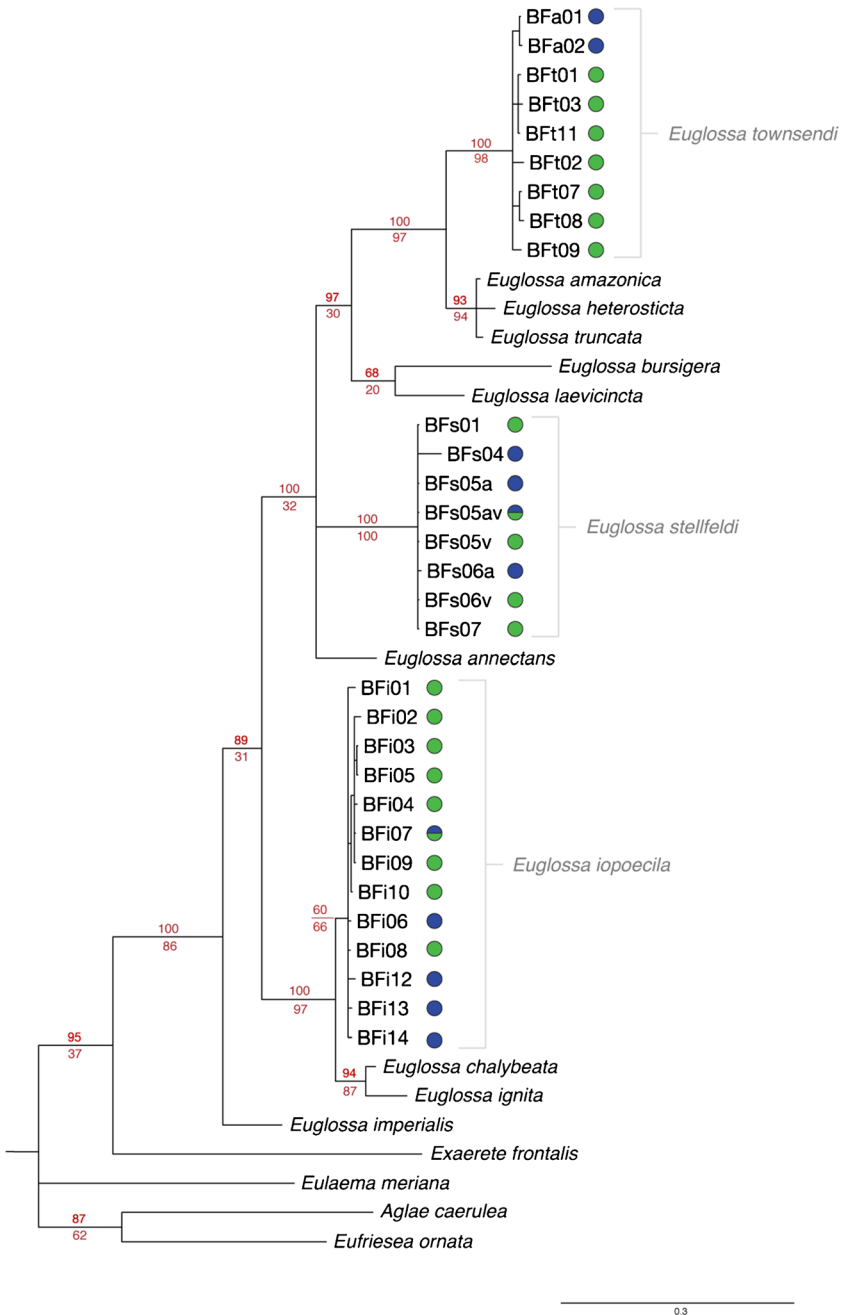
Phylogenetic reconstructions based on maximum likelihood and Bayesian inference exhibited similar topologies. The consensus tree resulting from the Bayesian analysis, with its posterior probability support over the branches and with the maximum likelihood bootstrap values beneath them, is shown in Figure 5. For illustration purposes, due to the long branches involved, the terminals belonging to other Apini subtribes are not shown.

As can be seen in Figure 5, for the two cases involving *E. iopoecila* and *E. stellfeldi*, the consensus tree showed very little or no internal topology resolution, with all terminal taxa collapsed together. In both cases, there is no support for separation between green and blue forms. A single specimen of *E. stellfeldi*, BF04, showed a disproportionally longer branch, compared to the other terminals. This

blue specimen from Paraná had a maximum uncorrected distance of 1.1 % with the remaining terminals of *E. stellfeldi*.

In the *E. townsendi* case, some internal resolution has been recovered, with the blue morph samples (BFa01 and BFa02, corresponding to the taxon described as *E. anodorhynchi*) and the Mexican specimens (BFt07 and B Ft08) being more closely related to each other, respectively. This seems simply a result of these samples being more similar to each other, when compared to the remaining terminals, due to their close geographic proximity (Figure 3). In any case, here also, no resolution indicative of separate lineages was evidenced in the phylogenetic analysis.

Within the studied cases, average pairwise genetic distance was 0.31 % ( $\pm 0.18$ ) for *E. iopoecila*, 0.28 % ( $\pm 0.40$ ) for *E. stellfeldi*, and



**Figure 5.** Consensus tree resulting from a Bayesian analysis of molecular data from the genes CO1 and cytb for the three case studies in the genus *Euglossa*. Posterior probability support is indicated over the branches and the maximum likelihood bootstrap values beneath them.

0.94 % ( $\pm 0.43$ ) for *E. townsendi*. Pairwise distances never exceeded 1.7 %, with the highest value observed within *E. townsendi*. Comparisons between different colored individ-

uals in *E. townsendi* revealed smaller genetic distances (e.g., 0.5 % between BFa01 and BFt02) than similarly colored individuals (e.g., 1.7 % between BFt07, BFt08, or BFt09 and BFt01), suggesting that both morphs should belong to a single taxonomic unit. The two blue specimens of *E. townsendi* differed from the remaining green individuals by an average distance of 0.82 % ( $\pm 0.18$ ) and the two Mexican specimens from the remaining ones by 1.21 % ( $\pm 0.33$ ).

#### 4. DISCUSSION

Increased popularization of DNA amplification and sequencing techniques has shed new light on species limits. Many studies have attempted to measure the amount of genetic divergence indicative of independent evolutionary lineages traditionally recognized as separate species, sometimes called the “bar code gap” when referring to divergence in the CO1 gene (Meyer and Paulay 2005). Hebert et al. (2003), when studying Lepidoptera, noticed that 98 % of morphologically valid species presented genetic distances greater than 3 %, and the remaining 2 % were from congeneric individuals, with clear morphological distinction, despite their lower genetic distances, suggesting more recent divergence. Among many metazoan groups, Meier et al. (2008) estimated a mean intraspecific variation of 1.8 % for Hymenoptera, in contrast to a minimum distance of 3.8 % ( $\pm 4.2$ ) between different species.

For orchid bees, there is no study comparing the amount of genetic variation within species with that among different species of a given group, in particular, involving taxa whose divergence time spans over a continuous range from more recent to older divergences. Estimates of intraspecific variation were published by Dick et al. (2004), based on a fragment of the CO1 gene, for 14 non-closely related euglossine species, with values ranging from 0.0 to 2.0 %. Only for a single pair of taxa, involving *Euglossa mixta* and *Euglossa cognata*, their CO1 data failed to sort the specimens into the two species recognized through mor-

phological features. However, the group to which these two species belong, the analis group, contains cryptic undescribed species (Melo, unpublished data) and, judging from the collecting data, some of the specimens studied by Dick et al. (2004) belong to these undescribed taxa. More recently, Eltz et al. (2011) also showed that sequence data from a CO1 fragment could not resolve the relationships between two closely related forms in *Euglossa*, treated by them as separate species. In their case, the two species were distinguished based in the chemical composition of the perfumes found in the hind tibia as well as microsatellite genotyping and the number of mandibular teeth of males.

The divergence values for the two mitochondrial genes found here among individuals within each of the case studies, all below 2.0 %, are compatible with those expected for a variation within a single species. Indeed, the average values within *E. iopoecila* and *E. stellfeldi*, both around 0.3 %, are very small and reveal a reduced differentiation among populations stretching for over 1,500 km along the coastal forests of eastern Brazil. Even the higher values observed within *E. townsendi*, as, for example, that of 1.2 % between the Mexican specimens and those from eastern Brazil, are relatively small, considering that the samples came from sites about 7,000 km apart.

Despite these results, one could argue that the mitochondrial genes are not adequate for sorting recently diverged lineages in orchid bees as found by Eltz et al. (2011) for the CO1 gene. Differently from their study, in which only the CO1 gene was sequenced and the two forms could be distinguished by a structural character, we used an additional mitochondrial gene, and the forms here studied cannot be morphologically differentiated, except for their integumental color. In this respect, it is important also to emphasize that the blue morphs of the three studied species all occur in the same region, being mostly sympatric in the southern portion of the Atlantic forest. As documented by Faria and Melo (2007), this distribution pattern points to strong selective pressure favoring blue color

phenotypes in orchid bees of the genus *Euglossa* present in this region.

Therefore, we conclude that the recognition of separate taxa for the different color morphs is not supported by the molecular evidence. The current evidence strongly suggests that taxonomic delimitation of orchid bee species based only on general integument coloration does not correctly reflect interspecific relations within the genera. Taking into consideration the potential intraspecific color variation, taxonomists should use these characters secondarily. Continued investigations concerning factors that lead to these color variations and the latitudinal pattern of their distributions are necessary.

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**Couleurs trompeuses: la reconnaissance de morphes différent par la couleur comme des espèces séparées chez les abeilles à orchidées n'a pas de fondement moléculaire**

**Forêt atlantique / Brésil / Euglossini / ADN mitochondrial / taxonomie moléculaire**

**Trägerische Farben: die Anerkennung von Prachtbienen-Farbmorphen als getrennte Arten wird durch molekulare Daten nicht unterstützt**

**Atlantischer Wald / Euglossini / mitochondriale DNA / molekulare Taxonomie**

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