1	Geometric morphometrics discriminates Eastern and Western populations of
2	Partamona rustica (Hymenoptera, Apidae, Meliponini) separated by São Francisco
3	River
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22	Running title: Morphometric variation in Partamona rustica populations
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25 Abstract

26 Wing morphology has been used in taxonomic and systematic studies of insects, often enabling the identification of groups based on variation. In this study, wing Geometric 27 Morphometrics was used to verify if eastern and western populations of Partamona 28 *rustica*, separated by the São Francisco River, are discriminated, thus confirming previous 29 molecular data. The two groups of P. rustica exhibited significant differences in wing 30 size and shape. Better differentiation of populations and groups was achieved with the 31 centroid size. We generated dendrograms using Mahalanobis and Procrustes distances, 32 33 which discriminated the eastern and western populations. Isolation by distance between morphometric and geographic distances was found. The confirmation of the two 34 35 population groups points out the need of further studies investigating the occurrence of barriers to gene flow and colonization history in the semiarid region by this stingless bee. 36 37

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Keywords: geometric morphometrics, population differentiation, stingless bees,
semiarid region, wing variation

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44 Introduction

45 The characterization of diversity and population structure is necessary to implement properly conservation strategies (Frankham et al. 2010). The use of different 46 methods for estimating the degree of variation of traits and its distribution in populations 47 enables an accurate assessment of their genetic status, the influence of environmental 48 factors on the expression of phenotypic characteristics, and the adaptation of populations 49 50 to specific ecotypes (Hurtado-Burillo et al., 2016; Nunes et al., 2013; Francoy et al., 2011). Such methods of diversity characterization also allow the identification of the 51 factors that may affect the size and shape of biological structures, such as geographic 52 53 barriers, climate, temperature, altitude, and genetic differences (Dellicour et al., 2017).

54 Pollinators are among the most important organisms for the maintenance of forest ecosystems and stingless bees (Meliponini, Apidae) are one the most important bee 55 56 pollinators in the tropical and subtropical region (Grüter, 2020). In Brazil, 207 species of stingless bees' genera have been described (Silveira et al. 2002), but the diversity in the 57 Neotropics reached to 426 species (Grüter, 2020). Assessing the diversity and population 58 structure of stingless bees using genetic and geometric morphometrics tools have been 59 60 successfully achieved (Francisco et al., 2008; Halcroft et al., 2016; Hurtado-Burillo et al., 61 2016; Galaschi-Teixeira et al., 2018). Those studies allow the discrimination of populations and are critical to understand the biodiversity of this group and point out 62 important areas of bees' conservation (Miranda et al., 2019). There is a need for more 63 64 comprehensive studies on the biology and conservation efforts directed at protecting stingless bees' biodiversity in the Neotropics, as it is expected that stingless bee's 65 diversity is even richer than it has been described (Gruter 2020). 66

Stingless bees of the genus *Partamona* Schwarz 1939 are grouped into 32
recognized species (Camargo & Pedro, 2003, 2013; Pedro & Camargo, 2003) distributed

from southern Mexico to southern Brazil. Partamona rustica Schwarz 1939 is endemic 69 70 to the Cerrado (savanna) and Caatinga (xeric scrubland forest) biomes in Brazil. Those 71 biomes have suffered profound anthropogenic changes and the fauna and the flora require 72 further knowledge as a first step towards conservation (Klink & Machado, 2005; Zanella & Martins, 2003). Although the geographic distribution of *P. rustica* was described to be 73 74 restricted from the northern portion of the state of Minas Gerais (Cerrado) to the 75 southwestern portion of the state of Bahia (Caatinga) (Camargo & Pedro, 2003), the occurrence of colonies of this species 150 km north of this limit was reported (Miranda 76 77 et al., 2015). Interestingly, 90% of P. rustica nests sampled were associated with active 78 termite mounds built in the upper portion of trees, usually in association with 79 Constrictotermes cyphergaster Silvestri.

In a previous population genetics study of *P. rustica* with colonies from eleven 80 81 locations in the states of Bahia and Minas Gerais, it was demonstrated the existence of two groups of genetically distinct populations based on sequences of four mitochondrial 82 genes and eight microsatellite loci (Miranda et al., 2016). The first group was composed 83 of two populations located western of the São Francisco River (SFR) and the second was 84 85 composed of nine populations located eastern of the river. Molecular analysis of variance 86 (AMOVA) based on gene sequences and microsatellite genotypes showed that much of the variation is between groups (ϕ CT= 0.468; ϕ CT = 0.218, respectively), indicating high 87 and moderate differentiation between the two groups of populations. However, given the 88 89 difference in number of populations between the two groups, the authors stressed the need for further studies as well as the use of a different analytical method to confirm the 90 91 findings.

92 The morphological variation of the wing has long been used in taxonomic and93 systematic studies of insects, making it possible to identify species comparing only the

morphology of this structure (Pretorius, 2005). In recent years, studies on morphological 94 95 variation have predominantly employed geometric morphometrics (GM) of Cartesian geometric coordinates rather than linear measurements (Tatsuta et al., 2018). A large 96 97 number of wasp and bee species has been studied in this way (Aytekin et al., 2007; Tofilski, 2008; Owen, 2012; Falamarzi et al., 2016; Žikićc et al., 2017; Dellicour et al., 98 99 2017), and GM has been used as a taxonomic tool to discriminate from morphotypes and 100 lineages inside populations to genera of bees, particularly stingless bees (Francoy et al., 101 2009; Nunes et al., 2013; Combey et al., 2013; Bonatti et al., 2014; Quezada-Euán et al., 102 2015; Halcroft et al., 2016; Francoy et al., 2016; Galaschi-Teixeira et al., 2018; Santos et 103 al., 2019).

104 Therefore, the present study aimed to verify whether wing geometric 105 morphometrics discriminate *P. rustica* populations located at western and eastern sides 106 of SFR. In this work, we included more samples located at the west side of the SFR to 107 confirm the occurrence of the two groups. This would provide greater support to the 108 notion that the SFR may act as a barrier to gene flow among populations of *P. rustica*. 109 The establishment of possible proximal causes of interpopulation differentiation in this 100 bee species provides relevance to the present study.

111

112 Material and methods

113 Sampling

We obtained 161 colonies of *P. rustica* collected from 14 localities (Table S1 and Figure S1). We used the 143 colonies from 11 localities previously analyzed (Miranda et al., 2016) and we increased the sampling with 18 new colonies located at the western side of the SFR (including the localities of Coribe, São Félix do Coribe, and Montalvânia). Permits necessary for the fieldwork and collection of samples were issued by the Brazilian 119 Institute for Biodiversity Conservation (ICMBio) (number 31750). The field studies did

120 not involve endangered or protected species.

121 Morphometric analysis

Three adult workers from each of the 161 nests sampled at the 14 locations (12 located in the state of Bahia and two in Minas Gerais) were analyzed (Table S1, Figure S1). The right forewing of each adult worker was removed and mounted between microscope slides. Images were captured using a Leica S6D digital camera coupled to a Leica DFC450 stereomicroscope. For the analysis of partial deformations, a database was created using tps format to store the wing image information at the tpsUtil64 software, version 1.79 (Rohlf, 2015).

129 To reduce possible human errors, seventeen landmarks (LM 9, 10, and 17 of type III, sensu Bookstein 1991) were manually digitized twice (independently) at the wing 130 131 vein intersections using the tpsDig2 software, version 2.16 (Rohlf, 2015) (Figure S2). The data used for analysis correspond to the average of the two markings performed on each 132 wing. In the MorphoJ software, version 1.6 (Klingenberg, 2011), the images underwent 133 Procrustes adjustment, enabling discriminant function analysis (DFA), principal 134 135 component analysis (PCA), and canonical variate analysis (CVA). ANOVA was 136 performed using two classifiers: i) considering the 14 populations independently and ii) considering the two population groups (from the eastern and western sides of the SFR). 137 138 Kaiser-Meyer-Olkin (KMO) test was used in order to determine the suitability of the data 139 for the multivariate analyses. The function KMO in the package psych was used. The overall Measure of Sampling Adequacy (MSA) was 0.5, meaning all coordinates may 140 141 reasonably be retained for the multivariate analyses.

142 Kruskal-Wallis one-way ANOVA on ranks was performed using the
143 STATISTICA 6.0 software (StatSoft 2001) to determine whether the mean values of

144 centroid size (CS) in the samples from the 14 populations were statistically different.
145 Kruskal-Wallis analyses among populations were assessed conducting pairwise
146 comparisons and Bonferroni correction for multiple comparisons. Additionally, a t-test
147 was performed to compare the mean centroid size in samples from eastern (occurring
148 predominantly in *Caatinga* areas) and western populations (predominantly in *Cerrado*149 areas) of the SFR.

Mahalanobis and Procrustes distances were used to generate interpopulation similarity dendrograms based on the neighbor-joining algorithm using the Mega software, version 6.0 (Tamura et al., 2011). The correlation between morphological and geographic distances, obtained using Google Earth version 6.1.0.5001 (Google Inc. 2011), was verified using a Mantel test with the TFPGA software (Miller, 1997).

All software used in our morphometric analysis are freely accessible and available
at http://life.bio.sunysb.edu/morph and http://www.flywings.org.uk/MorphoJ.

157

158 **Results**

159 We analyzed 483 forewings of P. rustica. Based on the shape covariance data matrix derived from the Procrustes fit, the PCA of the seventeen anatomical landmarks 160 161 revealed 30 components responsible for the total variation. The first 16 explained 92.16% of the total variation, with the first two PC axis explaining 43.30% of the variation (PC1: 162 26.84%; PC2: 16.46%) (Figure S3). For data visualization, we showed the first two axes 163 of the CVA (Figure 1) explaining 66.1% of the total variance in the data (CV1: 42.2%; 164 CV2: 23.9%). The histogram of the first CV, obtained in the MorphoJ, showed a 165 166 separation of the two groups located western and eastern of the SFR, with some overlaps (Figure S4). 167

168 The Mahalanobis distances between pairs of populations ranged from 2.1961 169 (TNO x MAC) to 7.2428 (IRA x MTV), whereas the Procrustes distances ranged from 170 0.0064 (MAC x ITU) to 0.0271 (CSI x SFC) (Table S2).

The discriminant function analysis resulted in 98.91%, demonstrating that nearly
all workers were correctly assigned to their original populations. Accuracy in the crossvalidation test was 87.16%.

Differences in size and shape of the wings of adult females of *P. rustica* were observed. ANOVA performed considering the 14 populations independently generated a statistically significant F (P < 0.0001^{***}) for centroid size (Figure 2) and shape (Table 1A). When populations were grouped into eastern and western groups, the ANOVA results were equally significant (P < 0.0001^{***}) for centroid size and shape (Table 1B), with a significant increase in the F value for wing shape as well as a marked decrease in the F value for centroid size in this second approach.

The discriminant analysis correctly assigned 95.73% of the individuals to their respective groups of origin (eastern or western), whereas the correct assignment rate in the cross-validation was 94.17%. As the PCA analyzed the same covariance matrix of the general data, the results for the two population groups were the same as described above for the populations taken as independent units.

The Kruskal-Wallis one-way ANOVA on ranks showed that centroid values differed significantly between populations ($H_{13} = 184.687$, P < 0.001***). The populations from Coribe and São Félix do Coribe (located western of the SFR) had higher values of centroid size than the other populations. Comparing mean centroid size in the two population groups, it appears that the females from the western group (predominantly *Cerrado* area) have a significantly higher mean centroid value than females from the colonies/populations from the east of the SFR (predominance of *Caatinga* areas) (Figure

S5), as confirmed by the Student's t test (t = 8.512, df = 452, P < 0.001***; 95% CI =
0.121 to 0.0756).

195 The Mantel test revealed a positive correlation between geographic distances and Mahalanobis (r = 0.6117; P < 0.0001^{***}) and Procrustes (r = 0.5317; P < 0.0001^{***}) 196 distances, which is consistent with the usually smaller Mahalanobis and Procrustes 197 distances between populations of the same group (eastern or western) and larger 198 199 Mahalanobis and Procrustes distances between populations of different groups (Table S2), as the groups were separated by the São Francisco river which could impose a 200 201 geographical barrier. These results are reflected in the similarity dendrograms (Figure 3) 202 generated from the Mahalanobis and Procrustes distances, which show the separation of 203 populations into two groups, eastern and western populations of the SFR.

204

205 **Discussion**

206 Geometric morphometric analyses using wing size and shape discriminate the populations 207 of P. rustica. As we expected based on our previous population genetics study (Miranda 208 et al. 2016), the Mahalanobis and Procrustes distances discriminate eastern and western 209 populations of Partamona rustica separated by São Francisco River. The differentiation 210 of populations located on opposite banks of the San Francisco River was improved in the 211 present work with the inclusion of 18 colonies of *P. rustica* from three new sites located 212 to the western of the SFR, giving new support to the results previously reported based on 213 molecular data (Miranda et al., 2016).

Wing size is a good estimator of body size (Dellicour et al. 2017) and survival, resource acquisition and reproductive success are generally size-dependent traits (Takahashi & Blanckenhorn, 2015). Our analyses of wing size assessed by centroid size significantly exhibited higher variation among populations of *P. rustica* than wing shape

(Table 1A). This finding was expected, as size variation in insects is related to the quality 218 219 and quantity of food given to the larvae (Peruquetti, 2003; Campos et al., 2018), and to the foraging range of colonies (Veiga et al., 2013). Colony fitness in stingless bees is 220 221 highly associated with the variation in worker body size, which is dependent on trophic resources stored within the colony, as at least 75% of the variation are attributed not to 222 223 phylogenetic effects but rather to food requirements (Pignata & Diniz-Filho, 1996). Thus, 224 as wing size variation may reflect the availability of trophic resources in each environment, this makes sense as the supply dynamics certainly vary temporally in the 225 226 Cerrado and Caatinga biomes (Campos et al., 2018; Miranda et al., 2021), which have 227 distinct characteristics in terms of terrain, climate and vegetation composition, as well as 228 the idiosyncratic evolutionary history of *P. rustica* (see Miranda et al., 2015; Miranda et 229 al., 2016). Alternatively, this variation in body size has been also associated with a 230 different response of these populations to specific features of their local environments (Grassi-Sella et al., 2018; Ribeiro et al., 2019). 231

232 Canonical variate analyses revealed little overlap between samples of the two groups. A broader range of variation was found among individuals from the eastern group 233 234 compared to those from the western group is consistent with the larger number of colonies 235 from the eastern side as well as the larger number of haplotypes identified (n = 22)compared to the western group (n = 8) (Miranda et al., 2016). However, these authors 236 237 found a different result regarding the microsatellite data, showing greater genetic 238 diversity of these markers among populations in the western group despite the small number of populations on this side of the SFR (Miranda et al., 2016). The agreement 239 240 between the similarity dendrograms and the characterization of the two groups previously defined by population genetic analysis denotes a high resolution of geometric 241

morphometrics to capture subtle differences in wing size and shape between close groups, 242 243 corroborating with other studies in bees (Quezada-Euán et al., 2015; Francoy et al., 2016). 244 In the analysis of variance (ANOVA) performed with Procrustes distances the 245 estimated F was greater for centroid size than shape of the wing of P. rustica workers. 246 The large reduction in the F value for centroid size and the large increase in the F value 247 for shape when the analysis was performed with the two groups compared to the analysis 248 considering the 14 populations independently is noteworthy. These results seem to be 249 coherent, since a large variation in centroid size is expected in samples from different 250 locations (first analysis considering the 14 populations) due to the different environments 251 to which the respective local colonies are exposed. When analyzing the two groups (second analysis), the F value decreases because we are now comparing the average of 252 253 the environments experienced by the populations east and west of the SFR. On the other 254 hand, the significant increase in the F value found in the two groups can be attributed to the differences in genetic composition between population groups demonstrated 255 256 previously (Miranda et al., 2016) and analyzing the shape of the wing in the present study. 257 Ontogenetic aspects linked to maternal and feeding effects (Peruquetti, 2003), climate 258 and temperature may be directly related to size variation among individuals from different 259 populations and may be inducing adaptive responses in these populations (Nunes et al., 2013). While environmental factors certainly contribute to the differences in size, the 260 261 shape of a structure is a trait of greater complexity that involves environmental and 262 genetic factors that are subject to developmental constraints (Klingenberg, 2016). So, shape differences may be linked to local adaptive responses to foraging behaviors, flight 263 264 dynamics and different environments to which populations are exposed (Benítez et al., 265 2013; Nunes et al., 2013).

The Mantel test supports the association between the variation in wing 266 267 morphology and biotic as well as abiotic factors by revealing a positive correlation 268 between morphological and geographic distances. However, one cannot rule out possible 269 effects of phenotypic plasticity on the expression of individual characteristics (Nunes et al., 2013). Isolation by distance – reported here for morphometric data and elsewhere for 270 271 microsatellite data (Miranda et al., 2016) – also explains some reduction in gene flow. 272 Other factors, such as the mode of reproduction in Meliponini colonies, with the temporary dependence of daughter colonies on the mother colony (Nogueira-Neto, 1954; 273 274 Engels & Imperatriz-Fonseca, 1990; Cronin et al., 2013), a small flight radius (Wille & 275 Orozco, 1975; Araújo et al., 2004; but see Zayed et al., 2005 about the distance wild bees 276 cover during foraging trips is related to their dispersal ability) and geographic barriers (in 277 this case, the SFR valley and/or different phytophysiognomies) are additional factors that 278 can lead to evolutionary processes that differentiate populations over time (May-Itzá et al., 2012; Hurtado-Burillo et al., 2016). As males, to some extent, ensure the dispersion 279 280 of genes in populations, a certain level of genetic homogeneity must be produced, which is consistent with the moderate gene flow estimated by the microsatellite loci (Miranda 281 282 et al., 2016) and the low overlap found between population groups in the geometric 283 morphometric analysis.

According to our previous work (Miranda et al., 2016), the eastern and western groups split recently – at the end of the Pleistocene about 102 kya (95% HPD: 45,588– 979,902 kya) – and phylogenetic reconstruction indicated that *P. rustica* possibly originated western of the SFR valley, with the subsequent colonization of the eastern region. The SFR or isolation by distance may be affecting gene flow and isolating the populations studied here. This argument is supported by the fact that this region has low potential for the historical occurrence of the species, as seen in the ecological niche

modeling analysis, as well as for the termite that builds the substrate in which this bee 291 292 nest (Miranda et al., 2015). On the other hand, in a study using geometric morphometrics 293 on populations of Melipona mandaçaia, which is a stingless bee that also occurs in 294 *Caatinga* areas along the São Francisco River, it was found no evidence that the valley or the river itself was a barrier to gene flow between populations sampled on the different 295 296 banks of the river (Prado-Silva et al., 2016). Alternatively, the differences between the 297 western (predominantly *Cerrado*) and eastern (predominantly *Caatinga*) phytophysiognomies of the SFR may be valid arguments for the differentiation between 298 the groups observed herein, as differences in rainfall, floral types, substrates and altitudes 299 300 between the two regions may be limiting factors for the occurrence of the species, which 301 has preferences for certain environments and substrates (termite nests) (Miranda et al., 302 2015).

The geometric morphometric differences between the two groups of populations provide support to the hypothesis that *P. rustica* originated in areas of the *Cerrado* and subsequently colonized areas of the *Caatinga* (Miranda et al., 2016). Thus, the previous hypothesis that the genus *Partamona* originated in Amazon and Andean areas (Camargo & Pedro, 2003), along with evidence that the biota of the *Cerrado* is more related to the biota found in the Amazon (Werneck et al. 2011) support the idea that the group located western of the SFR is older and gave rise to the eastern group.

Concluding, geometric morphometrics was effective in demonstrating differences in wing size and shape among colonies of *P. rustica* from different geographical locations. The geometric morphometric data further supported the distinction between the two groups of *P. rustica* previously suggested by genetic analysis based on molecular markers (mtDNA and microsatellite loci). Despite the new evidence, it is not possible to confirm that the São Francisco River constituted an effective geographic barrier that induced

genetic differentiation processes, especially regarding wing shape, as the level of genetic 316 317 isolation among populations in the two groups was not estimated, considering the possible recent separation between them. However, the observed geometric morphometric 318 319 variation appears to be, at least partially, the result of interpopulation genetic variation. Thus, subsequent studies are needed to assess how much of this variation may be 320 321 attributed to genetic and/or environmental factors as well as determine the possible 322 meaning of this variation, which is an under explored subject in bees, despite being one 323 of the central goals of evolutionary biology.

324

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562 Tables

Table 1. (A) ANOVA table including Procrustes distances for centroid size (CS) and
shape (SH) using *Partamona rustica* wings considering the 14 populations. (B)
ANOVA table including Procrustes distances for centroid size (CS) and shape (SH)
using *P. rustica* wings considering the two groups (western and eastern side of SFR).
Sum of squares (SS); mean squares (MS); degrees of freedom (dF). The F values have P
< 0.0001***.

Effect SS MS dF F CS Individual 28951189.154814 2227014.550370 13 217. Residual 4778672.443366 10254.661896 466 217. SH Individual 0.06004763 0.0001539683 390 13.3 Residual 0.16124608 0.0000115341 13980 13.3 B - ANOVA (considering Western x Eastern populations) Effect SS MS dF F CS Individual 6199655.653226 6199655.65322 1 107. CS Residual 27530205.944955 57594.573107 478 107. SH Individual 0.02122182 0.0007073941 30 50.7 SH Residual 0.20007189 0.0000139520 14340 50.7		Α	- ANOVA (considerin	g the 14 populations)	
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	зн	Residual	0.20007189	0.0000139520	14340	50.7





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Figure 1. Scatter plot of the fourteen populations of *Partamona rustica* analyzed, generated from the first two canonical variate analyses (CVA). Ellipses indicated 95% confidence intervals. The green circles represent the western populations and the red circles the eastern populations.

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Figure 2. Boxplot of the wing centroid sizes for each population of *Partamona rustica*. Vertical bars represent 95% confidence intervals. Pairwise comparisons among populations are indicated by the letters of significance: SFC (a); COR (bcd); MTV (bcdefg); CMA (bcd); COC (bcd); TNO (bcd); CSI (ef); ITU (bc); MAC (b); IRA (cdg); MIL (eg); RBA (deg); MVT (f); BVT (efg). The green colors represent the western populations and the red colors the eastern populations. (median \pm quartiles; whiskers: data range; circles: outliers).





Figure 3. Neighbour-joining dendrogram showing the relationships of similarity among

606 populations of *Partamona rustica* based in Mahalanobis (A) and Procrustes (B) distances

607 (in green, western group and in red eastern group).