

Chromosome morphometry of *Camponotus renggeri* Emery, 1894 (Hymenoptera: Formicidae)

Morfometria cromossômica de *Camponotus renggeri* Emery, 1894 (Hymenoptera: Formicidae)

Talles Fillipe Barcelos Vieira^I  | Flávia Assumpção Santana^{II} 

^IUniversidade Federal de Uberlândia. Uberlândia, Minas Gerais, Brasil

^{II}Universidade Estadual de Goiás. Quirinópolis, Goiás, Brasil

Abstract: Both the amount and the morphology of chromosomes are important aspects for the specific genomic organization of each organism. Data show that chromosomal evolution, which happens in higher rates in eusocial insects, tends to decrease the size of chromosomes during genetic diversification. Ants have a high karyotypic plasticity, and the genus *Camponotus*, one of the most speciose genus among the Formicidae, has little cytogenetic information available regarding its abundance. Therefore, this study aimed to assess morphometrically the karyotype of *Camponotus renggeri*. The chromosomes were obtained from the brain ganglia of prepupae, following a combination of two existent methodologies. Morphometric analysis of the karyotype revealed chromosomes from 0,31 μm to 1,22 μm , which reflects the chromosomal evolution trend towards considerably small chromosomes.

Keywords: Karyotype. Ants. Cytogenetics.

Resumo: A quantidade e a morfologia cromossômica são aspectos importantes para organização genômica de cada organismo. Dados mostram que a evolução cromossômica, que ocorre em taxas mais altas em insetos eusociais, tende a reduzir o tamanho dos cromossomos durante a diversificação genética. As formigas apresentam alta plasticidade cariotípica e o gênero *Camponotus*, um dos mais especiosos entre os Formicídeos, apresenta poucos dados citogenéticos em relação à sua abundância. Este estudo teve como objetivo realizar análises morfométricas dos cromossomos de *Camponotus renggeri*. Os cromossomos foram obtidos a partir dos gânglios cerebrais de pré-pupas, seguindo uma combinação de duas metodologias já descritas. A análise do cariótipo revelou cromossomos de 0,31 μm até 1,22 μm e reflete a tendência de evolução cromossômica, em direção a cromossomos consideravelmente pequenos.

Palavras-chave: Cariótipo. Formiga. Citogenética.

VIEIRA, T. F. B. & F. A. SANTANA, 2020. Chromosome morphometry of *Camponotus renggeri* Emery, 1894 (Hymenoptera: Formicidae). **Boletim do Museu Paraense Emílio Goeldi. Ciências Naturais** 15(1): 231-235. DOI: <http://doi.org/10.46357/bcnaturais.v15i1.243>.

Autor para correspondência: Talles Fillipe Barcelos Vieira. Av Terezina, 1150. Uberlândia, MG, Brasil. CEP 38400-744 (tallesbarcellos@hotmail.com).

Recebido em 19/12/2019

Aprovado em 06/04/2020

Responsabilidade editorial: Livia Pires do Prado



INTRODUCTION

Chromosomes are units of inheritance organized within the nucleus of eukaryotic cells and their amount and morphology are important aspects for the specific genomic organization of each organism (Cristiano *et al.*, 2013; Cardoso *et al.*, 2014). Both numerical and structural chromosomal variation is important for systematic and evolutionary studies and may lead to species identification and differentiation, favoring phylogenetic updating (Silveira *et al.*, 2006; Barros *et al.*, 2010; Menezes *et al.*, 2014; Correia *et al.*, 2016).

Cytogenetic data shows that chromosomal evolution tends to decrease the size of chromosomes, reducing genetic risks, such as translocation, during genetic diversification (Aguiar *et al.*, 2016; Mariano *et al.*, 2003). The evolution of chromosome in eusocial insects shows higher rates compared to other organisms and some genera may even display intraspecific variations (Lorite & Palomeque, 2010; Ross *et al.*, 2015; Barros *et al.*, 2016).

Ants have a large numerical and structural variety of chromosomes, with species exhibiting $2n = 2$ to species with $2n = 120$ (Cristiano *et al.*, 2013). The genus *Camponotus*, with 1,042 described species (Bolton, 2020), is one of the most specious genus among Formicidae and it features a considerable karyotypic variety and has little cytogenetic information available regarding its abundance (Aguiar *et al.*, 2017).

Although it is still scarce, morphometric analysis on ants chromosomes is an important tool for the updating of taxonomic status, once it allows the evaluation of measurements and variations of such structures (Gokhman, 2006; Fornel & Estrela, 2012; Cardoso *et al.*, 2017). Therefore, due to ants high karyotypic plasticity, mainly among *Camponotus*, and the lack of morphometric studies, this work aimed to morphometric assess the karyotype of *Camponotus renggeri* (Emery, 1894), that recently has been the subject of a wide discussion (Aguiar *et al.*, 2017), and we believe that our results may be useful as a mean of comparison for understanding

chromosomal variations or rearrangements that might be found in further studies.

MATERIAL AND METHODS

The biological materials were collected nearby Quirinópolis, state of Goiás, Brazil, in four different colonies, found in a preserved fragment of Cerrado surrounded by pasture fields. Chromosomes were obtained from the brain ganglia (BG) of 10 prepupae from each colony, following a combination of two methodologies (Imai *et al.*, 1988; Guerra & Souza, 2002), not described by other authors so far, which best suits our laboratory conditions.

Using dissecting needles, the BG were removed under a stereomicroscope and transferred to 500 μ l tubes with colchicine at 0.005% and allowed to rest for one hour to interrupt the spindle fibers. Later, colchicine was removed and replaced by an hypotonic solution, making cells more turgid. After 15 minutes, the hypotonic solution was removed and 10 drops of carnoy fixative (ethyl alcohol, acetic acid, 3: 1) were added as well.

After a 10 minutes rest, the BG were transferred to 500 μ l tubes with fresh carnoy fixative, where they were held for 30 minutes. Then, using dissecting needles, each BG was macerated with a drop of acetic acid at 45% on separate slides and allowed to dry at room temperature for one day and then stained with a solution of Giemsa at 4% for 10 minutes.

The slides were observed using an optical microscope (Leica DM 500 ®) and the eight metaphases with best chromosome scattering were photographed and characterized according to number and morphology, following to the nomenclature proposed by Levan *et al.* (1964). The morphometric analyzes were performed using the ImageJ software, measuring the whole extension of chromosomes, using a 5 μ m scale, and the resulting data were organized in table.

RESULTS AND DISCUSSION

The chromosome number found for *C. renggeri* was $2n = 40$, of which two pairs are submetacentric (SM), 17 pairs are subtelocentric (TS) and one is telocentric (T) (Figure 1). The karyotype corresponds to existent descriptions for the same species, performed in Nova Mutum-MT and Macapá-AP, both in number and chromosomal morphology (Aguiar *et al.*, 2016, 2017), however, no study has provided morphometric data so far.

Morphometric analysis of the karyotype revealed chromosomes from $0,31 \mu\text{m}$ to $1,22 \mu\text{m}$ (Table 1). The high rate of karyotype evolution in eusocial insects, whose aim is to decrease genetic risks, may explain the reduced size of chromosomes in relation to other insect and animal species (Mariano *et al.*, 2003; Ross *et al.*, 2015; Barros *et al.*, 2016; Aguiar *et al.*, 2016, 2017). It is also noteworthy that individuals of the same species, collected and karyotyped in other regions, may present variations in chromosome morphology, since some organisms may have intraspecific variations (Lorite & Palomeque, 2010; Barros *et al.*, 2016), and therefore might also present variations in size (Cardoso *et al.*, 2018).

Even though there are not many studies about the karyotype of *C. renggeri*, the available informations has shown that it undergoes a considerable rate of chromosome rearrangements, as expected (Aguiar *et al.*, 2016, 2017). Thus, the measurements presented here allow accurate comparisons and might open new paths that'll help further evolutionary investigations.

Table 1. Morphometric analysis of the chromosomes of *Camponotus renggeri*.

Chromosome number	size (μm)	Type
1	1,22	T
2	1,03	SM
3	0,88	ST
4	0,86	ST
5	0,86	ST
6	0,85	ST
7	0,84	ST
8	0,82	ST
9	0,76	ST
10	0,73	SM
11	0,72	ST
12	0,72	ST
13	0,71	ST
14	0,69	ST
15	0,66	ST
16	0,59	ST
17	0,50	ST
18	0,46	ST
19	0,42	ST
20	0,31	ST

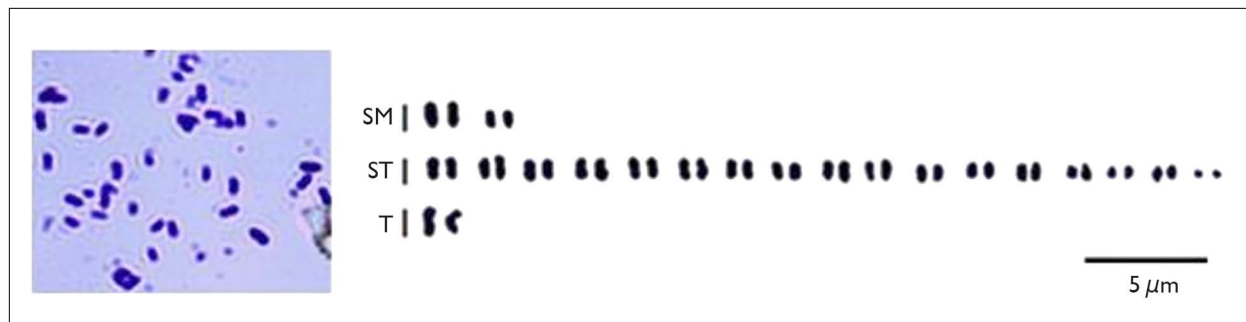


Figure 1. Conventional cytogenetics of mitotic cells of *Camponotus renggeri* (1000X). Bar = $5 \mu\text{m}$.

ACKNOWLEDGMENT

We thank Professor Rodrigo M. Feitosa (UFPR) for identifying the species.

REFERENCES

- AGUIAR, H. J. A. C., L. A. C. BARROS, F. A. F. SOARES, C. R. CARVALHO & S. G. POMPOLO, 2016. Estimation of nuclear genome size of three species of *Camponotus* (Mayr, 1861) (Hymenoptera: Formicidae: Formicinae) and their cytogenetic relationship. **Sociobiology** 63(2): 777-782. DOI: <http://doi.org/10.13102/sociobiology.v63i2.948>.
- AGUIAR, H. J. A. C., L. A. C. BARROS, D. R. ALVES, C. S. F. MARIANO, J. H. C. DELABIE & S. G. POMPOLO, 2017. Cytogenetic studies on populations of *Camponotus rufipes* (Fabricius, 1775) and *Camponotus renggeri* Emery, 1894 (Formicidae: Formicinae). **Plos One** 12(5): e0177702. DOI: <https://doi.org/10.1371/journal.pone.0177702>.
- BARROS, L. A. C., H. J. A. C. AGUIAR, C. S. F. MARIANO, J. H. C. DELABIE & S. G. POMPOLO, 2010. Cytogenetic characterization of the lower-attine *Mycocepurus goeldii* (Formicidae: Myrmicinae: Attini). **Sociobiology** 56(1): 57-66. DOI: <http://dx.doi.org/10.13102/sociobiology.v56i1.2214>.
- BARROS, L. A. C., H. J. A. C. AGUIAR, C. S. F. MARIANO, V. A. SOUZA, M. A. COSTA, J. H. C. DELABIE & S. G. POMPOLO, 2016. Cytogenetic data on six leafcutter ants of the genus *Acromyrmex* Mayr, 1865 (Hymenoptera, Formicidae, Myrmicinae): insights into chromosome evolution and taxonomic implications. **Comparative Cytogenetics** 10(2): 229-243. DOI: <https://doi.org/10.3897/CompCytogen.v10i2.7612>.
- BOLTON, B., 2020. **An online catalog of the ants of the world**. Available at: <http://antcat.org>. Access on: April 6, 2020.
- CARDOSO, D. C., S. G. POMPOLO, M. P. CRISTIANO & M. G. TAVARES, 2014. The role of fusion in ant chromosome evolution: insights from cytogenetic analysis using a molecular phylogenetic approach in the genus *Mycetophylax*. **Plos One** 9(1): e95408. DOI: <https://doi.org/10.1371/journal.pone.0087473>.
- CARDOSO, D. C., T. T. P. PEREIRA, A. L. CORDEIRO & M. P. CRISTIANO, 2017. Cytogenetic data on the agro-predatory ant *Megalomyrmex incisus* Smith, 1947 and its host, *Mycetophylax conformis* (Mayr, 1884) (Hymenoptera, Formicidae). **Comparative Cytogenetics** 11(1): 45-53. DOI: <https://doi.org/10.3897/CompCytogen.v11i1.10842>.
- CARDOSO, D. C., J. HEINZE, M. N. MOURA & M. P. CRISTIANO, 2018. Chromosomal variation among populations of a fungus-farming ant: implications for karyotype evolution and potential restriction to gene flow. **BMC Evolutionary Biology** 18: 146. DOI: <https://doi.org/10.1186/s12862-018-1247-5>.
- CORREIA, J. P. S. O., C. S. F. MARIANO, J. H. C. DELABIE, S. LACAU & M. A. COSTA, 2016. Cytogenetic analysis of *Pseudoponera stigma* and *Pseudoponera gilberti* (Hymenoptera: Formicidae: Ponerinae): a taxonomic approach. **Florida Entomologist** 99(4): 718-721. DOI: <https://doi.org/10.1653/024.099.0422>.
- CRISTIANO, M. P., D. C. CARDOSO & T. M. F. SALOMÃO, 2013. Cytogenetic and molecular analyses reveal a divergence between *Acromyrmex striatus* (Roger, 1863) and other congeneric species: taxonomic implications. **Plos One** 8(3): e59784. DOI: <https://doi.org/10.1371/journal.pone.0059784>.
- EMERY, C., 1894. Viaggio del dottor Alfredo Borelli nella Repubblica Argentina e nel Paraguay. VIII. Formiche. **Bollettino dei Musei di Zoologia ed Anatomia Comparata della Reale Università di Torino** 9(186): 1-4.
- FORNEL, R. & P. C. ESTRELA, 2012. Morfometria geométrica e a quantificação da forma dos organismos. In: J. R. MARINHO, L. U. HEPP & R. FORNEL (Ed.): **Temas em Biologia**: 101-120. EDIFAPES, Erechim.
- GOKHMAN, V. E., 2006. Implication of chromosomal analysis for the taxonomy of parasitic wasps (Hymenoptera). **Entomological Review** 86(1): 38-47. DOI: <https://doi.org/10.1134/S0013873806010015>.
- GUERRA, M. & M. J. SOUZA, 2002. **Como observar cromossomos**: um guia de técnicas em citogenética vegetal, animal e humana: 1-131. FUNPEC, Ribeirão Preto.
- IMAI, H. T., R. W. TAYLOR, M. W. J. CROSLAND & R. H. CROZIER, 1988. Modes of spontaneous chromosomal mutation and karyotype evolution in ants with reference to the minimum interaction hypothesis. **Japanese Journal of Genetics** 63(2): 159-185. DOI: <https://doi.org/10.1266/jjg.63.159>.
- LEVAN, A., K. FREDGA & A. A. SANDBERG, A. A., 1964. Nomenclature for centromeric position on chromosomes. **Hereditas** 52(2): 201-220. DOI: <https://doi.org/10.1111/j.1601-5223.1964.tb01953.x>.
- LORITE, P. & T. PALOMEQUE, 2010. Karyotype evolution in ants (Hymenoptera: Formicidae), with a review of the known ant chromosome numbers. **Myrmecological News** 13: 89-102.
- MARIANO, C. S. F., J. H. C. DELABIE, L. A. O. CAMPOS & S. G. POMPOLO, 2003. Trends in karyotype evolution in the ant genus *Camponotus* (Hymenoptera: Formicidae). **Sociobiology** 42(3): 831-839.
- MENEZES, R. S. T., A. F. CARVALHO, J. P. S. O. CORREIA, T. S. SILVA, A. SOMAVILLA & M. A. COSTA, 2014. Evolutionary trends in the chromosome numbers of swarm-founding social wasps. **Insectes Sociaux** 61(4): 385-393. DOI: <https://doi.org/10.1007/s00040-014-0365-3>.



ROSS, L., H. BLACKMON, P. LORITE, V. E. GOKHMAN & N. B. HARDY, 2015. Recombination, chromosome number and eusociality in the Hymenoptera. **Journal of Evolutionary Biology** 28(1): 105-116. DOI: <https://doi.org/10.1111/jeb.12543>.

SILVEIRA, F. T., F. A. ORTOLANI, M. F. MATAQUEIRO & J. R. MORO, 2006. Caracterização citogenética em duas espécies do gênero *Myrciaria*. **Revista de Biologia e Ciências da Terra** 6(2): 327-333.

