



Karyosystematic and karyotype evolution of *Panstrongylus lutzi* (Neiva & Pinto, 1923) (Hemiptera, Triatominae)

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1. Scientific Note

Currently, there are 153 species of triatomines, distributed in 18 genera, being all species considered as potential vector of Chagas disease (Alevi et al., 2016; Rosa et al., 2017). The genus *Panstrongylus* Berg, 1879 is composed of 15 species, being 14 species alive and one fossil. Cytogenetic analyses in *Panstrongylus* were initiated in 1950 with the karyotype description of *P. megistus* (Schreiber and Pellegrino, 1950). Until now the number of chromosomes in seven species of *Panstrongylus* was described, of which with the exception of *P. megistus* which has 21 chromosomes ($2n = 18A + X_1X_2Y$), all other species analyzed (*P. chinai*, *P. geniculatus*, *P. howardi*, *P. lignarius*, *P. rufotuberculatus* and *P. tupynambai*) have 23 chromosomes ($2n = 20A + X_1X_2Y$) (Schreiber and Pellegrino, 1950; Pérez et al., 2002; Panzera et al., 2010).

Based on homogeneity of the number of chromosomes ($2n = 23$) and sex determination system (X_1X_2Y) of the genus *Panstrongylus*, Perez et al. (2002) suggested that these triatomines were possibly originated from ancestors of North America, because all species of South America [except *Triatoma melanocephala* ($2n = 24$), *T. vitticeps* ($2n = 24$) and *T. tibiamaculata* ($2n = 23$) (Alevi et al., 2012)] have $2n = 22$ chromosomes and XY sex determination system (Panzera et al., 2010). These results were recently confirmed based on molecular analysis (Justi et al., 2014).

Thus, in order to assist in the chromosomal and evolutionary knowledge of the genus *Panstrongylus* and Triatominae subfamily, this study aimed to analyze the karyotype of *P. lutzi* and compare with karyotypes already described for other species of the triatomines.

One adult male of *P. lutzi* was collected in wild environment in the State of Bahia, Brazil (S 12.41'407", W 039.26'210" and elevation 167 meters). We justify that only one specimen was analyzed by the absence of *P. lutzi* in Brazilian insectaries and mainly by the difficulty of collecting and maintaining of these species in the

laboratory, since for cytogenetic analyzes the insects might not be killed or fixed in alcohol (as occurs for molecular analysis). The seminiferous tubules of adult males were torn and fixed to a cover slip. They then underwent the cytogenetic technique of Lacto-acetic orcein (De Vaio et al., 1985 with modifications according to Alevi et al., 2012) and analyzed using a Jenaval light microscope (Zeiss). For the characterization of the karyotype were analyzed 50 mitotic metaphases (I and II).

As well as was observed recently by Santos et al. (2016), *P. lutzi* presented a different karyotype of all species of the genus *Panstrongylus*, namely, $2n = 24$ ($20A + X_1X_2X_3Y$), being the Y sex chromosome heteropycnotic (Figure 1). This number of chromosomes is very peculiar because it was described to only three other species in subfamily Triatominae: *T. melanocephala* (Alevi et al., 2012), *T. vitticeps* (Schreiber and Pellegrino, 1950) and *T. eratyrisiformis* (Ueshima, 1966).

Starting from the principle that the ancestral karyotype of *Panstrongylus* is $2n = 23$ (Perez et al., 2002), during karyotype evolution of *P. megistus* and *P. lutzi* occurred simplicity (fusion) of a pair of autosomes (Perez et al., 2002) and agmatoploidy (fission) of X sex chromosome, respectively (Figure 2). The number of chromosomes of the *P. megistus* ($2n = 21$) and *P. lutzi* ($2n = 24$) can be used as a taxonomic tool to differentiate this species from all species of genus *Panstrongylus* ($2n = 23$), as well as allows distinguishing them from other 85 species of Triatominae subfamily that presents 22 (55 species) or 23 (30 species) chromosomes (Alevi et al., 2016; Bardella et al., 2016; Mendonça et al., 2016; Rosa et al., 2017).

Jurberg et al. (2001) based on chromatic and morphological analysis of only one specimen collected in Bahia described *P. sherlocki* as sister species of *P. lutzi*. However, Garcia et al. (2005) when analyze *P. lutzi* coming from the municipalities of Sobral (Bahia) and

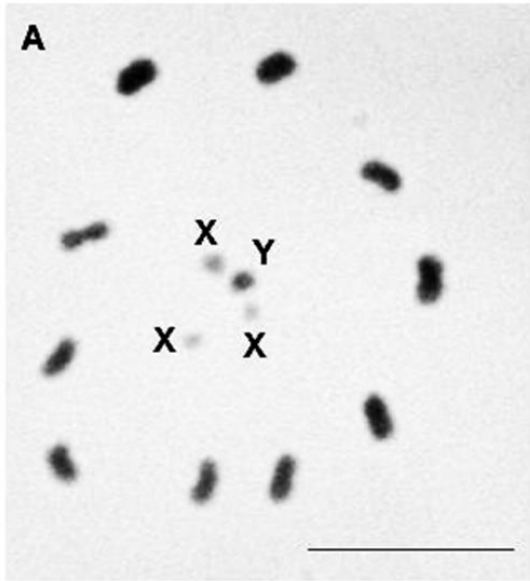


Figure 1. Karyotype of the *Panstrongylus lutzi*. Note $2n = 24$ ($20A + X_1X_2X_3Y$) chromosomes. X: X sex chromosome; Y: Y sex chromosome. Bar: 10 μ m.

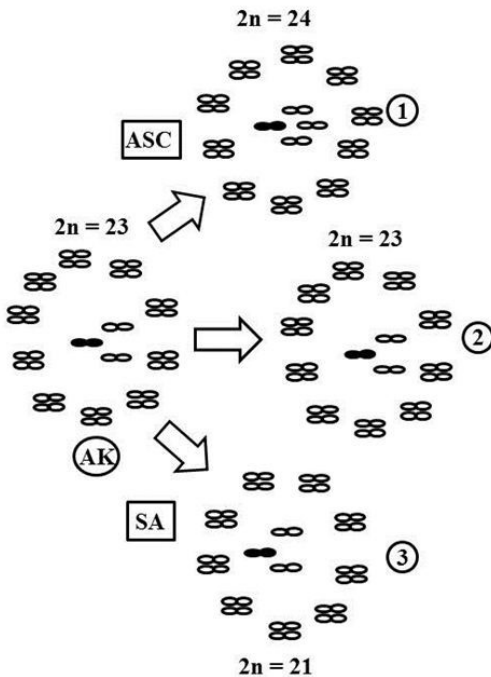


Figure 2. Karyotype evolution in the genus *Panstrongylus*. Note that from ancestral karyotype $2n = 23$, occurred three evolutionary events during the speciation of these vectors: (1) agmatoploidy in X sex chromosome, resulting in karyotype $2n = 24$ (*P. lutzi*); (2) absence of events that alter the karyotype numerically, keeping the same ancestor number $2n = 23$ (*P. chinai*, *P. geniculatus*, *P. howardi*, *P. lignarius*, *P. rufotuberculatus* and *P. tupynambai*); (3) simplidy in a pair of autosomes, resulting in karyotype $2n = 21$ (*P. megistus*). AK: ancestral karyotype; ASC: agmatoploidy in sex chromosome; SA: simplidy in autosomes.

Crateús (Ceará) observed high variability in morphological and morphometric characteristics and they classified the morphotypes that had the characteristics of *P. sherlocki* as *P. lutzi*. On that basis, *P. sherlocki* became considered as synonymous with *P. lutzi* (Schofield and Galvão, 2009). However, due to peculiarity observed in the karyotype of *P. lutzi*, we suggest that new karyotypic studies should be conducted on specimens initially classified as *P. sherlocki* by Jurberg et al. (2001), because if a different karyotype of $2n = 24$ is observed, the number of chromosomes would support the revalidation of the species.

Thus, this paper describes the number of chromosomes of *P. lutzi* [$2n = 24$ ($20A + X_1X_2X_3Y$)], suggests that karyotype arose from one agmatoploidy event of the X sex chromosome and mainly apply these data as taxonomic tool to differentiate this vector of other species of the genus *Panstrongylus*, as well as subfamily Triatominae.

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