



Short Communication

Molecular phylogeny of the *Drosophila tripunctata* and closely related species groups (Diptera: Drosophilidae)

Luciane Mendes Hatadani^a, James O. McInerney^b, Hermes Fonseca de Medeiros^a,
Ana Carolina Martins Junqueira^c, Ana Maria de Azeredo-Espin^{a,c}, Louis Bernard Klaczko^{a,*}

^a Departamento de Genética e Evolução, Instituto de Biologia, Universidade Estadual de Campinas (UNICAMP), P.O. Box 6109, Campinas, SP 13083-970, Brazil

^b Bioinformatics Laboratory, Department of Biology, National University of Ireland, Maynooth, Co. Kildare, Ireland

^c Laboratório de Genética Animal, Centro de Biologia Molecular e Engenharia Genética e Instituto de Biologia, Universidade Estadual de Campinas (UNICAMP), P.O. Box 6010, Campinas, SP 13083-875, Brazil

ARTICLE INFO

Article history:

Received 17 July 2008

Revised 27 February 2009

Accepted 28 February 2009

Available online 11 March 2009

Keywords:

Drosophila, *tripunctata*

Bayesian analysis

Mitochondrial

Neotropical

ABSTRACT

We suggest a new phylogenetic hypothesis for the *tripunctata* radiation based on sequences of mitochondrial genes. Phylogenetic trees were reconstructed by parsimony, maximum likelihood and Bayesian methods. We performed tests for hypotheses of monophyly for taxonomic groups and other specific hypotheses. Results reject the monophyly for the *tripunctata* group whereas monophyly is not rejected for the *tripunctata* radiation and other specific groups within the radiation. Although most of the basal nodes were unresolved we were able to identify four clusters within the *tripunctata* radiation. These results suggest the collection of additional data before a proper taxonomic revision could be proposed.

© 2009 Elsevier Inc. All rights reserved.

1. Introduction

The *Drosophila tripunctata* species group is presently the second largest Neotropical group of *Drosophila* (surpassed by the *D. repleta* group), comprising 78 species according to the Taxodros database of May 2008 (Bächli, 2008). Frota-Pessoa (1954) subdivided the group into four subgroups (I–IV) based on morphological characters. The *D. tripunctata* group is almost endemic to the Neotropics (Throckmorton, 1975), where its species are abundant, particularly in forest areas, and a dominant component of the drosophilid fauna (Ashburner et al., 2005; Klaczko, 2006).

The *tripunctata* radiation was created by Throckmorton (1975) and included the *tripunctata* group, as well as other groups (*calloptera*, *cardini*, *guarani*, *macroptera*, *pallidipenis*, *rubrifrons* and *sticta*). According to this author, a radiation which he called *immigrans-Hirtodrosophila* originated in the Paleotropics, where it initially diversified and from where it sent two separate lineages to the Neotropics: *tripunctata* (composing the *tripunctata* radiation) and *Hirtodrosophila*. Throckmorton (1975) also suggested that the *tripunctata* group itself should not be considered a monophyletic group. This statement is in agreement with cytological observations (Kastritsis et al., 1970) and recent molecular studies (Yotoko et al., 2003; Robe et al., 2005). The monophyly of the *tripunctata*

radiation as a whole has also been questioned (Remsen and O'Grady, 2002; Robe et al., 2005; Yotoko et al., 2003). In general, phylogenetic relationships among species belonging to the *tripunctata* radiation have been poorly studied, which has been pointed out by Markow and O'Grady (2006). Even though it seems clear that the *tripunctata* group is not monophyletic, the monophyly of the *tripunctata* radiation is still unresolved. Moreover, the studies mentioned previously were unable to recover a well supported phylogenetic hypothesis for relationships among the species groups within the radiation.

In this paper, we propose a new phylogenetic hypothesis for species of the *tripunctata* radiation of *Drosophila* based on sequences of mitochondrial genes of cytochrome oxidase subunits 1 and 2 (COI and COII) and test for different evolutionary hypotheses. Our aim was to improve the results obtained by Yotoko et al. (2003) and Robe et al. (2005) by adding both taxa and characters. In addition, we tested for monophyly of taxonomic groups (*calloptera*, *cardini*, *guarani* and *tripunctata*), of the *tripunctata* radiation, and of specific clades that appeared on the phylogenetic trees as monophyletic.

2. Materials and methods

2.1. COI and COII sequence data

Specific location of collection and taxonomic placement of each species are given in Table 1. All individuals included in the analysis

* Corresponding author. Fax: +55 19 3521 6235.

E-mail address: lbk@unicamp.br (L.B. Klaczko).

Table 1

Taxonomic placement and collection site of each species collected for DNA extraction and accession numbers of all sequences included in the phylogenetic analyses.

Subgenus	Group	Subgroup	Collection Site ^a	Species	Accession Number	
					COI	COII
<i>Drosophila</i>	<i>calloptera</i>		Mata Ribeirão Cachoeira	<i>D. atrata</i>	EF569988 *	EF570024 *
			—	<i>D. ornatipenis</i>	EF570010 *	EF570038 *
			Bosque dos Jequitibás	<i>D. schildi</i>	EF570016 *	AY162973
	<i>cardini</i>		Serra do Japi	<i>D. cardini</i>	EF569991 *	AY162974
			Brasília	<i>D. cardinoides</i>	EF569992 *	AY162975
			Bosque dos Jequitibás	<i>D. neocardini</i>	EF570006 *	EF570034
			Serra do Japi	<i>D. polymorpha</i>	EF570014 *	EF570040 *
	<i>guarani</i>	<i>guaramunu</i>	Serra do Japi	<i>D. griseolineata</i>	EF569995 *	EF570029 *
			Serra do Japi	<i>D. guaraja</i>	EF569996 *	EF570030
			Serra do Japi	<i>D. maculifrons</i>	EF569998 *	EF570031 *
		<i>guarani</i>	Mata Ribeirão Cachoeira	<i>D. guaru</i>	EF569997 *	EF570031 *
			Serra do Japi	<i>D. ornatifrons</i>	EF570009 *	AY162978
	<i>pallidipenis</i>		Serra do Japi	<i>D. pallidipenis</i>	EF570011 *	AY162982
	<i>sticta</i>		Mata Ribeirão Cachoeira	<i>D. sticta</i>	EF570018 *	EF570044 *
	<i>tripunctata</i>	I	Mata Ribeirão Cachoeira	<i>D. nappae</i>	EF570005 *	AY162983
			Mata Ribeirão Cachoeira	<i>D. neoguaramunu</i>	EF570007 *	EF570036 *
			Bosque dos Jequitibás	<i>D. setula</i>	EF570022 *	EF570042 *
			Serra do Japi	SP22 ^b	EF570017 *	EF570043 *
		II	Serra do Japi	<i>D. cuaso</i>	EF569993 *	EF570027 *
			Mata Ribeirão Cachoeira	<i>D. medioimpressa</i>	EF569999 *	AY162994
			Serra do Japi	<i>D. mediopunctata</i>	EF570001 *	AY162988
			Serra do Japi	<i>D. mediosignata</i>	EF570002 *	AY162985
			Serra do Japi	<i>D. paraguayensis</i>	EF570012 *	EF570039 *
			Serra do Japi	<i>D. roehrae</i>	EF570015 *	EF570041 *
			Mata Ribeirão Cachoeira	<i>D. unipunctata</i>	EF570020 *	EF570047 *
		III	Serra do Japi	<i>D. bandeirantorum</i>	EF569989 *	EF570025 *
			Bosque dos Jequitibás	<i>D. bifilum</i>	EF569990 *	EF570026 *
			Mata Ribeirão Cachoeira	<i>D. frotapessoai</i>	EF569994 *	EF570028 *
			Serra do Japi	<i>D. mediopicta</i>	EF570000 *	EF570033 *
			Serra do Japi	<i>D. mediotriata</i>	EF570003 *	EF570034 *
			Mata Ribeirão Cachoeira	<i>D. nigrincta</i>	EF570008 *	EF570037 *
			Serra do Japi	<i>D. paramediotriata</i>	EF570013 *	AY162995
			Mata Ribeirão Cachoeira	<i>D. trifilum</i>	EF570019 *	EF570046 *
		IV	Bosque dos Jequitibás	<i>D. metzii</i>	EF570004 *	AY162992
			—	<i>D. tripunctata</i>	EF570023 *	AF519343
	<i>quinaria</i>		—	<i>D. falleni</i>	AY541136	AF147117
			—	<i>D. innubila</i>	AY541192	AY541211
			—	<i>D. quinaria</i>	AY154400	AF478428
			—	<i>D. recens</i>	AY154456	AF147123
			—	<i>D. subquinaria</i>	AY154457	AY154457
	<i>immigrans</i> <i>repleta</i>	<i>immigrans</i> <i>hydei</i>	Mata Ribeirão Cachoeira	<i>D. immigrans</i>	EF570021 *	AY162993
			—	<i>D. eohydei</i>	DQ471601	AF145889
			—	<i>D. hydei</i>	DQ471602	DQ202020
<i>Sophophora</i>	<i>melanogaster</i>	<i>melanogaster</i>	—	<i>D. melanogaster</i>	NC001709	NC005779
			—	<i>D. mauritiana</i>	NC005779	NC001709
			—	<i>D. sechellia</i>	NC005780	NC005780
			—	<i>D. simulans</i>	NC005781	AF474082
			—	<i>D. yakuba</i>	NC001322	NC001322

^a Coordinates for each collection site are: 22°55' S, 47°03' W (Bosque dos Jequitibás, Campinas, SP); 15°46' S 47°55' W (Brasília, DF); 22°50' S, 46°55' W (Mata Ribeirão Cachoeira, Campinas, SP); 23°13' S, 46°53' W (Serra do Japi, Jundiá, SP).

^b Undescribed species. SP22 and *D. nappae* are sibling species.

* New sequences obtained in this study.

were adult males, identified by the aedeagus, the most reliable method of identification of these species (Vilela, 1992). In addition, prior to DNA extraction, the terminalia of each male was removed and preserved in 70% alcohol. This procedure would allow for future confirmation of species identification and reevaluation in case of taxonomic revisions.

Total DNA of each individual was extracted using a phenol–chloroform protocol (Azeredo-Espin et al., 1991). The primers used for amplification were TL2-N-3014 and C1-J-2195 (COI), and TL-2-J3037 and TK-N-3785 (COII), described in Simon et al. (1994). The amplified products were purified with the QIAquick PCR purification kit. With the exceptions of the 5' fragment of COI of *D. guaru*, *D. trifilum*, *D. maculifrons* and *D. setula*, and COII of *D. mediotriata*—in

which case PCR products were cloned into the PCR2.1 cloning vector using a TA Cloning Kit (Invitrogen)—all PCR products were directly sequenced. Sequencing was performed using BigDye (Applied Biosystems) chemistry on either an ABI377A or an ABI3700 automatic sequencer. At least two sequences of each fragment were obtained for each individual to ensure high quality of sequences. Except for the cloned samples (three clones per species), for which we used primers provided by the Cloning Kit, the primers used for sequencing were the same as in PCR. All resulting sequence chromatograms were evaluated and edited with the use of the programs Phred (Ewing et al., 1998), Phrap and Consed (Gordon et al., 1998).

Additional sequences were obtained from GenBank whereas individuals of *D. ornatipenis* were obtained from Tucson Fly Stock

Download English Version:

<https://daneshyari.com/en/article/2834711>

Download Persian Version:

<https://daneshyari.com/article/2834711>

[Daneshyari.com](https://daneshyari.com)