



# Unveiling South America

# ICO 2015



INTERNATIONAL CONGRESS  
OF ODONATOLOGY  
LA PLATA • BUENOS AIRES  
ARGENTINA

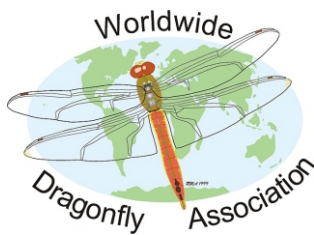
## Book of abstracts

# 2015 INTERNATIONAL CONGRESS OF ODONATOLOGY

La Plata, Buenos Aires, Argentina

15th to 20th November 2015

ICO 2015 is organized by the group of odonatologists lead by Javier Muzón. Although, this group has started their work several years ago at the Instituto de Limnología “Dr. R.A. Ringuelet” (CONICET – FCNyM, UNLP), most of their integrants are now part of BioGeA (Laboratorio de Biodiversidad y Genética Ambiental) of the Universidad Nacional de Avellaneda (UNDAV).



ICO 2015 is organized in consensus with the Worldwide Dragonfly Association (WDA) and the Societas Internationalis Odonatologica (SIO). This meeting is under the auspices of the Universidad Nacional de La Plata (UNLP) and its Facultad de Ciencias Naturales y Museo (FCNyM), the Universidad Nacional de Avellaneda (UNDAV), the National Research Council of Argentina (CONICET) and the Research Council of Buenos Aires province (CIC-BA). ICO 2015 has been supported by Seguros Rivadavia.

## ICO 2015 Book of Abstracts

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are close related to *H. superbum* and *H. croizati* and form a unstable clade topology in the analysis. Finally the results allow sustain species level for *H. sanguinipes* and *H. superbum* as lineages separated.

### The position of the former Neotropical "Protoneuridae" within Coenagrionoidea, a morphological cladistic analysis.

**Pablo Pessacq & Danielle Anjos dos Santos**

Protoneuridae and Coenagrionidae familiar status has been recently challenged by molecular and morphological phylogenetic analysis. There is coincidence in these analyses in considering Coenagrionidae as a paraphyletic clade that would include Neotropical Protoneuridae and Pseudostigmatidae. The monophyly of the former is strongly suggested by wing synapomorphies, such as the rectangular discoidal cell and the subarcus position at or proximal to Rp-Ma bifurcation, and its position as a subfamily is suggested by molecular data. In order to analyze the position of Neotropical Protoneuridae within Coenagrionoidea, its monophyly and the relation of its members, we constructed a data matrix of 61 morphological characters and 37 taxa. *Philogenia cassandra* (Megapodagrionidae) was selected as outgroup, while two Platystictidae, one Isostictidae, five Platycnemididae (including three of the former Paleotropical Protoneuridae), twelve Coenagrionidae and 17 Neotropical Protoneuridae species were included as outgroup. Analyses were conducted using TNT program, a posteriori weighting was chosen using the command "implied weighting". The analysis produced two very similar trees that support the inclusion of Neotropical Protoneuridae within Coenagrionidae. However, its members are recovered as a polyphyletic clade, with *Proneura*, *Junix*, and *Phasmoneura* nesting within rounded frons Coenagrionidae, and the remaining genera as a monophyletic clade within angulate frons Coenagrionidae. This unexpected result is coincident with previous morphological and molecular analyses that divide Coenagrionidae (plus Protoneuridae and Pseudostigmatidae) in two major clades based on the frons shape. Jackknife resamplings do not support most groups. *Telebasis willinki* and *Nehalennia irene* are the sister group to core Protoneuridae, and *Microneura caligata* and *Idioneura ancilla* the basal Protoneuridae. As in previous analyses, *Protoneura* appears as a polyphyletic group, while *Roppaneura beckeri*, *Psaironeura remisa*, *Amazonneura ehipigera*, *Forcepsioneura sancta* and *Lamproneura lucerna* conform a monophyletic clade and are the more derivate genera.

### Damselflies of Patagonia, a phylogeographic study utilizing EPIC DNA and mitochondrial sequence markers

**Pablo Pessacq, Seth M. Bybee, Taylor King, Preston Arnold, Danielle Anjos dos Santos & Mariana Morando.**

We conducted the first phylogeographic study of Patagonian insects, for which we selected the two most widely distributed species of Odonata in the region: *Rhionaeshna variegata* (Aeshnidae)



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and *Cyanallagma interruptum* (Coenagrionidae). First, we performed a preliminary analysis of nine populations of both species from most of their distribution range, and we sampled the nuclear genes H3 and 28S, and the mitochondrial genes 16S, COXI and COXII. While *R. variegata* showed no genetic structure, *C. interruptum* showed genetic structure for COXI/II and 16S. These results are consistent with a greater dispersal ability among aeshinds as compared with coenagrionids. Thus, we pursued further analyses for *C. interruptum*, for which we included eleven additional populations (20 populations and 54 specimens total) that cover most of its distributional range in Argentina. We performed network and phylogeographic analyses with the mitochondrial genes COXI/II and with the recently developed EPIC (exon-primed intron-crossing) nuclear genes PRMT, CDC5 and AgT. The mtDNA results show that *C. interruptum* consists of two major clades with considerable genetic differences, one distributed in the north (Northern Patagonia) and one in the south (central Patagonia). Individuals from a small area in between these two regions (southwestern Río Negro) have haplotypes recovered from both clades. This pattern is concordant with a separation of the ancestral population in the past and the posterior secondary contact in the intermediate localities. It is probable that events during the Pleistocene (glaciation cycles and associated changes in climate and/or other geological events) interrupted gene flow among northern and southern populations. The nuclear genes showed a high level of heterozygosity but low levels of genetic structure with no signals of geographic structure. The incongruence between the two types of markers allow us to elaborate two non-exclusive main hypotheses: 1) females may have lower dispersal capacity or high philopatry compared to males, 2) the temporal separation between the two populations was relatively brief providing enough time for mitochondrial markers to differentiate genetically, but not sufficiently long to be reflected by the more constrained evolutionary rates of the nuclear genes.

### A first look at the phylogenetic relationships of *Forcepsioneura* and related genera (Coenagrionidae: Protoneurinae)

**Ana Luiza Anes Pimenta, Ângelo Parise Pinto & Daniela Maeda Takiya**

The six valid species of *Forcepsioneura* Lencioni are restricted to Brazil and difficult to identify based on morphological characters. Recently collected material from Rio de Janeiro, São Paulo, and Bahia States are morphologically similar to the type species, *F. garrisoni* Lencioni, but differ slightly in some aspects, which can be used to separate them into three morphotypes. A previous morphological phylogenetic analysis of the Protoneurinae, shows *Forcepsioneura* within a clade (*i.e.* *Roppaeneura*+), supported by the uncarinated antennifer and long and incurved lobes of the genital ligula, together with other five Neotropical genera: *Amazoneura* Machado, *Lamproneura* De Marmels, *Phasmoneura* Williamson, *Psaironeura* Williamson and *Roppaeneura* Santos. The aim of this study was to add molecular data to hypothesize phylogenetic relationships among *Roppaeneura*+ genera and *Forcepsioneura* species and help delimit the taxonomic units through an integrative approach of the putative *F. garrisoni* species complex. Parsimony and Bayesian analyses were performed using two molecular markers: cytochrome oxidase I (COI) and 16S rDNA. Taxon sampling include specimens of