



## A new species of the *hysius* species-group of *Calisto* Hübner (Lepidoptera, Nymphalidae, Satyrinae) and insights into the status of different populations currently attributed to *C. grannus* Bates

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### Abstract

A species belonging to the *hysius* group of *Calisto* is newly described. *Calisto bahoruco* **new species** inhabits the eastern-most area of the southern Hispaniola Sierra de Bahoruco. The species is closely related to *C. hysius* Godart, another endemic from the southern mountains. The two species differ in average forewing length (larger in *C. hysius*), the relative size of ocelli (larger in *C. bahoruco*), and in the darker ground color with more contrasted paler edges of lines at underside of wings in *C. bahoruco* compared to *C. hysius*. Their male genitalia differ in the shape of the uncus and in the heavier sclerotization in *C. bahoruco*. COI barcodes bear a minimum of 15 differences between the two species. All species delimitation methods applied to the COI dataset, ABGD, BIN, bPTP, mPTP, and PTP yielded 8 species. The exception was the GMYC that failed to recognize the new taxon and oversplitted several other taxa. COI gene tree obtained by Maximum Likelihood and Bayesian have identical topologies agreeing with a multilocus phylogeny reconstructed in a previous work on *Calisto* and placing the new taxon as sister of *C. hysius*. Additionally, we provide new evidence of the conspecific nature of all named populations within *Calisto grannus* group.

Key words: Greater Antilles, Hispaniola, COI, ABGD, barcoding, Bayesian Inference, BIN, character base, diagnostic sites, GMYC, haplotype network, Maximum Likelihood, monophyly, new species, gen tree, phylogeny, PTP

### Introduction

The genus *Calisto* Hübner is the only representative of the Satyrinae in the Greater Antilles with 47 known species, most of them endemic from a single island (Matos–Maravi *et al.* 2014, Pérez–Asso *et al.* 2016, Núñez *et al.* in press). The island of Hispaniola possesses the highest species richness with several species groups commonly referred by authors in the rich bibliography on the genus (eg. Bates 1935, Munroe 1950, Galí 1985).

Intensive collecting efforts during the last decade together with the increasing number of molecular studies are bringing light into the genus taxonomy and phylogenetic relationships (Sourakov & Zakharov 2011, Núñez *et al.* 2012, 2013, in press, Matos–Maravi *et al.* 2014, Pérez–Asso *et al.* 2016). Currently, 39 species, 83% of the total known, have at least one gene sequenced.

The *hysius* species group, originally defined by Bates (1935), includes ten species. *Calisto confusa* Lathy, *C. obscura* Michener and *C. batesi* Michener are widespread across Hispaniola (Schwartz 1989, Smith *et al.* 1994). The remainder are known from a single mountain range or are restricted to one or few localities.

In the present work we describe the eleventh species of the group, a taxon closely related to *C. hysius* Godart. In addition, we test the species boundaries within the *hysius* group using 215 COI barcode sequences available from eight species applying several species delimitation methods, and provide additional evidence that populations within *Calisto grannus* group are conspecific.

## Material and methods

**Specimen collections.** The field work involved collecting trips from 2010 to 2014 across the Dominican Republic including the visit to the type localities, or their vicinity, for all species previously described, mentioned in detail by Schwartz (1989).

Morphological characters and species diagnosis. We investigated those taxonomic characters traditionally used in the work on the *hysius* group (Bates 1935, Michener 1943, Gonzalez 1987). As a starting point, we followed the species definition for each taxon of the *hysius* species group proposed by the latest authors (Johnson & Hedges 1998, Sourakov & Zakharov 2011).

**Molecular protocols and sequence editing.** Data acquisition and analysis DNA extraction, PCR amplification, and sequencing of the COI barcode region were performed at the Canadian Centre for DNA Barcoding (CCDB) and followed standard protocols (CCDB 2013). PCR and sequencing used a single pair of primers: LepF1 (ATTCAACCAATCATAAAGATATTGG) and LepR1 (TAAACTTCTGGATGTCCAAAAAATCA) (Hebert *et al.* 2004) which recovers a 658 bp region near the 5' end of COI including the 648 bp barcode region for the animal kingdom (Hebert *et al.* 2003).

Sequence editing and alignment were done manually using BioEdit v7.0.9 (Hall 1999). DNA sequences have been submitted to GenBank (see Table 1 for accession numbers). DNA voucher specimens are deposited at the Victor Gonzalez Research Collection, Puerto Rico.

Additional DNA sequences from *hysius* group members were downloaded from GenBank, <http://genbank.gov/> (Benson *et al.* 2014). However, we only used these from specimens with precise locality data, since some GenBank sequences have imprecise distribution data (Table 1).

**Phylogenetic reconstruction.** The phylogenetic reconstruction of the *hysius* species group was performed following Maximum Likelihood (ML) and Bayesian Inference (BI) methods. In both cases *Calisto eleleus* Bates was used as outgroup being one of the earliest divergent species of the genus (Matos–Maraví *et al.*, 2014). Our main goal was to assess the position of the new species described herein.

For the ML analysis, we used RAXML (Stamatakis *et al.* 2008) with 1000 rapid bootstrap replicates and a search for the maximum likelihood topology on the CIPRES portal (Miller *et al.* 2010). The data were modeled according to the GTR + G model.

In the BI approach, we infer the best-fitting model of molecular evolution and partition scheme to apply using PartitionFinder 1.0.1 (Lanfear *et al.* 2012). The best-fitting partition/substitution model scheme, as determined by the AICc, was implemented in a Bayesian inference analysis with MrBayes 3.2 (Ronquist *et al.* 2012). The independent MCMC analyses were run for 20 million generations and the sampling of trees and parameters was set to every 1000 generations at CIPRES. Convergence of the two runs was determined by the stationary distribution plot of the log likelihood values against number of generations and confirmed by the average standard deviation of split frequencies which in all the cases were lower than 0.05. We discarded the first 5 million generations as burn-in and trees were summarized under the 50 percent majority rule method.

**Species delimitation methods.** The species delimitation methods Automatic Barcode Gap Discovery (ABGD) (Puillandre *et al.* 2012), General Mixed Yule Coalescent model (GMYC) (Pons *et al.* 2006, Monaghan *et al.* 2009) and Poisson Tree Processes (PTP) (Zhang *et al.* 2013) were used to test the boundaries of species within the *hysius* groups as currently recognized.

The Automatic Barcode Gap Discovery method was used (Puillandre *et al.* 2011, 2012) to sort the available 215 sequences into genetic clusters or hypothetical species. This algorithm automatically finds the inflection point in the frequency distribution of ranked pairwise genetic distances between aligned homologous sequences, and does so recursively to get the finest partition of the data set into candidate species (Puillandre *et al.* 2011, 2012). A matrix of pairwise uncorrected p-distances in MEGA excluding all ambiguous positions between each pair of sequences was calculated. We used the ABGD web-interface available at: <http://www.wabi.snv.jussieu.fr/public/abgd/> using the default values for all parameters. The analysis was performed employing the three implemented models (Jukes–Cantor, K2P, and Simple Distance).

The Generalized Mixed Yule Coalescent (GMYC) method (Fujisawa & Barraclough 2013, Pons *et al.* 2006) is a likelihood method for delimiting independently evolving species. The GMYC method requires an ultrametric tree without identical sequences to avoid zero length terminal branches that hamper the likelihood estimation. The ultrametric tree was obtained in an analysis performed using BEAST v.1.8.2. (Drummond *et al.* 2012) at CIPRES

server with 100 million generations and sampling every 10000 generations, under a HKY substitution model. The GMYC was run as implemented in the GMYC web server (<http://species.h-its.org/gmyc/>).

The Poisson tree processes (PTP) is a new model that can delimit species using non ultrametric phylogenies (Zhang *et al.* 2013). The fundamental assumption of this method is that the number of substitutions is significantly higher between species than within species (Zhang *et al.* 2013). There are three variants of this method available in web servers and all were implemented. bPTP is a version of the original maximum likelihood PTP (maximum likelihood PTP search result is part of the bPTP results) that adds Bayesian support (BS) values to delimited species on the input tree. Higher BS value on a node indicates all descendants from this node are more likely to be from one species (Zhang *et al.* 2013). Analysis used the tree resulting in newick format from the BI analysis as input for the bPTP server, <http://species.h-its.org/> (Zhang *et al.* 2013). We also applied the Multi-rate PTP method, Kapli *et al.* (2016), using the ML analysis tree as input for the two variants, mPTP and PTP, available at <http://mptp.h-its.org/#/tree>.

We also compared the results with the output of the BIN system from BOLD. This system employs a two-stage algorithm (Refined Single Linkage) that couples single linkage and Markov clustering to assign sequences to a sequence cluster that is subsequently assigned a unique identifier termed a Barcode Index Number (Ratnasingham & Hebert 2013). The Refined Single Linkage algorithm matches the taxonomic performance of competing approaches, but couples this with protocols that are simple enough to allow the automated assignment of all new barcode records to a BIN (Ratnasingham & Hebert 2013).

**Character base.** We inspected visually the COI alignment to identify the presence or absence of discrete nucleotide substitutions, character states. These substitutions potentially allow the identification of species or even populations (Rach *et al.* 2008, Tavares & Baker, 2008, Brower 2010). We arranged the clustered sequences of each hypothetical species and then by localities in a single fasta file. Then this file was visually inspected in MEGA looking for unique substitutions at each site within hypothetical species as well as within populations.

Abbreviations and acronyms:

ABGD	Automatic Barcode Gap Discovery
BIN	Barcode Index Number
BS	Maximum Likelihood Bootstrap
FW	forewing
FWL	forewing length
GMYC	Generalize Mixed Yule Coalescent
HW	hindwing
K2P	Kimura 2 parameter
PP	Bayes posterior probability
PTP	Poisson Tree Process
VGRC	Victor González Research Collection, San Juan, Puerto Rico
ZSM	Zoologische Staatssammlung Muenchen, Munich, Germany

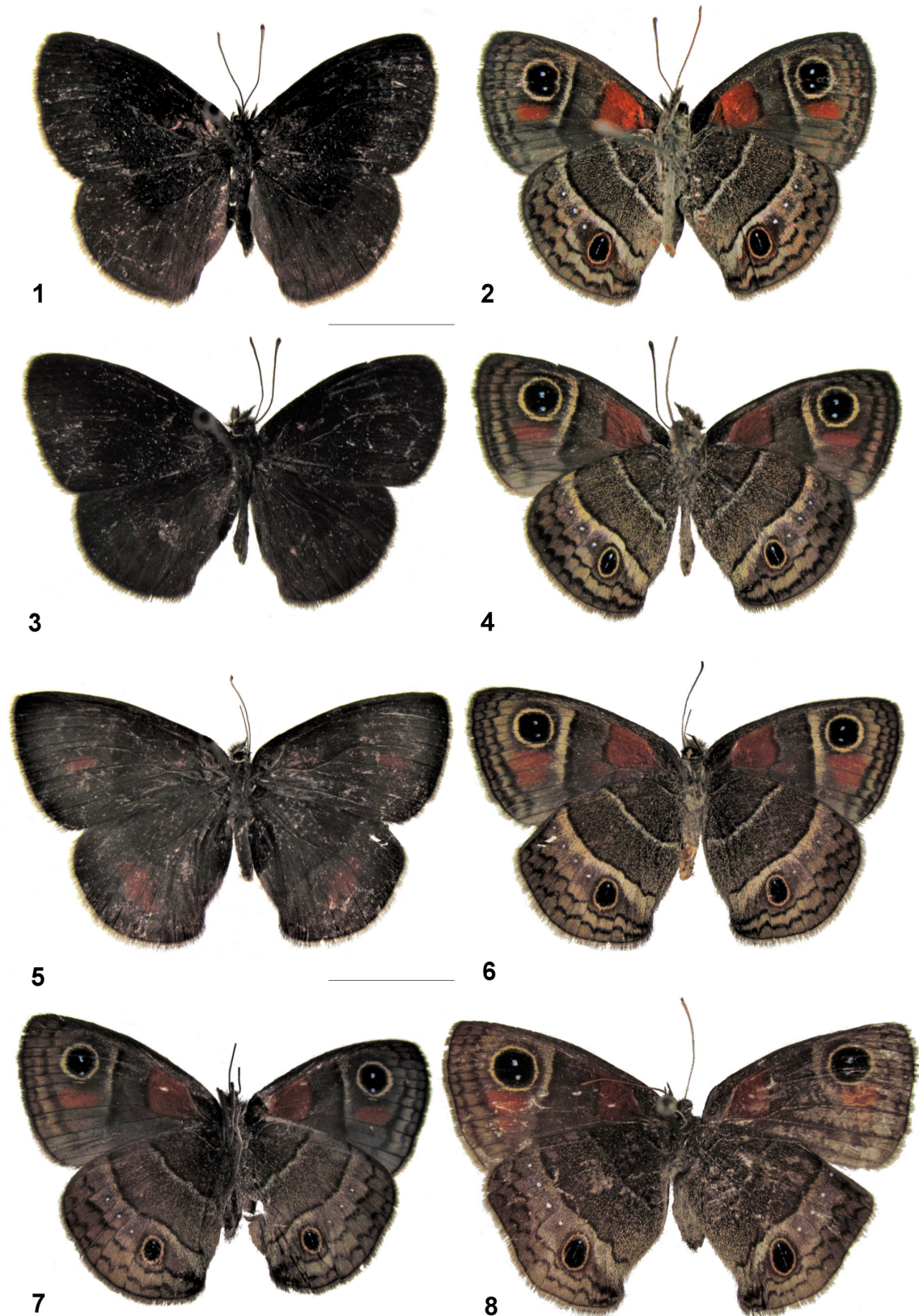
## Results

### Taxonomy

#### *Calisto bahoruco* Pérez–Asso, Núñez & Genaro, new species

Figures 1–6, 9–10

**Diagnosis.** *Calisto bahoruco* n. sp. requires comparison with its closest relative *C. hysius*. Both have a similar color pattern but differ in several characters. Average FWL is smaller in *C. bahoruco*, 15 mm in males (n=5) and 16.8 mm females (n=5), than in *C. hysius*, 16.5 mm in males (n=7), 18.3 mm in females (n=4). Ocelli are distinctly larger in *C. bahoruco* with a median of the ratio ocellus largest diameter/wing length of 0.20 at FW and 0.18 at HW. Values in *C. hysius* are 0.17 and 0.14 at FW and HW respectively. Wing pattern of *C. bahoruco* shows a darker background on the under surface, the discal of the HW is straighter and smooth, the overall pale scaling on



**FIGURES 1–8.** Adults of the *hysius* species group of *Calisto*. 1–2 *C. bahoruco* **new species**, male holotype, Villa Nizao, Paraíso, Barahona, República Dominicana: 1—upper surface, 2—under surface. 3–4 *C. bahoruco* **new species**, male paratype, same data: 3—upper surface, 4—under surface. 5–6 *C. bahoruco* **new species**, female paratype, same data: 5—upper surface, 6—under surface. 7–8 Under surface *C. hysius*, Los Arroyos, Pedernales, Sierra de Bahoruco, República Dominicana: 7—male, 8—female. Scale bar 10 mm. Pictures by Antonio R. Pérez-Asso.





**FIGURES 9–12.** Living adults of the *hysius* species group of *Calisto*. 9–10 *C. bahoruco* **new species**, Villa Nizao, Paraíso, Barahona, República Dominicana. 11–12 *C. hysius*, Los Arroyos, Pedernales, Sierra de Bahoruco, República Dominicana. Pictures by Pérez–Asso.

the distal edge of lines is much more contrasting compared to the equivalent in *C. hysius* which shows a paler ground colour, less contrasting distal edges of lines and the discal line more irregular than that in *C. bahoruco*. Genitalia are very similar in both sexes, however, the tegumen of *C. hysius* male broadly protrudes backwards compared to that of *C. bahoruco* (Figs. 13, 14), and in addition the male structure of the latter is notably more sclerotized (Fig. 13). The minimum pairwise K2P genetic distance among *C. bahoruco* **n. sp.** and a representative of the *hysius* group is to *C. hysius*, 2.3%, with intraspecific genetic distances averaging 0.14 and 0.05% respectively (Table 2). Comparison of COI barcodes belonging to both species showed *C. hysius* has a cytosine at positions 187 and 517, characters absent from any other *hysius* group member including *C. bahoruco* **n. sp.** (Table 3). The barcode of the latter species bears a thymine at position 220 whereas *C. hysius* possesses cytosine. However, this character is not exclusive since it is present in two sequences of *C. batesi*, all remaining 207 analyzed sequences bear a cytosine in that position. Additional non exclusive nucleotide positions distinguishing the COI barcodes of both species are mentioned in the Species delimitation methods section.

**Description.** Male (Figs 1–4): FWL 14.2–16.2 mm. Upper surface blackish brown, FW with triangular androconial patch from base to the cell on the area below the latter. Underside dark brown, paler beyond the post discal line on the FW. Discal cell with a red spot outwardly edged by a transverse blackish brown line. FW post discal line with a narrow pale yellow band on its outer edge. FW ocellus moderately large, circular, with two white pupils and edged below by a red spot. HW dark brown, background color formed by a mix of dark brown and pale yellow scales. HW discal line moderately straight outwardly edged by a narrow but distinctive band of white scales. HW ocellus elliptical, with a single basal white pupil and a trace of white scales along its larger axis; area

around external ring rusty colored. Area above ocellus with four tiny white dots being the one at Sc–Rs interspace the smaller. Post discal and subterminal lines edged by pale yellow contrasting scales on the outer and inner sides respectively.

Genitalia (Fig. 13). As illustrated.

Female (Figs 5, 6): FWL 15.7–17.9 mm. Similar to male except: Upperside of wings brown, outer half of wings paler. Outer third of the four wings with a rusty spot at central position.

Genitalia (Fig. 15). As illustrated.

HOLOTYPE. Male. Villa Nizao, Paraíso, Barahona, República Dominicana, 5–VIII–2014, A. R. Pérez–Asso & A. López coll., DNA voucher code JAGWI–1018 (VGRC).

PARATYPES. 4♂, 5♀, same data as holotype except DNA voucher codes JAGWI–1015, 1016, 1018, R–114, R–115 (VGRC). Genitalia slide preparations ♂: Rh1745, Rh1752, and ♀: Rh1747 (ZSM).



FIGURES 13–14. Male genitalia of the *hysius* species group of *Calisto*, lateral view 13—*C. bahoruco*, new species. 14—*C. hysius*. Scale bar 0.5 mm.

**Distribution** (Fig. 17). Only known from the type locality, Villa Nizao, Barahona province, at the foothills of eastern extreme of Sierra de Bahoruco, Dominican Republic. Apparently the species also inhabits several localities around the type locality, all at Barahona province (see Discussion).

**Natural history.** Unknown. The type series was collected only at the type locality, a secondary mesic forest mixed with coffee plantations.

**Comparative examined material.** *Calisto hysius*:

**Type.** *Satyrus hysius* 68, Godart (RSM). Reviewed through pictures available at Butterflies of America website (Warren *et al.* 2015).

Additional material (9♂, 4♀): camino de Los Arroyos a Ojo de Agua, Pedernales, República Dominicana, 28–VII–2010, A. López, A. R. Pérez–Asso & J. A. Genaro colls., DNA voucher codes WI–JAG–493–497 (5 ♂). Same data as anterior except July 2010, J. A. Genaro & A. R. Pérez–Asso colls., DNA voucher code WI–JAG–549 (♂). El Aguacate, 1055 m, pinar, Sierra de Bahoruco, Pedernales, República Dominicana, 9–Jun–2011, A. López & A. R. Pérez–Asso colls. (3 ♀). Zapoten, 1545 m, pinar, Sierra de Bahoruco, Pedernales, República Dominicana, 11–Jun–2011, A. López & A. R. Pérez–Asso colls. (1 ♂, 1 ♀). Las Abejas, pinar–latifoliado, PN Sierra de Bahoruco, Pedernales, República Dominicana, 20–11–2011, A. R. Pérez–Asso & A. López colls. (2 ♂). (VGRC).

Genitalia slide preparations ♂: Rh1743, Rh1746, and ♀: Rh1739, Rh1744 (ZSM).





**FIGURES 15–16.** Female genitalia of the *hysius* species group of *Calisto*, ventral view. 15—*C. bahoruco*, **new species**. 16—*C. hysius*. Scale bar 1 mm.



**FIGURE 17.** Geographic distribution of the *hysius* species group of *Calisto*. Black rhombus—type locality of *C. bahoruco*, **new species**; question marks—potential distribution of *C. bahoruco* following information by Schwartz (1989) and Warren et al. (2015); white rhombus—type locality of *C. hysius*, after Johnson & Hedges (1998); white circles—distribution of *C. hysius*, after Schwartz (1989).

### COI barcodes of the *hysius* group species

We obtained 150 COI barcodes and downloaded 59 additional sequences from GenBank. The 209 sequences in total were 570 to 658 bp long representing eight of the eleven species of the *hysius* group, including *C. bahoruco*. Only *C. loxias* Bates, *C. pauli* Johnson & Hedges and *C. thomasi* Johnson & Hedges lack sequences.

Barcodes had 166 variable sites, 25.2%, of which 153 were informative, 23.3%. Intraspecific variation ranged from 0.04 to 0.77% whereas minimum pairwise distances from 2.3 to 12.4%, or 15 to 65 differences (Table 2).

**TABLE 1.** List of specimens with COI barcode sequences analyzed and their corresponding collection and repository data and GenBank accession numbers. Voucher codes are unique identifiers referring to specimens at repositories and to individual records in the Barcode of Life Datasystems (BOLD, [www.boldsystems.org](http://www.boldsystems.org)).

Taxa	Voucher code	Locality	Genbank Accession Number
<i>Calisto grannus amazona</i>	WI-JAG-857	Dominican Republic, San Juan, Comparticion, Cordillera Central	MF172153
<i>Calisto grannus amazona</i>	WI-JAG-856	Dominican Republic, San Juan, Comparticion, Cordillera Central	MF172119
<i>Calisto grannus amazona</i>	WI-JAG-855	Dominican Republic, San Juan, Comparticion, Cordillera Central	MF172167
<i>Calisto grannus amazona</i>	WI-JAG-854	Dominican Republic, San Juan, Comparticion, Cordillera Central	MF172179
<i>Calisto grannus amazona</i>	WI-JAG-853	Dominican Republic, San Juan, Comparticion, Cordillera Central	MF172144
<i>Calisto grannus amazona</i>	WI-JAG-852	Dominican Republic, San Juan, Valle de Bao, Cordillera Central	MF172209
<i>Calisto grannus amazona</i>	WI-JAG-851	Dominican Republic, San Juan, Valle de Bao, Cordillera Central	MF172173
<i>Calisto grannus amazona</i>	WI-JAG-850	Dominican Republic, San Juan, Valle de Bao, Cordillera Central	MF172160
<i>Calisto grannus amazona</i>	WI-JAG-849	Dominican Republic, San Juan, Valle de Bao, Cordillera Central	MF172102
<i>Calisto grannus amazona</i>	WI-JAG-848	Dominican Republic, San Juan, Valle de Bao, Cordillera Central	MF172104
<i>Calisto bahoruco</i>	WI-JAG-1019	Dominican Republic, Barahona, Villa Nazao, Paraiso	MF172195
<i>Calisto bahoruco</i>	WI-JAG-1018	Dominican Republic, Barahona, Villa Nazao, Paraiso	MF172133
<i>Calisto bahoruco</i>	WI-JAG-1016	Dominican Republic, Barahona, Villa Nazao, Paraiso	MF172180
<i>Calisto bahoruco</i>	WI-JAG-1015	Dominican Republic, Barahona, Villa Nazao, Paraiso	MF172161
<i>Calisto bahoruco</i>	R-114	Dominican Republic, Barahona, Villa Nazao, Paraiso	MF172252
<i>Calisto bahoruco</i>	R-115	Dominican Republic, Barahona, Villa Nazao, Paraiso	MF172253
<i>Calisto batesi</i>	WI-JAG-517	Dominican Republic, Pico Diego de Ocampo	JN299994
<i>Calisto batesi</i>	WI-JAG-981	Dominican Republic, La Vega, Jarabacoa	MF172171
<i>Calisto batesi</i>	WI-JAG-515	Dominican Republic, camino a Playa Fronton, Samana	JN299992
<i>Calisto batesi</i>	WI-JAG-513	Dominican Republic, Puerto Plata, Pico Isabel de Torres	JN299990
<i>Calisto batesi</i>	WI-JAG-512	Dominican Republic, Las Abejas, Sierra Bahoruco	JN299989
<i>Calisto batesi</i>	WI-JAG-548	Dominican Republic, Las Abejas, Sierra Bahoruco	JN300024
<i>Calisto batesi</i>	WI-JAG-516	Dominican Republic, Pico Diego de Ocampo	JN299993
<i>Calisto batesi</i>	WI-JAG-514	Dominican Republic, camino a Playa Fronton, Samana	JN299991

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TABLE 1. (Continued)

Taxa	Voucher code	Locality	Genbank Accession Number
<i>Calisto batesi</i>	WI-JAG-911	Dominican Republic, Santiago Rodriguez, La Leonor	MF172192
<i>Calisto batesi</i>	WI-JAG-910	Dominican Republic, Santiago Rodriguez, La Leonor	MF172188
<i>Calisto batesi</i>	WI-JAG-909	Dominican Republic, Santiago Rodriguez, La Leonor	MF172156
<i>Calisto batesi</i>	WI-JAG-908	Dominican Republic, Santiago Rodriguez, La Leonor	MF172165
<i>Calisto batesi</i>	WI-JAG-907	Dominican Republic, Santiago Rodriguez, La Leonor	MF172189
<i>Calisto batesi</i>	WI-JAG-906	Dominican Republic, Santiago Rodriguez, La Leonor	MF172154
<i>Calisto batesi</i>	WI-JAG-905	Dominican Republic, Santiago Rodriguez, La Leonor	MF172185
<i>Calisto batesi</i>	WI-JAG-904	Dominican Republic, Santiago Rodriguez, La Leonor	MF172169
<i>Calisto batesi</i>	WI-JAG-903	Dominican Republic, Santiago Rodriguez, La Leonor	MF172113
<i>Calisto batesi</i>	WI-JAG-902	Dominican Republic, Santiago Rodriguez, La Leonor	MF172118
<i>Calisto batesi</i>	WI-JAG-901	Dominican Republic, Santiago, Pico El Rubio	MF172120
<i>Calisto batesi</i>	WI-JAG-900	Dominican Republic, Santiago, Pico El Rubio	MF172106
<i>Calisto batesi</i>	WI-JAG-899	Dominican Republic, Santiago, Pico El Rubio	MF172108
<i>Calisto batesi</i>	WI-JAG-898	Dominican Republic, Santiago Rodriguez, La Leonor	MF172124
<i>Calisto batesi</i>	WI-JAG-897	Dominican Republic, Santiago, Loma del Toro, Cordillera Central	MF172174
<i>Calisto batesi</i>	WI-JAG-896	Dominican Republic, Santiago, Loma del Toro, Cordillera Central	MF172105
<i>Calisto batesi</i>	WI-JAG-895	Dominican Republic, Santiago, Loma del Toro, Cordillera Central	MF172099
<i>Calisto batesi</i>	WI-JAG-894	Dominican Republic, La Vega, El Arroyazo, Ebano Verde	MF172182
<i>Calisto batesi</i>	WI-JAG-893	Dominican Republic, La Vega, El Arroyazo, Ebano Verde	MF172208
<i>Calisto batesi</i>	WI-JAG-892	Dominican Republic, La Vega, El Arroyazo, Ebano Verde	MF172181
<i>Calisto batesi</i>	McGuire09-CAL-Sat6	Dominican Republic, Santiago	JN197311
<i>Calisto batesi</i>	McGuire09-CAL-Sat7	Dominican Republic, Santiago	JN197312
<i>Calisto batesi</i>	McGuire09-CAL-Sat38	Dominican Republic, Elias Pina	JN197308
<i>Calisto batesi</i>	McGuire09-CAL-Sat64	Dominican Republic, Elias Pina	JN197307
<i>Calisto batesi</i>	McGuire09-CAL-Sat78	Dominican Republic, La Vega	JN197306

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TABLE 1. (Continued)

Taxa	Voucher code	Locality	Genbank Accession Number
<i>Calisto confusa</i>	WI-JAG-942	Dominican Republic, La Vega, El Aroyazo, Ebano Verde	MF172205
<i>Calisto confusa</i>	WI-JAG-939	Dominican Republic, Santiago, Loma del Toro	MF172159
<i>Calisto confusa</i>	WI-JAG-938	Dominican Republic, Santiago Rodriguez, La Leonor	MF172121
<i>Calisto confusa</i>	WI-JAG-937	Dominican Republic, Santiago Rodriguez, La Leonor	MF172135
<i>Calisto confusa</i>	WI-JAG-1017	Dominican Republic, Barahona, Villa Nizao, Paraiso	MF172101
<i>Calisto confusa</i>	WI-JAG-543	Dominican Republic, Mirador de Paraiso, Barahona	JN300019
<i>Calisto confusa</i>	WI-JAG-969	Dominican Republic, Independencia, Zapoten, Sierra de Bahoruco	MF172206
<i>Calisto confusa</i>	WI-JAG-967	Dominican Republic, La Vega, PN Armando Bermudez, La Cienaga	MF172177
<i>Calisto confusa</i>	WI-JAG-940	Dominican Republic, Santiago, Loma del Toro	MF172139
<i>Calisto confusa</i>	WI-JAG-511	Dominican Republic, salto La Demajagua	JN299988
<i>Calisto confusa</i>	WI-JAG-510	Dominican Republic, salto La Demajagua	JN299987
<i>Calisto confusa</i>	WI-JAG-508	Dominican Republic, camino a Playa Fronton, Samana	JN299985
<i>Calisto confusa</i>	WI-JAG-970	Dominican Republic, Independencia, Las Abejas, Sierra de Bahoruco	MF172157
<i>Calisto confusa</i>	NW149-18	Dominican Republic	KF054329
<i>Calisto confusa</i>	DR016	Dominican Republic	JN881879
<i>Calisto confusa</i>	DR032	Dominican Republic	KF054319
<i>Calisto confusa</i>	McGuire09-CAL-Sat35	Dominican Republic, Puerto Plata	JN197331
<i>Calisto confusa</i>	McGuire09-CAL-Sat45	Dominican Republic, La Vega	JN197330
<i>Calisto confusa</i>	McGuire09-CAL-Sat46	Dominican Republic, La Vega	JN197329
<i>Calisto confusa</i>	McGuire09-CAL-Sat58	Dominican Republic, Elias Pina	JN197328
<i>Calisto confusa</i>	McGuire09-CAL-Sat113	Dominican Republic, Sierra de Bahoruco	JN197327
<i>Calisto debarriera</i>	WI-JAG-979	Dominican Republic, Santiago, La Leonor, Moncion	MF172107
<i>Calisto debarriera</i>	WI-JAG-944	Dominican Republic, La Vega, El Aroyazo, Ebano Verde	MF172112
<i>Calisto debarriera</i>	WI-JAG-968	Dominican Republic, La Vega, La Nuez, Valle Nuevo	MF172176
<i>Calisto debarriera</i>	WI-JAG-963	Dominican Republic, La Vega, La Cienaga	MF172142

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TABLE 1. (Continued)

Taxa	Voucher code	Locality	Genbank Accession Number
<i>Calisto debarriera</i>	WI-JAG-962	Dominican Republic, La Vega, La Cienaga	MF172200
<i>Calisto debarriera</i>	WI-JAG-533	Dominican Republic, Puerto Plata, Pico Isabel de Torres	JN300009
<i>Calisto debarriera</i>	WI-JAG-945	Dominican Republic, La Vega, El Aroyazo, Ebano Verde	MF172170
<i>Calisto debarriera</i>	WI-JAG-943	Dominican Republic, La Vega, El Aroyazo, Ebano Verde	MF172109
<i>Calisto debarriera</i>	WI-JAG-941	Dominican Republic, La Vega, El Aroyazo, Ebano Verde	MF172098
<i>Calisto debarriera</i>	WI-JAG-509	Dominican Republic, Puerto Plata, Pico Isabel de Torres	JN299986
<i>Calisto debarriera</i>	WI-JAG-507	Dominican Republic, Parque Nacional A Bermudez, La Cienaga	JN299984
<i>Calisto debarriera</i>	WI-JAG-818	Dominican Republic, Puesto Piramide 204, Sierra de Neiba	MF172125
<i>Calisto debarriera</i>	McGuire09-CAL-Sat5	Dominican Republic, Santiago	JN197341
<i>Calisto debarriera</i>	McGuire09-CAL-Sat50	Dominican Republic, La Vega	JN197340
<i>Calisto debarriera</i>	McGuire09-CAL-Sat51	Dominican Republic, La Vega	JN197339
<i>Calisto debarriera</i>	McGuire09-CAL-Sat59	Dominican Republic, Elias Pina	JN197338
<i>Calisto debarriera</i>	McGuire09-CAL-Sat75	Dominican Republic, La Vega	JN197337
<i>Calisto debarriera</i>	DR019	Dominican Republic	KF054318
<i>Calisto debarriera</i>	McGuire09-CAL-Sat112	Dominican Republic, Sierra de Bahoruco	JN197380
<i>Calisto grannus dilemma</i>	WI-JAG-837	Dominican Republic, La Vega, 8 km colonia japonesa, Valle Nuevo	MF172150
<i>Calisto grannus dilemma</i>	WI-JAG-836	Dominican Republic, La Vega, 8 km colonia japonesa, Valle Nuevo	MF172175
<i>Calisto grannus dilemma</i>	WI-JAG-835	Dominican Republic, La Vega, 8 km colonia japonesa, Valle Nuevo	MF172134
<i>Calisto grannus dilemma</i>	WI-JAG-834	Dominican Republic, La Vega, 8 km colonia japonesa, Valle Nuevo	MF172122
<i>Calisto grannus dilemma</i>	WI-JAG-833	Dominican Republic, La Vega, 8 km colonia japonesa, Valle Nuevo	MF172132
<i>Calisto grannus dilemma</i>	McGuire09-CAL-Sat2	Dominican Republic, Santiago	JN197365
<i>Calisto grannus dilemma</i>	McGuire09-CAL-Sat4	Dominican Republic, Santiago	JN197364
<i>Calisto grannus dilemma</i>	McGuire09-CAL-Sat8	Dominican Republic, Santiago	JN197363
<i>Calisto grannus dilemma</i>	McGuire09-CAL-Sat37	Dominican Republic, Elias Pina	JN197362
<i>Calisto grannus dilemma</i>	McGuire09-CAL-Sat39	Dominican Republic, Elias Pina	JN197361

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**TABLE 1.** (Continued)

<b>Taxa</b>	<b>Voucher code</b>	<b>Locality</b>	<b>Genbank Accession Number</b>
<i>Calisto grannus dilemma</i>	McGuire09-CAL-Sat42	Dominican Republic, Elias Pina	JN197360
<i>Calisto grannus dilemma</i>	McGuire09-CAL-Sat43	Dominican Republic, Elias Pina	JN197359
<i>Calisto grannus dilemma</i>	McGuire09-CAL-Sat44	Dominican Republic, Elias Pina	JN197358
<i>Calisto grannus dilemma</i>	McGuire09-CAL-Sat74	Dominican Republic, La Vega	JN197357
<i>Calisto grannus dilemma</i>	McGuire09-CAL-Sat76	Dominican Republic, La Vega	JN197356
<i>Calisto grannus dilemma</i>	McGuire09-CAL-Sat77	Dominican Republic, La Vega	JN197355
<i>Calisto grannus dilemma</i>	McGuire09-CAL-Sat79	Dominican Republic, La Vega	JN197354
<i>Calisto grannus dilemma</i>	McGuire09-CAL-Sat80	Dominican Republic, La Vega	JN197353
<i>Calisto grannus dilemma</i>	McGuire09-CAL-Sat82	Dominican Republic, Elias Pina	JN197352
<i>Calisto grannus dystacta</i>	WI-JAG-847	Dominican Republic, Santiago, La Leonor	MF172168
<i>Calisto grannus dystacta</i>	WI-JAG-846	Dominican Republic, Santiago, La Leonor	MF172163
<i>Calisto grannus dystacta</i>	WI-JAG-845	Dominican Republic, Santiago, La Leonor	MF172187
<i>Calisto grannus dystacta</i>	WI-JAG-844	Dominican Republic, Santiago, La Leonor	MF172136
<i>Calisto grannus grannus</i>	WI-JAG-551	Dominican Republic, Valle Nuevo, Constanza	JN300027
<i>Calisto grannus grannus</i>	WI-JAG-946	Dominican Republic, La Vega, 8 km colonia japonesa, Valle Nuevo	MF172184
<i>Calisto grannus grannus</i>	WI-JAG-814	Dominican Republic, La Vega, La Nuez, Valle Nuevo	MF172114
<i>Calisto grannus grannus</i>	WI-JAG-813	Dominican Republic, La Vega, La Nuez, Valle Nuevo	MF172207
<i>Calisto grannus grannus</i>	WI-JAG-812	Dominican Republic, La Vega, La Nuez, Valle Nuevo	MF172097
<i>Calisto grannus grannus</i>	WI-JAG-811	Dominican Republic, La Vega, La Piramide, Valle Nuevo	MF172115
<i>Calisto grannus grannus</i>	WI-JAG-810	Dominican Republic, La Vega, La Piramide, Valle Nuevo	MF172155
<i>Calisto grannus grannus</i>	McGuire09-CAL-Sat27	Dominican Republic, La Vega	JN197351
<i>Calisto grannus grannus</i>	McGuire09-CAL-Sat	Dominican Republic, La Vega	JN197350
<i>Calisto grannus grannus</i>	McGuire09-CAL-Sat67	Dominican Republic, La Vega	JN197349
<i>Calisto grannus grannus</i>	McGuire09-CAL-Sat69	Dominican Republic, La Vega	JN197348
<i>Calisto grannus grannus</i>	McGuire09-CAL-Sat70	Dominican Republic, La Vega	JN197347

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TABLE 1. (Continued)

Taxa	Voucher code	Locality	Genbank Accession Number
<i>Calisto grannus grannus</i>	McGuire09-CAL-Sat95	Dominican Republic, La Vega	JN197346
<i>Calisto grannus grannus</i>	McGuire09-CAL-Sat96	Dominican Republic, La Vega	JN197345
<i>Calisto grannus grannus</i>	McGuire09-CAL-Sat47	Dominican Republic, La Vega	JN197366
<i>Calisto hysius</i>	WI-JAG-497	Dominican Republic, Pedernales, camino de Los Arroyos a Ojo de Agua	JN299974
<i>Calisto hysius</i>	WI-JAG-496	Dominican Republic, Pedernales, camino de Los Arroyos a Ojo de Agua	JN299973
<i>Calisto hysius</i>	WI-JAG-495	Dominican Republic, Pedernales, camino de Los Arroyos a Ojo de Agua	JN299972
<i>Calisto hysius</i>	WI-JAG-494	Dominican Republic, Pedernales, camino de Los Arroyos a Ojo de Agua	JN299971
<i>Calisto hysius</i>	WI-JAG-493	Dominican Republic, Pedernales, camino de Los Arroyos a Ojo de Agua	JN299970
<i>Calisto hysius</i>	WI-JAG-549	Dominican Republic, camino de Los Arroyos a Ojo de Agua, Sierra de Bahoruco	JN300025
<i>Calisto hysius</i>	McGuire09-CAL-Sat83	Dominican Republic, Pedernales	JN197375
<i>Calisto hysius</i>	McGuire09-CAL-Sat84	Dominican Republic, Pedernales	JN197374
<i>Calisto grannus micheneri</i>	WI-JAG-832	Dominican Republic, Santiago, Loma del Toro, Cordillera Central	MF172141
<i>Calisto grannus micheneri</i>	WI-JAG-831	Dominican Republic, Santiago, Loma del Toro, Cordillera Central	MF172172
<i>Calisto grannus micheneri</i>	WI-JAG-830	Dominican Republic, Santiago, Loma del Toro, Cordillera Central	MF172197
<i>Calisto grannus micheneri</i>	WI-JAG-829	Dominican Republic, Santiago, Loma del Toro, Cordillera Central	MF172117
<i>Calisto grannus micheneri</i>	WI-JAG-828	Dominican Republic, Santiago, Loma del Toro, Cordillera Central	MF172100
<i>Calisto grannus micrommata</i>	WI-JAG-822	Dominican Republic, Puesto Piramide 204, Sierra de Neiba	MF172193
<i>Calisto grannus micrommata</i>	WI-JAG-821	Dominican Republic, Puesto Piramide 204, Sierra de Neiba	MF172127
<i>Calisto grannus micrommata</i>	WI-JAG-820	Dominican Republic, Puesto Piramide 204, Sierra de Neiba	MF172166
<i>Calisto grannus micrommata</i>	WI-JAG-819	Dominican Republic, Puesto Piramide 204, Sierra de Neiba	MF172190
<i>Calisto obscura</i>	WI-JAG-936	Dominican Republic, Santiago, Pico El Rubio	MF172151
<i>Calisto obscura</i>	WI-JAG-935	Dominican Republic, Santiago, Pico El Rubio	MF172191
<i>Calisto obscura</i>	WI-JAG-934	Dominican Republic, Santiago, Pico El Rubio	MF172130
<i>Calisto obscura</i>	WI-JAG-933	Dominican Republic, Santiago, Pico El Rubio	MF172186

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TABLE 1. (Continued)

Taxa	Voucher code	Locality	Genbank Accession Number
<i>Calisto obscura</i>	WI-JAG-932	Dominican Republic, Santiago, Pico El Rubio	MF172138
<i>Calisto obscura</i>	WI-JAG-544	Dominican Republic, Las Mercedes, Pedernales,	JN300020
<i>Calisto obscura</i>	WI-JAG-542	Dominican Republic, Las Abejas, Sierra Bahoruco	JN300018
<i>Calisto obscura</i>	WI-JAG-532	Dominican Republic, Fondo Paradi, Jaragua	JN300008
<i>Calisto obscura</i>	WI-JAG-531	Dominican Republic, Mirador de Paraiso, Barahona	JN300007
<i>Calisto obscura</i>	WI-JAG-530	Dominican Republic, Mirador de Paraiso, Barahona	JN300006
<i>Calisto obscura</i>	WI-JAG-529	Dominican Republic, camino de Pedernales, a Ojo de Agua, Sierra Bahoruco	JN300005
<i>Calisto obscura</i>	WI-JAG-522	Dominican Republic, Las Abejas, Sierra Bahoruco	JN299999
<i>Calisto obscura</i>	WI-JAG-521	Dominican Republic, Las Abejas, Sierra Bahoruco	JN299998
<i>Calisto obscura</i>	WI-JAG-520	Dominican Republic, Las Abejas, Sierra Bahoruco	JN299997
<i>Calisto obscura</i>	WI-JAG-519	Dominican Republic, Las Abejas, Sierra Bahoruco	JN299996
<i>Calisto obscura</i>	WI-JAG-772	Dominican Republic, Pedernales, Mapioro, Oviedo	MF172199
<i>Calisto obscura</i>	WI-JAG-771	Dominican Republic, Pedernales, Fondo Paradi, Oviedo	MF172198
<i>Calisto obscura</i>	WI-JAG-770	Dominican Republic, Pedernales, Aceitillar, Sierra de Bahoruco	MF172183
<i>Calisto obscura</i>	WI-JAG-769	Dominican Republic, Pedernales, Caseta 1, Sierra de Bahoruco	MF172162
<i>Calisto obscura</i>	WI-JAG-768	Dominican Republic, Pedernales, Las Abejas Sierra de Bahoruco	MF172147
<i>Calisto obscura</i>	WI-JAG-767	Dominican Republic, Pedernales, Las Abejas Sierra de Bahoruco	MF172103
<i>Calisto obscura</i>	WI-JAG-766	Dominican Republic, Pedernales, Las Abejas Sierra de Bahoruco	MF172210
<i>Calisto obscura</i>	McGuire09-CAL-Sat9	Dominican Republic, Santiago	JN197392
<i>Calisto obscura</i>	McGuire09-CAL-Sat10	Dominican Republic, Santiago	JN197391
<i>Calisto obscura</i>	McGuire09-CAL-Sat13	Dominican Republic, Santiago	JN197390
<i>Calisto obscura</i>	McGuire09-CAL-Sat34	Dominican Republic, La Altagracia	JN197389
<i>Calisto obscura</i>	McGuire09-CAL-Sat40	Dominican Republic, Elias Pina	JN197388
<i>Calisto obscura</i>	McGuire09-CAL-Sat122	Dominican Republic, Pedernales	JN197386

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TABLE 1. (Continued)

Taxa	Voucher code	Locality	Genbank Accession Number
<i>Calisto obscura</i>	NW149-12	Dominican Republic	KF054324
<i>Calisto obscura</i>	NW150-1	Dominican Republic	KF054330
<i>Calisto grannus phoinix</i>	WI-JAG-843	Dominican Republic, La Vega, El Arroyazo, Ebano Verde	MF172129
<i>Calisto grannus phoinix</i>	WI-JAG-842	Dominican Republic, La Vega, El Arroyazo, Ebano Verde	MF172145
<i>Calisto grannus phoinix</i>	WI-JAG-841	Dominican Republic, La Vega, El Arroyazo, Ebano Verde	MF172196
<i>Calisto grannus phoinix</i>	WI-JAG-840	Dominican Republic, La Vega, El Arroyazo, Ebano Verde	MF172146
<i>Calisto grannus phoinix</i>	WI-JAG-839	Dominican Republic, La Vega, El Arroyazo, Ebano Verde	MF172158
<i>Calisto grannus phoinix</i>	WI-JAG-838	Dominican Republic, La Vega, El Arroyazo, Ebano Verde	MF172194
<i>Calisto sommeri</i>	WI-JAG-550	Dominican Republic, camino entre Las Abejas y caseta 2, Sierra Bahoruco	JN300026
<i>Calisto sommeri</i>	WI-JAG-506	Dominican Republic, pinar entre Las Abejas y caseta 2, Sierra Bahoruco	JN299983
<i>Calisto sommeri</i>	WI-JAG-505	Dominican Republic, pinar entre Las Abejas y caseta 2, Sierra Bahoruco	JN299982
<i>Calisto sommeri</i>	WI-JAG-504	Dominican Republic, pinar entre Las Abejas y caseta 2, Sierra Bahoruco	JN299981
<i>Calisto sommeri</i>	WI-JAG-503	Dominican Republic, Pedernales, Los Arroyos, Sierra Bahoruco	JN299980
<i>Calisto sommeri</i>	WI-JAG-502	Dominican Republic, Pedernales, Los Arroyos, Sierra Bahoruco	JN299979
<i>Calisto sommeri</i>	WI-JAG-501	Dominican Republic, Pedernales, Los Arroyos, Sierra Bahoruco	JN299978
<i>Calisto sommeri</i>	WI-JAG-492	Dominican Republic, Pedernales, Los Arroyos, Sierra Bahoruco	JN299969
<i>Calisto sommeri</i>	WI-JAG-827	Dominican Republic, Pedernales, Loma El Toro, Sierra de Bahoruco	MF172148
<i>Calisto sommeri</i>	WI-JAG-817	Dominican Republic, Pedernales, Loma El Toro, Sierra de Bahoruco	MF172201
<i>Calisto sommeri</i>	WI-JAG-816	Dominican Republic, Pedernales, Sierra de Bahoruco	MF172149
<i>Calisto sommeri</i>	WI-JAG-815	Dominican Republic, Pedernales, caseta 2, Sierra de Bahoruco	MF172137
<i>Calisto sommeri</i>	McGuire09-CAL-Sat52	Dominican Republic, Pedernales	JN197401
<i>Calisto sommeri</i>	McGuire09-CAL-Sat53	Dominican Republic, Pedernales	JN197400
<i>Calisto sommeri</i>	McGuire09-CAL-Sat54	Dominican Republic, Pedernales	JN197399
<i>Calisto sommeri</i>	McGuire09-CAL-Sat55	Dominican Republic, Pedernales	JN197398
<i>Calisto sommeri</i>	McGuire09-CAL-Sat93	Dominican Republic, Pedernales	JN197397

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**TABLE 1.** (Continued)

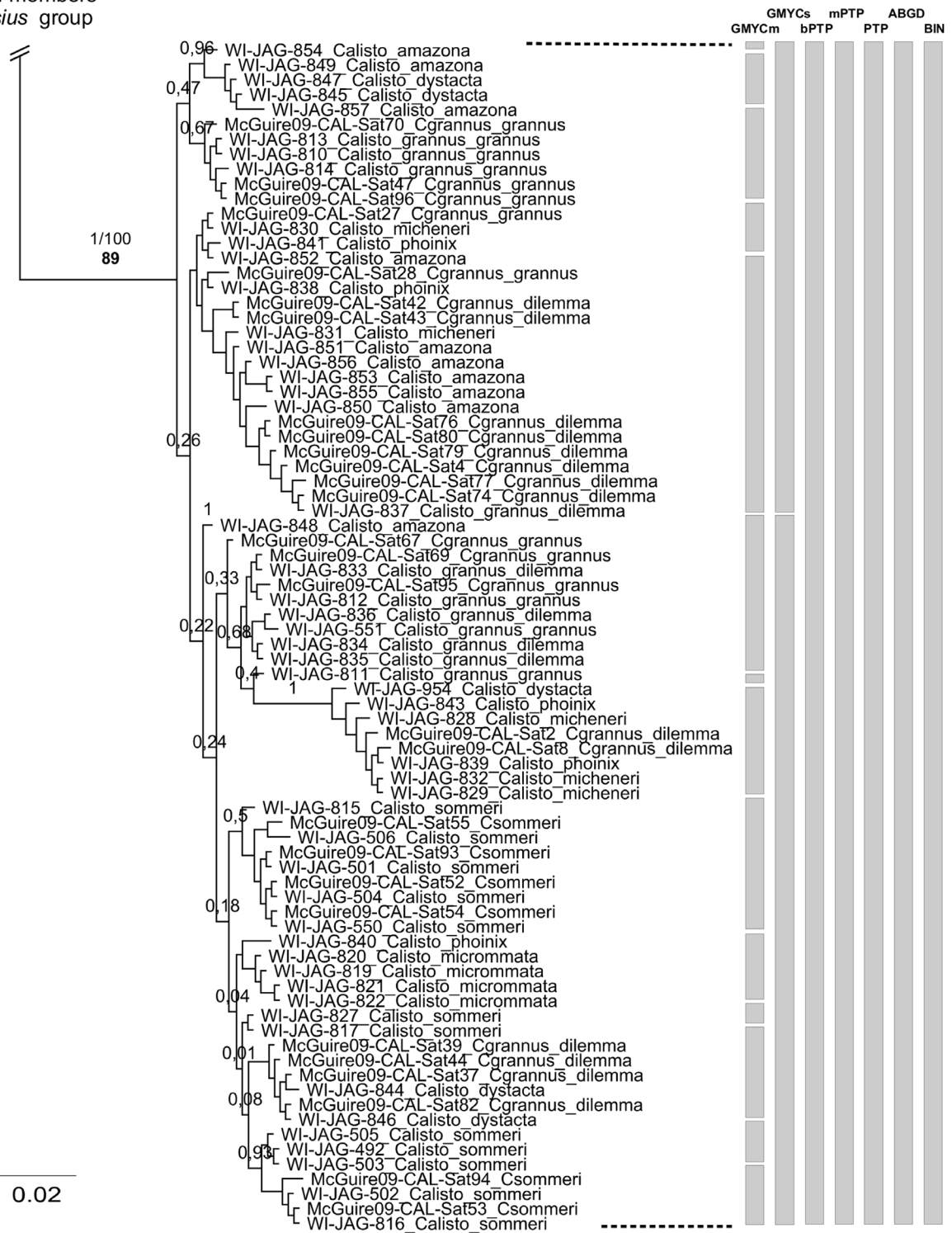
<b>Taxa</b>	<b>Voucher code</b>	<b>Locality</b>	<b>Genbank Accession Number</b>
<i>Calisto somneri</i>	McGuire09-CAL-Sat94	Dominican Republic, Pedernales	JN197396
<i>Calisto tragus</i>	WI-JAG-989	Dominican Republic, Independencia, caseta 3, Bahoruco	MF172126
<i>Calisto tragus</i>	WI-JAG-988	Dominican Republic, Independencia, caseta 3, Bahoruco	MF172111
<i>Calisto tragus</i>	WI-JAG-987	Dominican Republic, Independencia, caseta 3, Bahoruco	MF172110
<i>Calisto tragus</i>	WI-JAG-986	Dominican Republic, Independencia, caseta 3, Bahoruco	MF172140
<i>Calisto tragus</i>	WI-JAG-982	Dominican Republic, Pedernales, Loma El Toro, Sierra de Bahoruco	MF172123
<i>Calisto tragus</i>	WI-JAG-826	Dominican Republic, Pedernales, Loma El Toro, Sierra de Bahoruco	MF172131
<i>Calisto tragus</i>	WI-JAG-825	Dominican Republic, Pedernales, Loma El Toro, Sierra de Bahoruco	MF172204
<i>Calisto tragus</i>	WI-JAG-824	Dominican Republic, Pedernales, Loma El Toro, Sierra de Bahoruco	MF172152
<i>Calisto tragus</i>	WI-JAG-823	Dominican Republic, Pedernales, Loma El Toro, Sierra de Bahoruco	MF172178
<i>Calisto tragus</i>	RN02-18	Dominican Republic	KF054342
<i>Calisto eleleus</i>	WI-JAG-538	Dominican Republic	JN300014





**FIGURE 18.** Bayesian COI barcodes gen tree reconstructed by MrBayes showing the relationships among taxa belonging to the *hysius* species group of *Calisto*. Numbers above branches represent the posterior probabilities / bootstrap values of Bayesian Inference / Maximum Likelihood. Bold numbers at species clades represent the support values for each species calculated by the Bayesian Poisson Tree Process (bPTP) species delimitation method. Gray box indicating the position of the species described herein, *C. bahoruco*. Gray bars at the right side of tree showing the species hypothesis obtained by the different species delimitation methods applied: Generalize Mixed Yule Coalescent single and multiple threshold (GMYCs, GMYCm), Poisson Tree Process, PTP, variants: Bayesian (bPTP), Maximum Likelihood (mPTP), and standard (PTP), Automatic Barcode Gap Discovery (ABGD), and Barcode Index Number (BIN).

rest of members  
of *hysius* group



18 (cont.)

**Table 2.** COI genetic distance values among taxa of the *hysius* group. Bottom right Kimura 2- parameters (K2P) minimum pairwise distances, upper left minimum number of differences. Columns heading showing below each taxon the number sequences (n) and average K2P intraspecific distance.

	<i>C. batesi</i> n=33, 0.59	<i>C. confusa</i> n=21, 0.46	<i>C. debarriera</i> n=26, 0.23	<i>C. bahoruco n. sp.</i> n=6, 0.14	<i>C. hysius</i> n=8, 0.05	<i>C. obscura</i> n=31, 0.47	<i>C. grannus</i> n=80, 0.77	<i>C. tragijs</i> n=10, 0.04
<i>C. batesi</i>		56	47	32	38	48	49	31
<i>C. confusa</i>	9.8		33	49	49	64	65	48
<i>C. debarriera</i>	8.9	6.4		50	54	64	60	58
<i>C. bahoruco n. sp.</i>	5.1	8.5	9.5		15	48	50	35
<i>C. hysius</i>	6.1	8.5	10.3	2.3		47	54	35
<i>C. obscura</i>	8.5	12.1	12.4	8.7	8.3		29	55
<i>C. grannus</i>	8.8	11.9	12.4	9	9.8	5.4		52
<i>C. tragijs</i>	5.7	9.8	11.5	6.5	6.5	10.9	11.1	

**Table 3.** Nucleotide sites with unique fixed states present in COI barcodes of species belonging to the *hysius* group of *Calisto*.

Taxa/Positions	10	25	38	49	67	100	127	187	208	214	238	256	281	319	325	328	334	346	352	367	373	385	
<i>C. confusa</i> n=21	C	T	G	T	A	A	T	T	T	A	A	T	A	T	A	A	T	T	T	T	T	C	T
<i>C. batesi</i> n=33	T	C	G	T	T	A	A	T	A	A	T	T	A/G	T	A	T	T	C	A	A	T	A	T
<i>C. debarriera</i> n=26	T	T	A	C	A/G	T	T	T	A	A	C	A	C	T	A	A	C	T	C	T	A	A	C
<i>C. obscura</i> n=31	T	T	G	T	A	A	C	T	A	C	T	T	A	T	A	T	T	G	A	A	T	A	T
<i>C. hysius</i> n=8	T	T	G	T	A	A	A	C	A	A	C	T	A	T	A	T	T	T	A	T	A	A	T
<i>C. grannus</i> n=80	T	T	G	T	A/G	A/G	T	T	A	T	C	T	A/G	C	A	T	G	A	A	A	T	A/G	T
<i>C. tragius</i> n=10	T	T	G	T	A	A	A	T	A	A	T	T	G	T	T	C	T	T	A	C	A	A	T
<i>C. bahoruco</i> n. sp. n=6	T	T	G	T	A	A	A	T	A	A	C	T	A	T	A	T	T	T	A	T	A	A	T

(cont.)	397	400	412	421	436	446	482	499	500	505	517	520	529	539	542	544	556	557	559	604	637	653	
<i>C. confusa</i> n=21	T	A	C	A	T	C	T	C	C	T	T	A	C	T	C	T	A	T	A	T	T	T	T
<i>C. batesi</i> n=33	T	C	T	A	T	T	T	A	T	T	A	A	T	T	C	T	A	T	G	T	C	T	T
<i>C. debarriera</i> n=26	T	C	A	A	T	T	T	T	T	C	T	A	G/T	T	C	T	A	T	A	T	T	C	C
<i>C. obscura</i> n=31	T	T	A	T	T	T	T	A/G	T	T	A	A	A	C	C	T	A/C	C	A	T	T	T	T
<i>C. hysius</i> n=8	T	T	T	A	T	T	T	A	T	T	C	A	A	T	C	T	A	T	A	T	T	T	T
<i>C. grannus</i> n=80	C	C	A	A	C	T	A/G	A	T	T	A	A	A	T	T	A/G	A	T	A	C	T	T	T
<i>C. tragius</i> n=10	T	T	T	C	T	T	T	A	T	T	T	T	A	T	C	T	T	T	A	T	T	T	T
<i>C. bahoruco</i> n. sp. n=6	T	C	T	A	T	T	T	A	T	T	T	A	A	T	C	T	A	T	A	T	T	T	T



## Phylogenetic reconstruction with COI

Both phylogenetic methods recovered the same topology with all relationships strongly supported (Fig. 18). The only differences were evidenced within some species clades. *Calisto confusa* and *C. debarriera* were placed as sister species (PP= 1, BS=100) and the sister of all other *hysius* group species (1, 95). All other species were grouped in two clades (1, 100). *Calisto obscura* and *C. grannus* are sister species (1, 100) while the remaining four species were included in another clade (1, 94). The latter cluster is composed by other two species pairs: *C. hysius* and *C. bahoruco* (1, 87) and *C. tragus* and *C. batesi* (1, 76).

## Species delimitation methods in the *hysius* group

Most species delimitation methods yielded results matching the current accepted species within the *hysius* group (Fig. 18, Appendix). The exception was the GMYC, mainly the multiple threshold variant that splitted all species except *C. confusa*. Both GMYC variants failed to recognize the new species here described, *C. bahoruco*. The new taxon was delimited by all other methods employed (Fig. 18, Appendix).

The character base approach revealed the existence of 2 to 11 diagnostic fixed nucleotide positions in the barcodes of each species belonging to the *hysius* group except *C. bahoruco* (Table 3). However, COI barcodes of the latter can be easily separated from these of its sister species, *C. hysius*. They differ by the change on nucleotide positions 187 and 517, which are diagnostic for *C. hysius* among all group members, but also in other 13 positions (*C. hysius/C. bahoruco*): 82 (T/C), 118 (C/T), 166 (G/A), 184 (G/A), 202 (T/C), 220 (C/T), 271 (C/T), 349 (C/T), 355 (C/T), 364 (T/C), 400 (T/C), 562 (A/G) and 634 (T/C). Within *C. grannus* the only diagnosable population is *C. grannus micrommata*, Sierra de Neiba, which bears a thymine at position 622 whereas specimens from all other populations have an adenine.

## The *C. grannus* populations

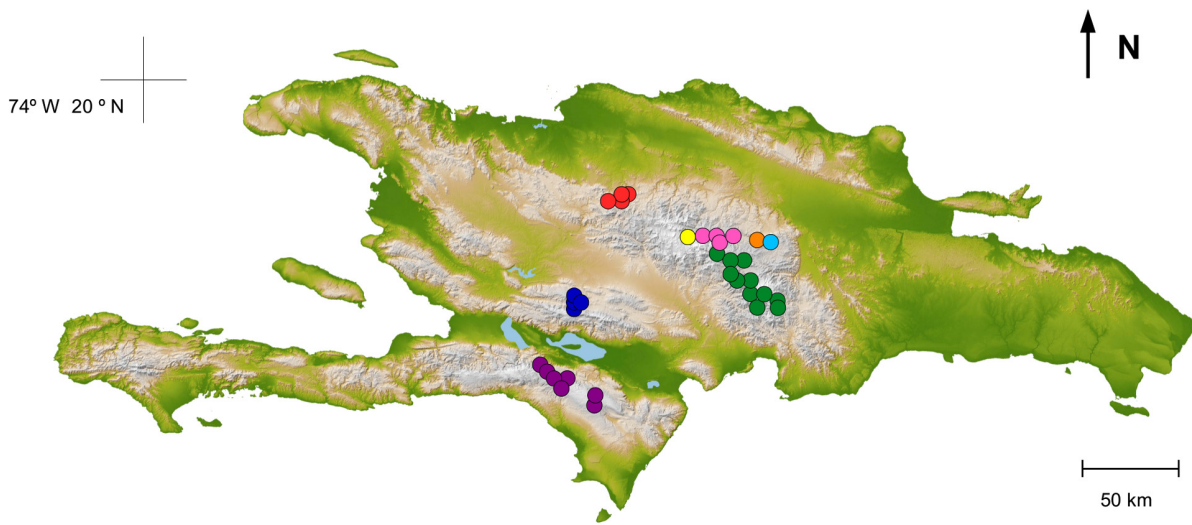
We analyzed 58 sequences belonging to the eight taxa included in the former *C. grannus* complex or species group due its genitalic morphology and the possession of two circled ocelli with central pupils at the under surface of HW (Schwartz & Gali 1984, Gonzalez 1987). Some were originally described as separate species from localities separated a few kilometers at the major mountain range of Hispaniola, the Cordillera Central (*C. grannus grannus* M. Bates, 1939, *C. grannus dilemma* González, 1987, *C. grannus phoinix* González, 1987, *C. grannus amazona* González, 1987, *C. grannus micheneri* Clench, 1944) whereas others were discovered at more distant places of the C. Central (*C. grannus dystacta* González, 1987), the middle Sierra de Neiba (*C. grannus micrommata* Schwartz & Gali, 1984) or the southern Sierra de Bahoruco (*C. grannus sommeri* Schwartz & Gali, 1984) (Fig. 19). Sourakov & Zakharov (2011), based on COI barcode sequences obtained from 28 specimens, lowered the status of most of these taxa from species to subspecies level using mitochondrial DNA as evidence of low divergence level between them. We did not include sequences from the latter study in our analysis as they lacked precise geographical data, with the exception of six sequences representing *C. grannus sommeri*, which we included in our dataset.

No Bayesian, Maximum Likelihood or Neighbor Joining produced a single cluster formed only by specimens from the same locality or belonging to a single taxon with most clades weakly supported (Fig. 18). K2P pairwise distances values were between 0 and 2.1%, or 0 to 12 differences, with intra-taxon minimum pairwise distances ranging from 0 (*C. grannus micrommata*) to 1.1% (*C. grannus phoinix*) and intertaxa minimum pairwise distances from 0.3 (*C. grannus micrommata*–*C. grannus sommeri*) to 1.2% (*C. grannus amazona*–*C. grannus micheneri*).

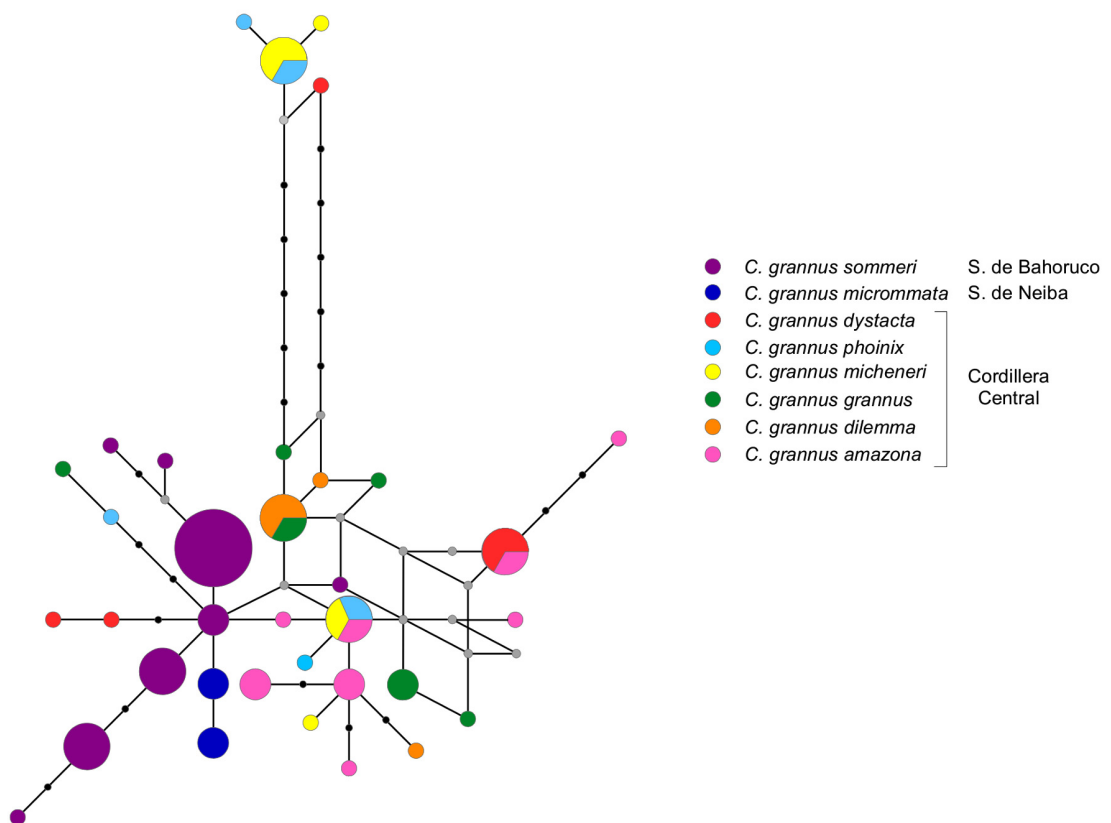
The species identification methods recovered a single entity (all PTP variants, ABGD, BIN) or two and as much as 14 entities, GMYC single and multiple threshold respectively (Fig. 18). The later method also mixed specimens from different named populations mixed within the delimited entities.

The Median Joining haplotype network shed some light on the relationships of these populations (Fig. 20). The analysis identified 36 haplotypes. *Calisto grannus sommeri* and *C. grannus micrommata* were represented by 8, 18 sequences, and 2, 4 sequences, haplotypes respectively. These haplotypes are unique from their respective

geographic ranges, Sierra de Bahoruco and Sierra de Neiba. Populations of the northern Cordillera Central included 26 haplotypes, 36 sequences, 19 of them represented by unique sequences. Four haplotypes of these populations are shared by two or three named populations (Fig. 20).



19



20

**FIGURES 19–20.** 19—Geographic distribution of *C. grannus* populations, nomenclature follows Sourakov & Zakharov (2011). 20—Median Joining Haplotype network obtained in Network v. 5.0; circles size proportional to number of sequences; gray circles are hypothetical haplotypes; black circles represent changes; colors represent subspecies sensu Sourakov & Zakharov (2011).

## Discussion

More information about the new species described herein and its sister *C. hysius* is needed to assess how their ancestral populations splitted in a seemingly continuous mountain habitat. Needed data include additional molecular markers, habitat, immature stages, and distribution. Several markers besides COI were sequenced by Matos–Maravi et al (2014) for two *C. hysius* specimens but at present only COI barcodes are available for *C. bahoruco*. In the same way, the immature stages of *C. hysius* were described by Sourakov (1996) but those of *C. bahoruco* remain unknown.

Regarding distribution, although we found *C. bahoruco* at a single locality we suspect the species inhabits other low to middle elevation localities at the Barahona province depicted by Schwartz (1989) for *C. hysius*. All these localities are at the extreme eastern area of Sierra de Bahoruco. *Calisto hysius* range seems to occupy most of the southern Hispaniolan mountain range west of Barahona, from Pedernales and Independencia provinces of Dominican Republic along the Tiburon Peninsula to the Massif de la Hotte, Haiti. Our main clue to assert this is the fact that *C. bahoruco* type specimens match three specimens identified as *C. hysius* from two other localities of the Barahona province illustrated on the Butterflies of America website (Warren et al. 2016). In the website there is another specimen with a different color pattern also attributed to *C. hysius*. We think it probably represents the northern subspecies of *C. hysius*, *C. hysius aleucosticha* Correa & Schwartz, a taxon for which both sequences and specimens are lacking for present study. One *C. hysius* adult from 1.5 km S Los Arroyos, Pedernales province, illustrated by Sourakov (1996) match our *C. hysius* specimens from a nearby locality. In addition, the male genitalia of our *C. hysius* from Los Arroyos match better the drawing of Haitian specimens by Johnson & Hedges (1998) than the male structures of *C. bahoruco* type series, mainly the prominent shape of the tegumen base. Evidently the species were confused in the past due to their similar wing pattern and close distribution.

Phylogenetic relationships reconstructed by both methods concur with the topology resulting from six genes obtained by Matos–Maraví et al. (2014). *Calisto confusa* and *C. debarriera* species pair is sister of all other species. The rest splits in two, with *C. grannus* and *C. obscura* being sister of the remaining species. Despite using COI barcodes, there was a good phylogenetic signal. The only change is the position of *C. bahoruco* **n. sp.** as sister species of *C. hysius*.

Concerning *Calisto grannus*, there is no doubt that all known populations are monophyletic, descendants from a common ancestor. According to the COI data, populations within *C. grannus* seem to have an ongoing gene exchange or it continued until recently. The latter is evident at Cordillera Central where several haplotypes can be shared between two or even three populations and where individuals of the same population may have different haplotypes suggesting introgression. We found cases of such genetic introgression among populations of *C. g. phoinix*, *C. g. micheneri* and *C. g. dystacta*, the latter being moderately isolated from all other *C. Central* populations. In fact, all *C. Central* populations except the westernmost *C. g. dystacta*, are so close to each other that the gene exchange almost certainly is ongoing. Haplotypes from Sierra de Neiba and Sierra de Bahoruco are found, as could be expected, exclusively in their respective ranges, suggesting a prolonged geographic isolation. These results are also supported by observations on the immature stages: Sourakov & Emmel (1995) and Sourakov (1996) described immature stages of *C. grannus grannus*, *C. g. dilemma* and *C. g. sommeri*, and found that while the first two taxa share morphology, *C. g. sommeri* exhibited a spotted form of caterpillars not found in *C. Central* subspecies.

While our DNA analysis overall confirms the results obtained by Sourakov & Zakharov (2011), our study significantly increases the dataset and provides a more precise locations data for the studied populations. Nevertheless, we feel that only with further morphological studies and DNA analyses involving additional markers will we be able to reassess the taxonomic status of *C. grannus* populations.

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## Literature cited

- Bates, M. (1935) The satyrid genus *Calisto*. *Occasional Papers Boston Society of Natural History*, 8, 229–248.
- Benson, D.A., Clark, K., Karsch-Mizrachi, I., Lipman, D.J., Ostell, J. & Sayers, E.W. (2014) GenBank. *Nucleic Acids Research*, 42, 32–37.  
<https://doi.org/10.1093/nar/gkt1030>
- Brower, A.V.Z. (2010) Alleviating the taxonomic impediment of DNA barcoding and setting a bad precedent: names for ten species of ‘*Astrartes fulgerator*’ (Lepidoptera: Hesperiiidae: Eudaminae) with DNA-based diagnoses. *Systematics and Biodiversity*, 8 (4), 485–491.  
<https://doi.org/10.1080/14772000.2010.534512>
- Drummond, A.J., Suchard, M.A., Xie, D. & Rambaut, A. (2012) Bayesian Phylogenetics with BEAUti and the BEAST 1.7. *Molecular Biology and Evolution*, 29, 1969–1973.  
<https://doi.org/10.1093/molbev/mss075>
- Fujisawa, T. & Barraclough, T.G. (2013) Delimiting species using Single-Locus Data and the Generalized Mixed Yule Coalescent Approach: a revised method and evaluation on simulated data sets. *Systematic Biology*, 65, 707–724.  
<https://doi.org/10.1093/sysbio/syt033>
- Gali, F. (1985) Five new species of *Calisto* (Lepidoptera: Satyridae) from Hispaniola. *Milwaukee Public Museum Contributions to Biology and Geology*, 63, 1–16.
- Gonzalez, F.L. (1987) Three new species and one new subspecies in the grannus complex of Hispaniolan *Calisto* (Lepidoptera: Satyridae). *Bulletin of the Allyn Museum*, 108, 1–17.
- Hall, T.A. (1999) BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. *Nucleic Acids Symposium Series*, 41, 95–98.
- Hebert, P.D.N., Cywinska, A., Ball, S.L. & deWaard, J.R. (2003) Biological identifications through DNA barcodes. *Proceedings of the Royal Society of London, Series B, Biological Sciences*, 270, 313–321.  
<https://doi.org/10.1098/rspb.2002.2218>
- Hebert, P.D.N., Penton, E.H., Burns, J.M., Janzen, D.H. & Hallwachs, W. (2004) Ten Species in One: DNA Barcoding Reveals Cryptic Species in the Neotropical Skipper Butterfly *Astrartes fulgerator*. *Proceedings of the National Academy of Sciences of the United States of America*, 101 (41), 14812–14817.  
<https://doi.org/10.1073/pnas.0406166101>
- Johnson, K. & Hedges, S.B. (1998) Three new species of *Calisto* from Southwestern Haiti (Lepidoptera: Nymphalidae: Satyrinae). *Tropical Lepidoptera*, 9 (2), 45–53.
- Kapli, P., Lutteropp, S., Zhang, J., Kobert, K., Pavlidis, P., Stamatakis, A. & Flouri, T. (2016) Multi-rate Poisson tree processes for single-locus species delimitation under maximum likelihood and Markov chain Monte Carlo. *bioRxiv*, 2016, 063875.  
<https://doi.org/10.1101/063875>
- Lanfear, R., Calcott, B., Ho, S.Y.W. & Guindon, S. (2012) Partition Finder: Combined Selection of Partitioning Schemes and Substitution Models for Phylogenetic Analyses. *Molecular Biology and Evolution*, 29 (6), 1695–1701.  
<https://doi.org/10.1093/molbev/mss020>
- Matos-Maraví, P.F., Núñez, R., Peña, C., Miller, J.Y., Sourakov, A. & Wahlberg, N. (2014) Causes of endemic radiation in the Caribbean: evidence from the historical biogeography and diversification of the butterfly genus *Calisto* (Nymphalidae: Satyrinae: Satyrini). *BMC Evolutionary Biology* 14 (199), 1–18.  
<https://doi.org/10.1186/s12862-014-0199-7>
- Michener, C.D. (1943) A review of the genus *Calisto* (Lepidoptera, Satyrinae). *American Museum Novitates*, 1236, 1–6.
- Miller, M.A., Pfeiffer, W. & Schwartz, T. (2010) Creating the CIPRES Science Gateway for inference of large phylogenetic trees. In: *Proceedings of the Gateway Computing Environments Workshop (GCE)*, New Orleans, 2010, pp. 1–8.  
<https://doi.org/10.1109/gce.2010.5676129>
- Monaghan, M.T., Wild, R., Elliot, M., Fujisawa, T., Balke, M., Inward, D.J., Lees, D.C., Ranaivosolo, R., Eggleton, P., Barraclough, T.G. & Vogler, A.P. (2009) Accelerated species inventory on Madagascar using coalescent-based models of species delineation. *Systematic Biology*, 58, 298–311.  
<https://doi.org/10.1093/sysbio/syp027>
- Munroe, E.G. (1951) The systematics of *Calisto* (Lepidoptera, Satyrinae), with remarks on the evolutionary and zoogeographic significance of the genus. *Journal of the New York Entomological Society*, 58 (4), 211–241.
- Núñez, R., Matos-Maraví, P.F. & Wahlberg, N. (2013) New *Calisto* species from Cuba, with insights on the relationships of



- Cuban and Bahamian taxa (Lepidoptera, Nymphalidae, Satyrinae). *Zootaxa*, 3669 (4), 503–521.  
<https://doi.org/10.11646/zootaxa.3669.4.5>
- Núñez, R., Oliva, E., Matos-Maraví, P.F. & Wahlberg, N. (2012) Cuban *Calisto* (Lepidoptera, Nymphalidae, Satyrinae), a review based on morphological and DNA data. *ZooKeys*, 165, 57–105.  
<https://doi.org/10.3897/zookeys.165.2206>
- Núñez, R., Perez-Asso, A.R. & Genaro, J.A. (2017) Taxonomic reassessment of species within the *chrysaoros* group of *Calisto* (Lepidoptera, Nymphalidae, Satyrinae). *Invertebrate Systematics*. [in press]
- Perez-Asso, A.R., Núñez, R. & Genaro, J.A. (2016) Morphology and COI barcodes reveal four new species in the *lycieus* group of *Calisto* (Lepidoptera, Nymphalidae, Satyrinae). *Zootaxa*, 4170 (3), 401–450.  
<https://doi.org/10.11646/zootaxa.4170.3.1>
- Pons, J., Barraclough, T., Gomez-Zurita, J., Cardoso, A., Duran, D., Hazell, S., Kamoun, S., Sumlin, W. & Vogler, A. (2006) Sequence-based species delimitation for the DNA taxonomy of undescribed insects. *Systematic Biology*, 55, 595–610.  
<https://doi.org/10.1080/10635150600852011>
- Puillandre, N., Lambert, A., Brouillet, S. & Achaz, G. (2011) ABGD, Automatic Barcode Gap Discovery for primary species delimitation. *Molecular Ecology*, 21 (8), 1864–1877.  
<https://doi.org/10.1111/j.1365-294X.2011.05239.x>
- Puillandre, N., Modica, M.V., Zhang, Y., Sirovich, L., Boisselier, M.C., Cruaud, C., Holford, M. & Samadi, S. (2012) Largescale species delimitation method for hyperdiverse groups. *Molecular Ecology*, 21 (11), 2671–2691.  
<https://doi.org/10.1111/j.1365-294X.2012.05559.x>
- Rach, R., DeSalle, R., Sarkar, I.N., Schierwater, B. & Hadrys, H. (2008) Character-based DNA barcoding allows discrimination of genera, species and populations in Odonata. *Proceedings of the Royal Society of London, Series B (Biological Sciences)*, 275, 237–247.  
<https://doi.org/10.1098/rspb.2007.1290>
- Ronquist, F., Teslenko, M., van der Mark, P., Ayres, D.L., Darling, A., Höhna, S., Larget, B., Liu, L., Suchard, M.A. & Huelsenbeck, J.P. (2012) MrBayes 3.2: Efficient Bayesian phylogenetic inference and model choice across a large model space. *Systematic Biology*, 61 (3), 539–542.  
<http://dx.doi.org/10.1093/sysbio/sys029>
- Schwartz, A. (1989) *The butterflies of Hispaniola*. University of Florida Press, Gainesville, Florida, xiv + 580 pp.
- Schwartz, A. & Gali, F. (1984) Five new species of *Calisto* (Satyridae) from Hispaniola. *Bulletin of the Allyn Museum*, 85, 1–18.
- Smith, D.S., Miller, L.D. & Miller, J.Y. (1994) *The Butterflies of the West Indies and South Florida*. Oxford University Press, New York, 284 pp.
- Sourakov, A. (1996) Notes on the genus *Calisto*, with descriptions of the immature stages (part 1) (Lepidoptera: Nymphalidae: Satyrinae). *Tropical Lepidoptera*, 7 (1), 91–111.
- Sourakov, A. & Emmel, T.C. (1995) Early stages of *Calisto granmus* Bates on Hispaniola (Lepidoptera: Nymphalidae: Satyrinae). *Tropical Lepidoptera*, 6 (1), 27–30.
- Sourakov, A. & Zakharov, E.V. (2011) “Darwin’s butterflies”? DNA barcoding and the radiation of the endemic Caribbean butterfly genus *Calisto* (Lepidoptera, Nymphalidae, Satyrinae). *Comparative Cytogenetics*, 5 (3), 191–210.  
<https://doi.org/10.3897/compcytogen.v5i3.1730>
- Stamatakis, A., Hoover, P. & Rougemont, J. (2008) A rapid bootstrap algorithm for the RAxML web-servers. *Systematic Biology*, 75, 758–771.  
<https://doi.org/10.1080/10635150802429642>
- Tavares, E.S. & Baker, A.J. (2008) Single mitochondrial gene barcodes reliably identify sister-species in diverse clades of birds. *BMC Evolutionary Biology*, 8, 81.  
<https://doi.org/10.1186/1471-2148-8-81>
- Warren, A.D., Davis, K.J., Stangeland, E.M., Pelham, J.P., Willmott, K.R. & Grishin, N.V. (2016) Illustrated Lists of American Butterflies. Butterflies of America Foundation. Available from: <http://www.butterfliesofamerica.com/> (accessed 15 September 2016)
- Zhang, J., Kapli, P., Pavlidis, P. & Stamatakis, A. (2013) A general species delimitation method with applications to phylogenetic placements. *Bioinformatics*, 29, 2869–2876.  
<https://doi.org/10.1093/bioinformatics/btt499>

**APPENDIX 1.** Output of the species delimitation methods applied using 214 COI barcodes belonging to eight species form *hysius* group of *Calisto*.

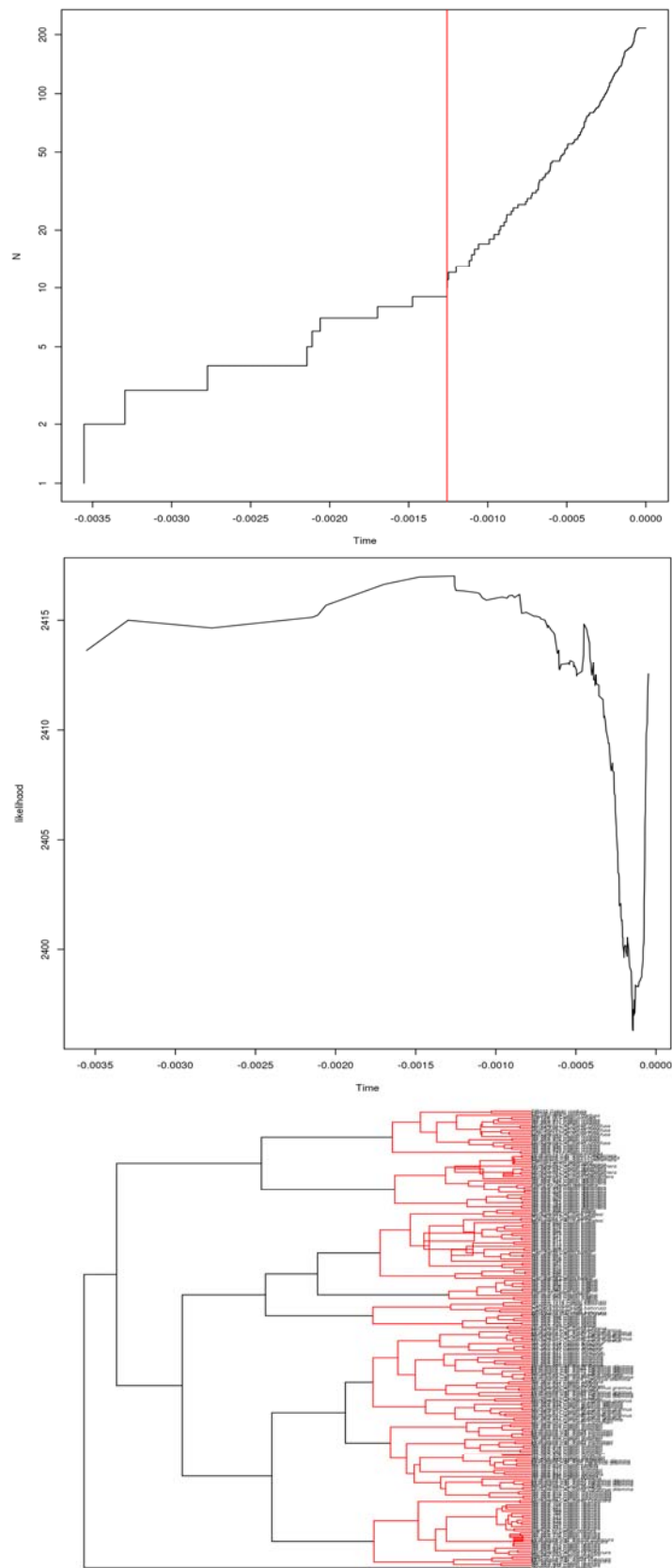
Generalized Mixed Yule Coalescent

Ultrametric starting tree obtained in BEAST software v.1.8.2





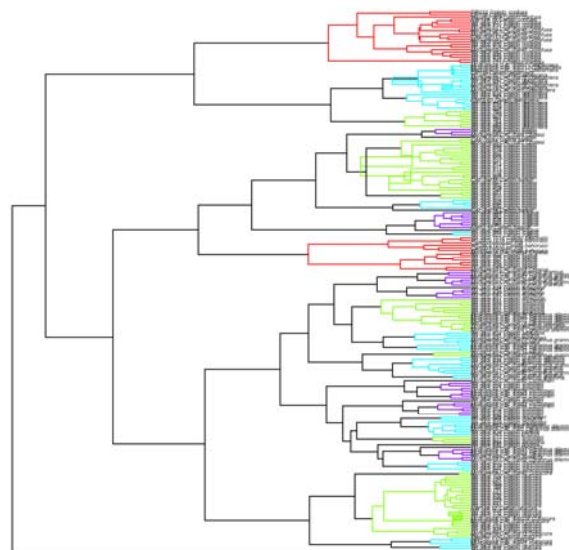
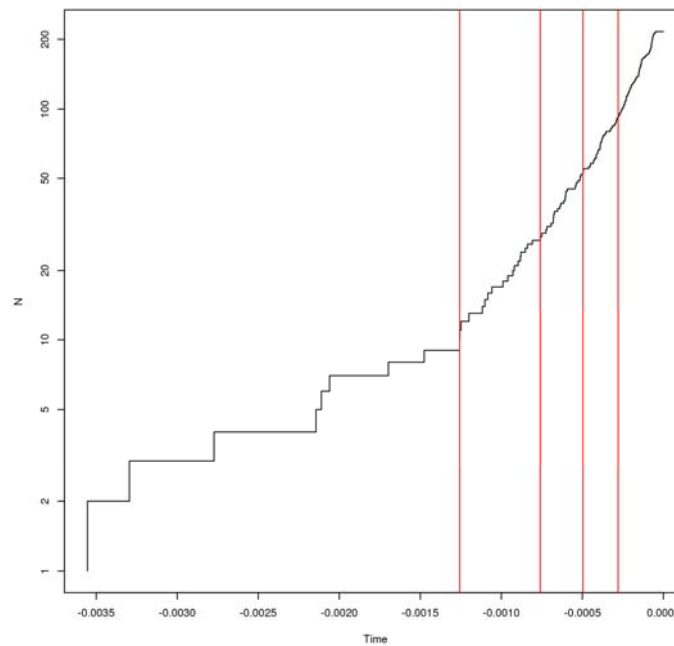
Graphic output of the GMYC single threshold method:



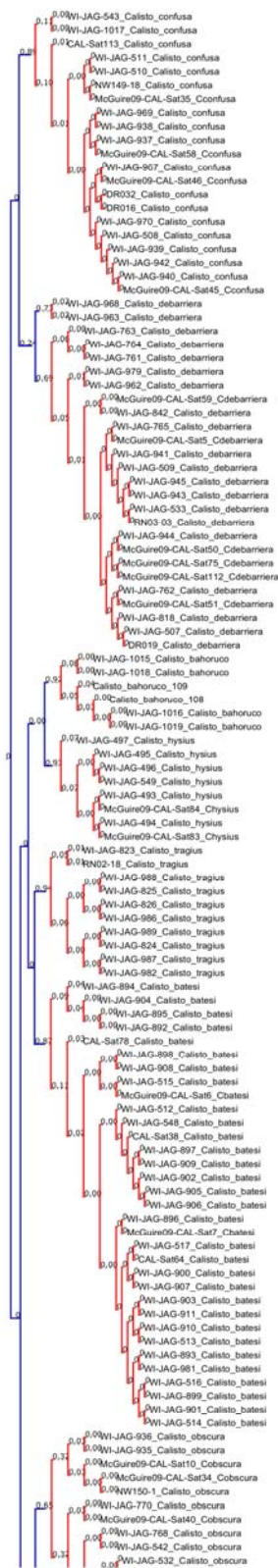
Parameters output of the GMYC multiple threshold method:

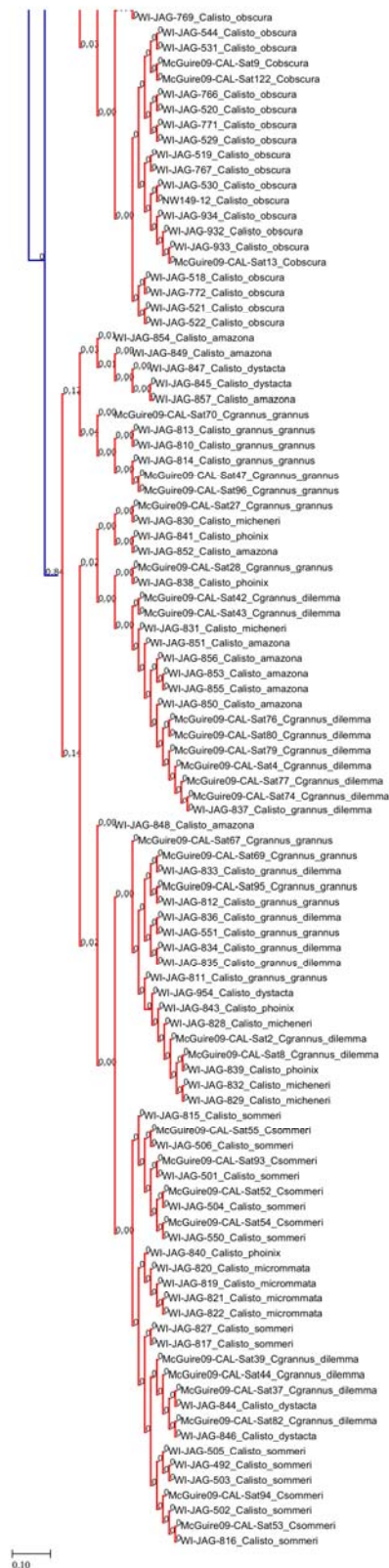
method: multiple  
likelihood of null model: 2413.628  
maximum likelihood of GMYC model: 2423.836  
likelihood ratio: 20.41686  
result of LR test: 3.68583e-05\*\*\*  
number of ML clusters: 33  
confidence interval: 29-44  
number of ML entities: 42  
confidence interval: 34-57  
threshold time: -0.001257703 -0.0007598622 -0.0004966197 -0.0002791752

Graphic output of the GMYC multiple threshold method:



Bayesian species delimitation using the Poisson Tree Process (bPTP) based on the distribution of nucleotide substitutions on the Bayesian Inference tree of hysius group species. Terminal branches in blue indicate lineages that stand as separate species and the clades in red are lumped into single species.

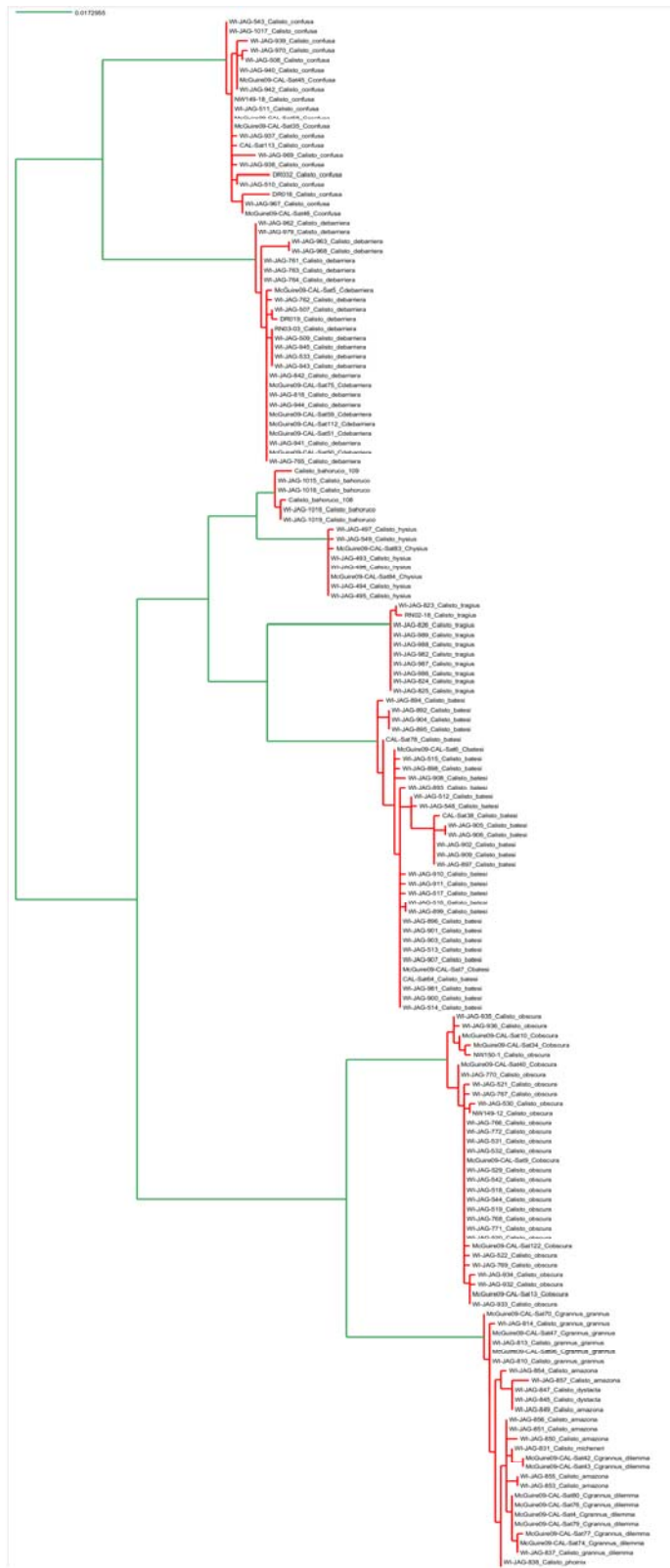


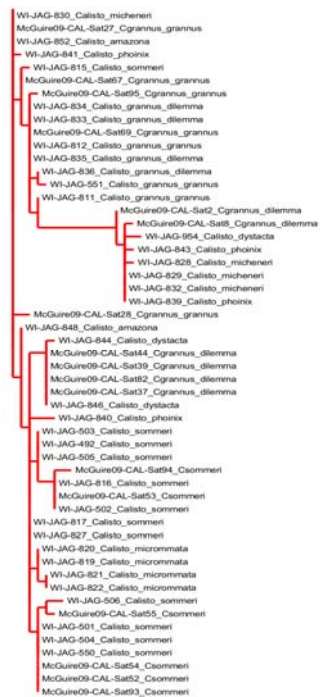


Multi-rate Poisson Tree Process (mPTP) delimitation. Terminal branches in red indicate lineages that stand as separate species and the clades in red are lumped into single species.



Graphic output





Output:

Command: `../bin/mptp mptp --ml --multi --outgroup JN300014_Calisto_eleus --outgroup_crop --svg_width 1366 --svg_marginleft 14 --svg_marginright 14 --tree_file ../uploads/f7516e8f2cit9sdur47eankbl2.newick --output_file ../uploads/f7516e8f2cit9sdur47eankbl2.1`

Number of edges greater than minimum branch length: 124 / 428

Null-model score: 516.549719

Best score for multi coalescent rate: 516.549719

Number of delimited species: 8

Species 1:

- WI-JAG-543\_Calisto\_confusa
- WI-JAG-1017\_Calisto\_confusa
- WI-JAG-939\_Calisto\_confusa
- WI-JAG-970\_Calisto\_confusa
- WI-JAG-508\_Calisto\_confusa
- WI-JAG-940\_Calisto\_confusa
- McGuire09-CAL-Sat45\_Cconfusa
- WI-JAG-942\_Calisto\_confusa
- NW149-18\_Calisto\_confusa
- WI-JAG-511\_Calisto\_confusa
- McGuire09-CAL-Sat58\_Cconfusa
- McGuire09-CAL-Sat35\_Cconfusa
- WI-JAG-937\_Calisto\_confusa
- CAL-Sat113\_Calisto\_confusa
- WI-JAG-969\_Calisto\_confusa
- WI-JAG-938\_Calisto\_confusa
- DR032\_Calisto\_confusa
- WI-JAG-510\_Calisto\_confusa

DR016\_Calisto\_confusa  
WI-JAG-967\_Calisto\_confusa  
McGuire09-CAL-Sat46\_Cconfusa

Species 2:

WI-JAG-962\_Calisto\_debarriera  
WI-JAG-979\_Calisto\_debarriera  
WI-JAG-963\_Calisto\_debarriera  
WI-JAG-968\_Calisto\_debarriera  
WI-JAG-761\_Calisto\_debarriera  
WI-JAG-763\_Calisto\_debarriera  
WI-JAG-764\_Calisto\_debarriera  
McGuire09-CAL-Sat5\_Cdebarriera  
WI-JAG-762\_Calisto\_debarriera  
WI-JAG-507\_Calisto\_debarriera  
DR019\_Calisto\_debarriera  
RN03-03\_Calisto\_debarriera  
WI-JAG-509\_Calisto\_debarriera  
WI-JAG-945\_Calisto\_debarriera  
WI-JAG-533\_Calisto\_debarriera  
WI-JAG-943\_Calisto\_debarriera  
WI-JAG-842\_Calisto\_debarriera  
McGuire09-CAL-Sat75\_Cdebarriera  
WI-JAG-818\_Calisto\_debarriera  
WI-JAG-944\_Calisto\_debarriera  
McGuire09-CAL-Sat59\_Cdebarriera  
McGuire09-CAL-Sat112\_Cdebarriera  
McGuire09-CAL-Sat51\_Cdebarriera  
WI-JAG-941\_Calisto\_debarriera  
McGuire09-CAL-Sat50\_Cdebarriera  
WI-JAG-765\_Calisto\_debarriera

Species 3:

Calisto\_bahoruco\_109  
WI-JAG-1015\_Calisto\_bahoruco  
WI-JAG-1018\_Calisto\_bahoruco  
Calisto\_bahoruco\_108  
WI-JAG-1016\_Calisto\_bahoruco  
WI-JAG-1019\_Calisto\_bahoruco

Species 4:

WI-JAG-497\_Calisto\_hysius  
WI-JAG-549\_Calisto\_hysius  
McGuire09-CAL-Sat83\_Chysius  
WI-JAG-493\_Calisto\_hysius  
WI-JAG-496\_Calisto\_hysius  
McGuire09-CAL-Sat84\_Chysius  
WI-JAG-494\_Calisto\_hysius  
WI-JAG-495\_Calisto\_hysius

Species 5:

WI-JAG-823\_Calisto\_tragius  
RN02-18\_Calisto\_tragius  
WI-JAG-826\_Calisto\_tragius  
WI-JAG-989\_Calisto\_tragius  
WI-JAG-988\_Calisto\_tragius

WI-JAG-982\_Calisto\_tragi  
WI-JAG-987\_Calisto\_tragi  
WI-JAG-986\_Calisto\_tragi  
WI-JAG-824\_Calisto\_tragi  
WI-JAG-825\_Calisto\_tragi

Species 6:

WI-JAG-894\_Calisto\_batesi  
WI-JAG-892\_Calisto\_batesi  
WI-JAG-904\_Calisto\_batesi  
WI-JAG-895\_Calisto\_batesi  
CAL-Sat78\_Calisto\_batesi  
McGuire09-CAL-Sat6\_Cbatesi  
WI-JAG-515\_Calisto\_batesi  
WI-JAG-898\_Calisto\_batesi  
WI-JAG-908\_Calisto\_batesi  
WI-JAG-893\_Calisto\_batesi  
WI-JAG-512\_Calisto\_batesi  
WI-JAG-548\_Calisto\_batesi  
CAL-Sat38\_Calisto\_batesi  
WI-JAG-905\_Calisto\_batesi  
WI-JAG-906\_Calisto\_batesi  
WI-JAG-902\_Calisto\_batesi  
WI-JAG-909\_Calisto\_batesi  
WI-JAG-897\_Calisto\_batesi  
WI-JAG-910\_Calisto\_batesi  
WI-JAG-911\_Calisto\_batesi  
WI-JAG-517\_Calisto\_batesi  
WI-JAG-516\_Calisto\_batesi  
WI-JAG-899\_Calisto\_batesi  
WI-JAG-896\_Calisto\_batesi  
WI-JAG-901\_Calisto\_batesi  
WI-JAG-903\_Calisto\_batesi  
WI-JAG-513\_Calisto\_batesi  
WI-JAG-907\_Calisto\_batesi  
McGuire09-CAL-Sat7\_Cbatesi  
CAL-Sat64\_Calisto\_batesi  
WI-JAG-981\_Calisto\_batesi  
WI-JAG-900\_Calisto\_batesi  
WI-JAG-514\_Calisto\_batesi

Species 7:

WI-JAG-935\_Calisto\_obscura  
WI-JAG-936\_Calisto\_obscura  
McGuire09-CAL-Sat10\_Cobscura  
McGuire09-CAL-Sat34\_Cobscura  
NW150-1\_Calisto\_obscura  
McGuire09-CAL-Sat40\_Cobscura  
WI-JAG-770\_Calisto\_obscura  
WI-JAG-521\_Calisto\_obscura  
WI-JAG-767\_Calisto\_obscura  
WI-JAG-530\_Calisto\_obscura  
NW149-12\_Calisto\_obscura  
WI-JAG-766\_Calisto\_obscura  
WI-JAG-772\_Calisto\_obscura  
WI-JAG-531\_Calisto\_obscura

WI-JAG-532\_Calisto\_obscura  
McGuire09-CAL-Sat9\_Cobscura  
WI-JAG-529\_Calisto\_obscura  
WI-JAG-542\_Calisto\_obscura  
WI-JAG-518\_Calisto\_obscura  
WI-JAG-544\_Calisto\_obscura  
WI-JAG-519\_Calisto\_obscura  
WI-JAG-768\_Calisto\_obscura  
WI-JAG-771\_Calisto\_obscura  
WI-JAG-520\_Calisto\_obscura  
McGuire09-CAL-Sat122\_Cobscura  
WI-JAG-522\_Calisto\_obscura  
WI-JAG-769\_Calisto\_obscura  
WI-JAG-934\_Calisto\_obscura  
WI-JAG-932\_Calisto\_obscura  
McGuire09-CAL-Sat13\_Cobscura  
WI-JAG-933\_Calisto\_obscura

Species 8:

McGuire09-CAL-Sat70\_Cgrannus\_grannus  
WI-JAG-814\_Calisto\_grannus\_grannus  
McGuire09-CAL-Sat47\_Cgrannus\_grannus  
WI-JAG-813\_Calisto\_grannus\_grannus  
McGuire09-CAL-Sat96\_Cgrannus\_grannus  
WI-JAG-810\_Calisto\_grannus\_grannus  
WI-JAG-854\_Calisto\_amazona  
WI-JAG-857\_Calisto\_amazona  
WI-JAG-847\_Calisto\_dystacta  
WI-JAG-845\_Calisto\_dystacta  
WI-JAG-849\_Calisto\_amazona  
WI-JAG-856\_Calisto\_amazona  
WI-JAG-851\_Calisto\_amazona  
WI-JAG-850\_Calisto\_amazona  
WI-JAG-831\_Calisto\_micheneri  
McGuire09-CAL-Sat42\_Cgrannus\_dilemma  
McGuire09-CAL-Sat43\_Cgrannus\_dilemma  
WI-JAG-855\_Calisto\_amazona  
WI-JAG-853\_Calisto\_amazona  
McGuire09-CAL-Sat80\_Cgrannus\_dilemma  
McGuire09-CAL-Sat76\_Cgrannus\_dilemma  
McGuire09-CAL-Sat4\_Cgrannus\_dilemma  
McGuire09-CAL-Sat79\_Cgrannus\_dilemma  
McGuire09-CAL-Sat77\_Cgrannus\_dilemma  
McGuire09-CAL-Sat74\_Cgrannus\_dilemma  
WI-JAG-837\_Calisto\_grannus\_dilemma  
WI-JAG-838\_Calisto\_phoinix  
WI-JAG-830\_Calisto\_micheneri  
McGuire09-CAL-Sat27\_Cgrannus\_grannus  
WI-JAG-852\_Calisto\_amazona  
WI-JAG-841\_Calisto\_phoinix  
WI-JAG-815\_Calisto\_sommeri  
McGuire09-CAL-Sat67\_Cgrannus\_grannus  
McGuire09-CAL-Sat95\_Cgrannus\_grannus  
WI-JAG-834\_Calisto\_grannus\_dilemma  
WI-JAG-833\_Calisto\_grannus\_dilemma  
McGuire09-CAL-Sat69\_Cgrannus\_grannus

WI-JAG-812\_Calisto\_grannus\_grannus  
WI-JAG-835\_Calisto\_grannus\_dilemma  
WI-JAG-836\_Calisto\_grannus\_dilemma  
WI-JAG-551\_Calisto\_grannus\_grannus  
WI-JAG-811\_Calisto\_grannus\_grannus  
McGuire09-CAL-Sat2\_Cgrannus\_dilemma  
McGuire09-CAL-Sat8\_Cgrannus\_dilemma  
WI-JAG-954\_Calisto\_dystacta  
WI-JAG-843\_Calisto\_phoinix  
WI-JAG-828\_Calisto\_micheneri  
WI-JAG-829\_Calisto\_micheneri  
WI-JAG-832\_Calisto\_micheneri  
WI-JAG-839\_Calisto\_phoinix  
McGuire09-CAL-Sat28\_Cgrannus\_grannus  
WI-JAG-848\_Calisto\_amazona  
WI-JAG-844\_Calisto\_dystacta  
McGuire09-CAL-Sat44\_Cgrannus\_dilemma  
McGuire09-CAL-Sat39\_Cgrannus\_dilemma  
McGuire09-CAL-Sat82\_Cgrannus\_dilemma  
McGuire09-CAL-Sat37\_Cgrannus\_dilemma  
WI-JAG-846\_Calisto\_dystacta  
WI-JAG-840\_Calisto\_phoinix  
WI-JAG-503\_Calisto\_sommeri  
WI-JAG-492\_Calisto\_sommeri  
WI-JAG-505\_Calisto\_sommeri  
McGuire09-CAL-Sat94\_Csommeri  
WI-JAG-816\_Calisto\_sommeri  
McGuire09-CAL-Sat53\_Csommeri  
WI-JAG-502\_Calisto\_sommeri  
WI-JAG-817\_Calisto\_sommeri  
WI-JAG-827\_Calisto\_sommeri  
WI-JAG-820\_Calisto\_micrommata  
WI-JAG-819\_Calisto\_micrommata  
WI-JAG-821\_Calisto\_micrommata  
WI-JAG-822\_Calisto\_micrommata  
WI-JAG-506\_Calisto\_sommeri  
McGuire09-CAL-Sat55\_Csommeri  
WI-JAG-501\_Calisto\_sommeri  
WI-JAG-504\_Calisto\_sommeri  
WI-JAG-550\_Calisto\_sommeri  
McGuire09-CAL-Sat54\_Csommeri  
McGuire09-CAL-Sat52\_Csommeri  
McGuire09-CAL-Sat93\_Csommeri

Poisson Tree Process (PTP) delimitation. Terminal branches in red indicate lineages that stand as separate species and the clades in red are lumped into single species.







Output:

Command: ../bin/mptp mptp --ml --single --pvalue 0.001 --outgroup JN300014\_Calisto\_eleleus --outgroup\_crop --svg\_width 1366 --svg\_marginleft 14 --svg\_marginright 14 --tree\_file ../uploads/f7516e8f2cit9sdur47eankbl2.newick --output\_file ../uploads/f7516e8f2cit9sdur47eankbl2.2

Number of edges greater than minimum branch length: 124 / 428

Null-model score: 516.549719

Best score for single coalescent rate: 584.466328

Number of delimited species: 8

Species 1:

- WI-JAG-543\_Calisto\_confusa
- WI-JAG-1017\_Calisto\_confusa
- WI-JAG-939\_Calisto\_confusa
- WI-JAG-970\_Calisto\_confusa
- WI-JAG-508\_Calisto\_confusa
- WI-JAG-940\_Calisto\_confusa
- McGuire09-CAL-Sat45\_Cconfusa
- WI-JAG-942\_Calisto\_confusa
- NW149-18\_Calisto\_confusa
- WI-JAG-511\_Calisto\_confusa
- McGuire09-CAL-Sat58\_Cconfusa
- McGuire09-CAL-Sat35\_Cconfusa
- WI-JAG-937\_Calisto\_confusa
- CAL-Sat113\_Calisto\_confusa
- WI-JAG-969\_Calisto\_confusa
- WI-JAG-938\_Calisto\_confusa
- DR032\_Calisto\_confusa
- WI-JAG-510\_Calisto\_confusa
- DR016\_Calisto\_confusa
- WI-JAG-967\_Calisto\_confusa

McGuire09-CAL-Sat46\_Cconfusa

Species 2:

WI-JAG-962\_Calisto\_debarriera  
WI-JAG-979\_Calisto\_debarriera  
WI-JAG-963\_Calisto\_debarriera  
WI-JAG-968\_Calisto\_debarriera  
WI-JAG-761\_Calisto\_debarriera  
WI-JAG-763\_Calisto\_debarriera  
WI-JAG-764\_Calisto\_debarriera  
McGuire09-CAL-Sat5\_Cdebarriera  
WI-JAG-762\_Calisto\_debarriera  
WI-JAG-507\_Calisto\_debarriera  
DR019\_Calisto\_debarriera  
RN03-03\_Calisto\_debarriera  
WI-JAG-509\_Calisto\_debarriera  
WI-JAG-945\_Calisto\_debarriera  
WI-JAG-533\_Calisto\_debarriera  
WI-JAG-943\_Calisto\_debarriera  
WI-JAG-842\_Calisto\_debarriera  
McGuire09-CAL-Sat75\_Cdebarriera  
WI-JAG-818\_Calisto\_debarriera  
WI-JAG-944\_Calisto\_debarriera  
McGuire09-CAL-Sat59\_Cdebarriera  
McGuire09-CAL-Sat112\_Cdebarriera  
McGuire09-CAL-Sat51\_Cdebarriera  
WI-JAG-941\_Calisto\_debarriera  
McGuire09-CAL-Sat50\_Cdebarriera  
WI-JAG-765\_Calisto\_debarriera

Species 3:

Calisto\_bahoruco\_109  
WI-JAG-1015\_Calisto\_bahoruco  
WI-JAG-1018\_Calisto\_bahoruco  
Calisto\_bahoruco\_108  
WI-JAG-1016\_Calisto\_bahoruco  
WI-JAG-1019\_Calisto\_bahoruco

Species 4:

WI-JAG-497\_Calisto\_hysius  
WI-JAG-549\_Calisto\_hysius  
McGuire09-CAL-Sat83\_Chysius  
WI-JAG-493\_Calisto\_hysius  
WI-JAG-496\_Calisto\_hysius  
McGuire09-CAL-Sat84\_Chysius  
WI-JAG-494\_Calisto\_hysius  
WI-JAG-495\_Calisto\_hysius

Species 5:

WI-JAG-823\_Calisto\_tragius  
RN02-18\_Calisto\_tragius  
WI-JAG-826\_Calisto\_tragius  
WI-JAG-989\_Calisto\_tragius  
WI-JAG-988\_Calisto\_tragius  
WI-JAG-982\_Calisto\_tragius  
WI-JAG-987\_Calisto\_tragius

WI-JAG-986\_Calisto\_tragi  
WI-JAG-824\_Calisto\_tragi  
WI-JAG-825\_Calisto\_tragi

Species 6:

WI-JAG-894\_Calisto\_batesi  
WI-JAG-892\_Calisto\_batesi  
WI-JAG-904\_Calisto\_batesi  
WI-JAG-895\_Calisto\_batesi  
CAL-Sat78\_Calisto\_batesi  
McGuire09-CAL-Sat6\_Cbatesi  
WI-JAG-515\_Calisto\_batesi  
WI-JAG-898\_Calisto\_batesi  
WI-JAG-908\_Calisto\_batesi  
WI-JAG-893\_Calisto\_batesi  
WI-JAG-512\_Calisto\_batesi  
WI-JAG-548\_Calisto\_batesi  
CAL-Sat38\_Calisto\_batesi  
WI-JAG-905\_Calisto\_batesi  
WI-JAG-906\_Calisto\_batesi  
WI-JAG-902\_Calisto\_batesi  
WI-JAG-909\_Calisto\_batesi  
WI-JAG-897\_Calisto\_batesi  
WI-JAG-910\_Calisto\_batesi  
WI-JAG-911\_Calisto\_batesi  
WI-JAG-517\_Calisto\_batesi  
WI-JAG-516\_Calisto\_batesi  
WI-JAG-899\_Calisto\_batesi  
WI-JAG-896\_Calisto\_batesi  
WI-JAG-901\_Calisto\_batesi  
WI-JAG-903\_Calisto\_batesi  
WI-JAG-513\_Calisto\_batesi  
WI-JAG-907\_Calisto\_batesi  
McGuire09-CAL-Sat7\_Cbatesi  
CAL-Sat64\_Calisto\_batesi  
WI-JAG-981\_Calisto\_batesi  
WI-JAG-900\_Calisto\_batesi  
WI-JAG-514\_Calisto\_batesi

Species 7:

WI-JAG-935\_Calisto\_obscura  
WI-JAG-936\_Calisto\_obscura  
McGuire09-CAL-Sat10\_Cobscura  
McGuire09-CAL-Sat34\_Cobscura  
NW150-1\_Calisto\_obscura  
McGuire09-CAL-Sat40\_Cobscura  
WI-JAG-770\_Calisto\_obscura  
WI-JAG-521\_Calisto\_obscura  
WI-JAG-767\_Calisto\_obscura  
WI-JAG-530\_Calisto\_obscura  
NW149-12\_Calisto\_obscura  
WI-JAG-766\_Calisto\_obscura  
WI-JAG-772\_Calisto\_obscura  
WI-JAG-531\_Calisto\_obscura  
WI-JAG-532\_Calisto\_obscura  
McGuire09-CAL-Sat9\_Cobscura

WI-JAG-529\_Calisto\_obscura  
WI-JAG-542\_Calisto\_obscura  
WI-JAG-518\_Calisto\_obscura  
WI-JAG-544\_Calisto\_obscura  
WI-JAG-519\_Calisto\_obscura  
WI-JAG-768\_Calisto\_obscura  
WI-JAG-771\_Calisto\_obscura  
WI-JAG-520\_Calisto\_obscura  
McGuire09-CAL-Sat122\_Cobscura  
WI-JAG-522\_Calisto\_obscura  
WI-JAG-769\_Calisto\_obscura  
WI-JAG-934\_Calisto\_obscura  
WI-JAG-932\_Calisto\_obscura  
McGuire09-CAL-Sat13\_Cobscura  
WI-JAG-933\_Calisto\_obscura

Species 8:

McGuire09-CAL-Sat70\_Cgrannus\_grannus  
WI-JAG-814\_Calisto\_grannus\_grannus  
McGuire09-CAL-Sat47\_Cgrannus\_grannus  
WI-JAG-813\_Calisto\_grannus\_grannus  
McGuire09-CAL-Sat96\_Cgrannus\_grannus  
WI-JAG-810\_Calisto\_grannus\_grannus  
WI-JAG-854\_Calisto\_amazona  
WI-JAG-857\_Calisto\_amazona  
WI-JAG-847\_Calisto\_dystacta  
WI-JAG-845\_Calisto\_dystacta  
WI-JAG-849\_Calisto\_amazona  
WI-JAG-856\_Calisto\_amazona  
WI-JAG-851\_Calisto\_amazona  
WI-JAG-850\_Calisto\_amazona  
WI-JAG-831\_Calisto\_micheneri  
McGuire09-CAL-Sat42\_Cgrannus\_dilemma  
McGuire09-CAL-Sat43\_Cgrannus\_dilemma  
WI-JAG-855\_Calisto\_amazona  
WI-JAG-853\_Calisto\_amazona  
McGuire09-CAL-Sat80\_Cgrannus\_dilemma  
McGuire09-CAL-Sat76\_Cgrannus\_dilemma  
McGuire09-CAL-Sat4\_Cgrannus\_dilemma  
McGuire09-CAL-Sat79\_Cgrannus\_dilemma  
McGuire09-CAL-Sat77\_Cgrannus\_dilemma  
McGuire09-CAL-Sat74\_Cgrannus\_dilemma  
WI-JAG-837\_Calisto\_grannus\_dilemma  
WI-JAG-838\_Calisto\_phoinix  
WI-JAG-830\_Calisto\_micheneri  
McGuire09-CAL-Sat27\_Cgrannus\_grannus  
WI-JAG-852\_Calisto\_amazona  
WI-JAG-841\_Calisto\_phoinix  
WI-JAG-815\_Calisto\_sommeri  
McGuire09-CAL-Sat67\_Cgrannus\_grannus  
McGuire09-CAL-Sat95\_Cgrannus\_grannus  
WI-JAG-834\_Calisto\_grannus\_dilemma  
WI-JAG-833\_Calisto\_grannus\_dilemma  
McGuire09-CAL-Sat69\_Cgrannus\_grannus  
WI-JAG-812\_Calisto\_grannus\_grannus  
WI-JAG-835\_Calisto\_grannus\_dilemma

WI-JAG-836\_Calisto\_grannus\_dilemma  
WI-JAG-551\_Calisto\_grannus\_grannus  
WI-JAG-811\_Calisto\_grannus\_grannus  
McGuire09-CAL-Sat2\_Cgrannus\_dilemma  
McGuire09-CAL-Sat8\_Cgrannus\_dilemma  
WI-JAG-954\_Calisto\_dystacta  
WI-JAG-843\_Calisto\_phoinix  
WI-JAG-828\_Calisto\_micheneri  
WI-JAG-829\_Calisto\_micheneri  
WI-JAG-832\_Calisto\_micheneri  
WI-JAG-839\_Calisto\_phoinix  
McGuire09-CAL-Sat28\_Cgrannus\_grannus  
WI-JAG-848\_Calisto\_amazona  
WI-JAG-844\_Calisto\_dystacta  
McGuire09-CAL-Sat44\_Cgrannus\_dilemma  
McGuire09-CAL-Sat39\_Cgrannus\_dilemma  
McGuire09-CAL-Sat82\_Cgrannus\_dilemma  
McGuire09-CAL-Sat37\_Cgrannus\_dilemma  
WI-JAG-846\_Calisto\_dystacta  
WI-JAG-840\_Calisto\_phoinix  
WI-JAG-503\_Calisto\_sommeri  
WI-JAG-492\_Calisto\_sommeri  
WI-JAG-505\_Calisto\_sommeri  
McGuire09-CAL-Sat94\_Csommeri  
WI-JAG-816\_Calisto\_sommeri  
McGuire09-CAL-Sat53\_Csommeri  
WI-JAG-502\_Calisto\_sommeri  
WI-JAG-817\_Calisto\_sommeri  
WI-JAG-827\_Calisto\_sommeri  
WI-JAG-820\_Calisto\_micrommata  
WI-JAG-819\_Calisto\_micrommata  
WI-JAG-821\_Calisto\_micrommata  
WI-JAG-822\_Calisto\_micrommata  
WI-JAG-506\_Calisto\_sommeri  
McGuire09-CAL-Sat55\_Csommeri  
WI-JAG-501\_Calisto\_sommeri  
WI-JAG-504\_Calisto\_sommeri  
WI-JAG-550\_Calisto\_sommeri  
McGuire09-CAL-Sat54\_Csommeri  
McGuire09-CAL-Sat52\_Csommeri  
McGuire09-CAL-Sat93\_Csommeri

Outputs generated by the ABGD web- interface (available at: <http://wwwabi.snv.jussieu.fr/public/abgd/>) for the available COI sequences of the hysius species group of *Calisto*.

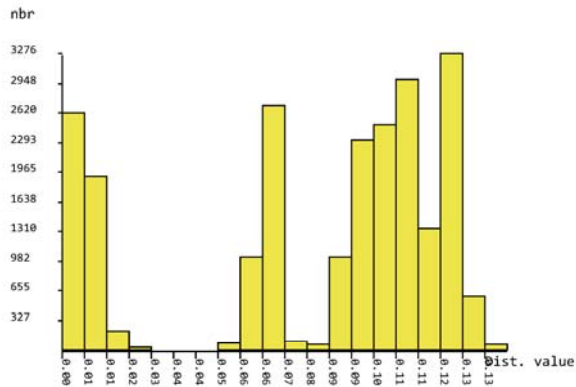
7/2/2017

abgd web

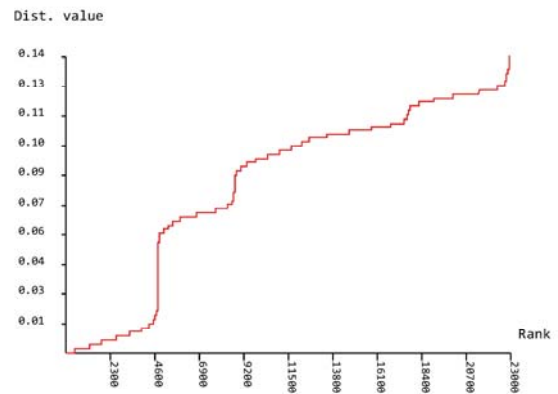
ABGD Web results using JC69 Jukes-Cantor mesure of distance Left click [here](#) to save matrix distance file

Data: DistanceDataHysius

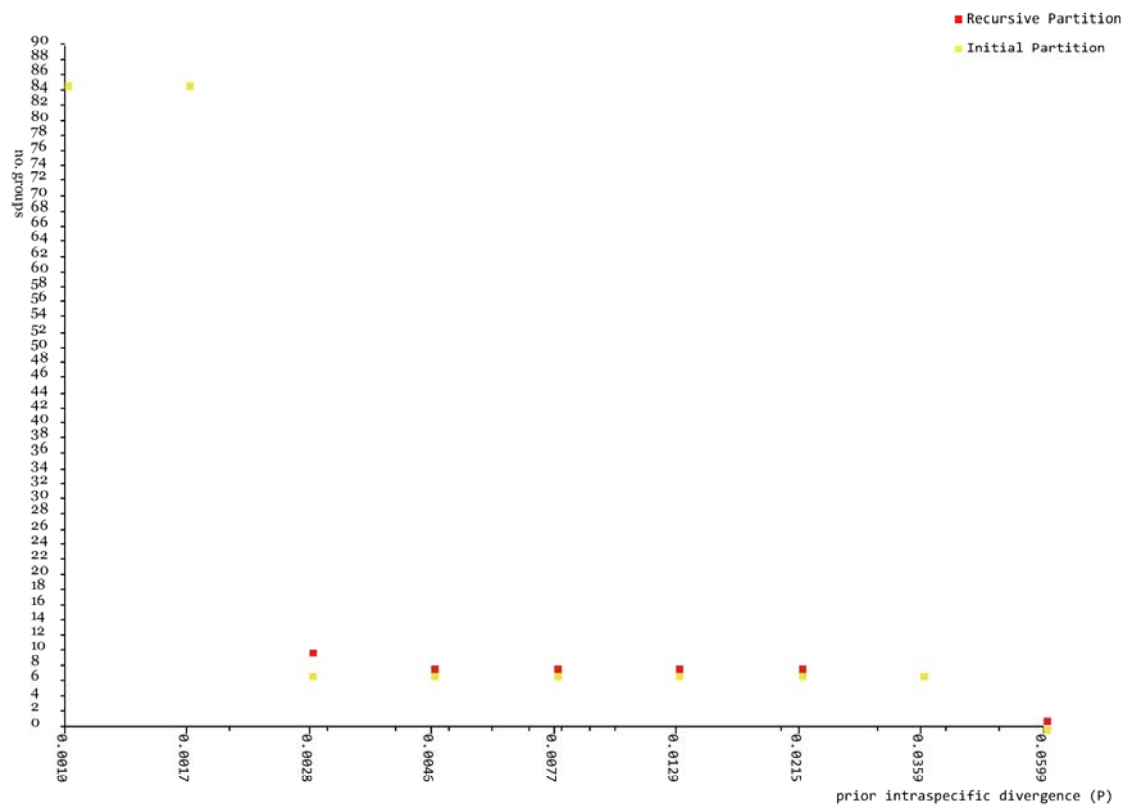
Histogram of distances [\[save\]](#)



Ranked distances [\[save\]](#)



A Click on a symbol will open a new tab/window showing the selected partition



<http://wwwabi.snv.jussieu.fr/public/abgd/temp/31216.1540297313/index.html>