***Cataracta*, a new monotipic genus segregated from *Physalis* L. (Solanaceae)**

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**APPENDIX**

**TABLE A1.** GenBank sequence numbers of the 22 species used in the phylogenetic inference to estimate the position of *Cataracta* gen. nov. \*cpDNA sequences that were extracted from plastomes generated by Sandoval-Padilla et al. (in prep.). Accession numbers in bold were newly generated for this work. NA = not available.

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| Species | *ITS* | *GBSSI* | *LEAFY* | *matK* | *rbcL* | *ndhF* | *rpl32-trnL* | *trnL* | *ycf1-3* |
| *Alkekengi officinarum* | AY665850 | AY665931 | MH822152 | EF438924 | U08617 | U08927 | MH045575 | MH752594 | MH045575 |
| *Brachistus stramonnifolius* | AY665845 | AY665924 | MH822159 | OR400638\* | OR400638\* | OR400638\* | OR400638\* | EU580963 | OR400638\* |
| *Calliphysalis carpenteri* | AY665852 | AY665932 | MH822160 | OR400639\* | OR400639\* | EU580926 | OR400639\* | EU581042 | OR400639\* |
| *Capsicophysalis potosina* | OK298970 | **OR521018** | NA | **OR521018** | **OR521028** | **OR521030** | **OR521009** | NA | **OR521000** |
| *Capsicum* | AY665841 | AY665923 | NA | JQ589211 | JX856306 | U08916 | NC018552 | NC018552 | NC018552 |
| *Cataracta microphysa* comb.nov. | AY665859 | AY665933 | MH822240 | **OR521029** | **OR520999** | **OR521033** | **OR521017** | MH752653 | **OR521008** |
| *Chamaesaracha coronopus* | AY665860 | AY665937 | MH822163 | **OR521022** | **OR520991** | EU580871 | **OR521010** | MH752598 | **OR521001** |
| *Chamaesaracha rzedowskiana* | OK298969 | **OR521019** | MH822166 | **OR521023** | **OR520992** | **OR521031** | **OR521011** | MH752601 | **OR521002** |
| *Iochroma* | AY665840 | AY665921 | DQ301559 | EF438902 | NA | EU580894 | NA | NA | NA |
| *Deprea* | AY665839 | AY665919 | NA | NA | NA | EU126022 | NA | NA | NA |
| *Leucophysalis grandiflora* | AY665846 | AY665929 | DQ301515 | **OR521024** | **OR520993** | EU58090 | **OR521012** | EU581013 | **OR521012** |
| *Leucophysalis nana* | AY665847 | AY665928 | NA | NA | **OR520994** | EU580906 | **OR521013** | EU581014 | NA |
| *Oryctes nevadensis* | AY665864 | AY665934 | NA | OR360845\* | OR360845\* | EU580923 | OR360845\* | EY581039 | OR360845\* |
| *Physaliastrum heterophyllum* | KC768878 | NA | NA | **OR521025** | **OR520995** | KC768882 | **OR521014** | KC768880 | **OR521004** |
| *Physalis campechiana* | AY665867 | AY665936 | MH822226 | **OR521026** | **OR520996** | NA | NA | MH752638 | OR521005 |
| *Physalis cinerascens* | AY665885 | AY665971 | NA | OR296713\* | OR296713\* | OR296713\* | OR296713\* | MH752640 | OR296713\* |
| *Physalis melanocystis* | AY665865 | **OR521020** | MH822239 | **OR521028** | **OR520998** | NA | **OR521016** | MH752652 | **OR521007** |
| *Physalis pubescens* | AY665917 | AY665951 | MH304895 | MH045576 | MH045576 | MH045576 | MH045576 | MH752660 | MH045576 |
| *Quincula lobata* | AY665863 | AY665935 | MH822257 | OR521027 | OR520997 | EU580936 | OR521015 | MH752668 | OR521006 |
| *Schraderanthus viscosus* | AY665848 | AY665927 | NA | OR360844\* | OR360844\* | OR360844\* | OR360844\* | OR360844\* | OR360844\* |
| *Tzeltalia amphitricha* | AY665853 | NA | NA | OR360842\* | OR360842\* | OR360842\* | OR360842\* | OR360842\* | OR360842\* |
| *Witheringia solanacea* | AY665858 | AY665926 | DQ301517 | JQ594187 | JQ594188 | U72755 | OR400643\* | EU581074 | OR400643\* |

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| **TABLE A2.** Voucher information of the specimens that were used to generate the new DNA sequences. |
| |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | | Species | Specimen voucher | Collected by | Collection date | Country | Identified by | Herbarium | | *Capsicophysalis potosina* | 331 PZT | Pilar Zamora y Mahinda Martinez | 02-sep-16 | Mexico | Mahinda Martinez | IBUG | | *Cataracta microphysa* comb.nov. | 330 PZT | Pilar Zamora y Mahinda Martinez | 02-sep-16 | Mexico | Pilar Zamora | IBUG | | *Chamaesaracha coronopus* | 300 PZT | Pilar Zamora y Mahinda Martinez | 16-sep-16 | Mexico | Mahinda Martinez | IBUG | | *Chamaesaracha rzedowskiana* | 227 PZT | Pilar Zamora y Mahinda Martinez | 21-sep-12 | Mexico | Mahinda Martinez | IBUG | | *Leucophysalis grandiflora* | 1424418\_NY | H.H. Bartlet and J.F. Grayson | 27/06/1952 | USA |  | NY | | *Leucophysalis nana* | 2781262\_NY | A. Tiehm 17631 | 10/08/2016 | USA |  | NY | | *Physaliastrum heterophyllum* | 1992\_MO | Tayaping Team Exp. 791 | 1992 | China |  | MO | | *Physalis campechiana* | SN IBUG | F. Ventura A | 04-dic-71 | Mexico | Mahinda Martinez | IBUG | | *Physalis melanocystis* | SN IBUG | Mahinda Martinez | 17-ago-21 | Mexico | Mahinda Martinez | IBUG | | *Quincula lobata* | 335 PZT | Pilar Zamora y Mahinda Martinez | 16-sep-16 | Mexico | Pilar Zamora | IBUG | |

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| **TABLE A3.** Dataset by regions, number of taxa of Physalidinae included, length in base pairs, and the best-fitting nucleotide substitution models based on the Akaike Information Criterion (AIC). |
| |  |  |  |  | | --- | --- | --- | --- | | Data set | Number of Physalidinae taxa | Length in base pairs | Best model (AIC) | | 5.8S RNA ribosomal | 19 | 703 | HKY+G | | *LEAFY* | 13 | 2141 | GTR+I+G | | *GBSSI* region between exons 8-10 | 18 | 773 | TPM2uf+G | | *mat*K | 18 | 789 | TVM+G | | *ndh*F | 17 | 758 | TPM1uf+G | | *rbc*L | 19 | 607 | HKY | | *rpl*32-*trn*L | 18 | 1213 | TPM1uf+G | | trnL*F* | 16 | 1028 | GTR+I+G | | *ycf*1-3 | 17 | 809 | GTR+G | |

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| **FIGURE** **A1.** The best tree obtained with Maximum Likelihood and 1000 bootstrap iterations with data of RNA ribosomal 5.8S region and 19 taxa of Physalidinae. |
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| **FIGURE** **A2.** The best tree obtained with Maximum Likelihood and 1000 bootstrap iterations with data of *LEAFY* and 13 taxa of Physalidinae. |
| Diagrama  Descripción generada automáticamente |

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| **FIGURE** **A3.** The best tree obtained with Maximum Likelihood and 1000 bootstrap iterations with data of GBSSI region between exons 8-10, and 18 taxa of Physalidinae. |
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| **FIGURE** **A4.** The best tree obtained with Maximum Likelihood and 1000 bootstrap iterations with data of *mat*K region and 18 taxa of Physalidinae. |
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| **FIGURE** **A5.** The best tree obtained with Maximum Likelihood and 1000 bootstrap iterations with data of *ndh*F region and 17 taxa of Physalidinae. |
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| **FIGURE** **A6.** The best tree obtained with Maximum Likelihood and 1000 bootstrap iterations with data of *rbc*L region and 19 taxa of Physalidinae. |
| Imagen que contiene Gráfico  Descripción generada automáticamente |

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| **FIGURE** **A7.** The best tree obtained with Maximum Likelihood and 1000 bootstrap iterations with data of *rpl*32*- trn*Lintergenic region and 18 taxa of Physalidinae. |
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| **FIGURE** **A8.** The best tree obtained with Maximum Likelihood and 1000 bootstrap iterations with data of *trnl*F region and 16 taxa of Physalidinae. |
| Diagrama  Descripción generada automáticamente |
| **FIGURE** **A9.** The best tree obtained with Maximum Likelihood and 1000 bootstrap iterations with data of *ycf*1-3 region and 17 taxa of Physalidinae. | |
| Interfaz de usuario gráfica, Texto, Aplicación  Descripción generada automáticamente con confianza media | |

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| **FIGURE** **A10.** Phylogenetic relationships of Physalidinae based on Bayesian 50% majority consensus tree and Maximum Likelihood with data of six cpDNA and three nDNA regions. The colored boxes indicate the subgeneric classification of *Physalis* proposed by Martinez (1998) and the phylogenetic position of *Cataracta gen. nov*. Numbers in the nodes are posterior probabilities and bootstrap values. |
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