

LIST OF PUBLICATIONS

Peer-reviewed / In Press

The Germline Mutational Process in Rhesus Macaque and Its Implications for Phylogenetic Dating Bergeron L., Besenbacher S., Bakker J., Zheng J., Li P., **Pacheco G.**, Sinding M. S., Gilbert M. T. P., Schierup M. H. & Zhang G. *GigaScience* / Vol. 10, pp. 1–14 • 2021

ROLE: I performed crucial lab work for this project, mainly working as the tutor of the leading author of this project ([Dr. Lucie Bergeron](#)) in our labs in Copenhagen, whom I introduced to some of the modern techniques that were used in this study. I also revised and approved the final version of this drafted article.

Why TRPV6 Currents Are Not Detectable in Native Cells – What Can We Learn from Bats? Wolske K, Fecher-Trost C., Wesely C., Löhr H., Philipp S., Flockerzi V., **Pacheco G.** & Wissenbach U. *Cell Calcium* / Vol. 92, Article Nr. 102302 • 2020

ROLE: I conducted some lab work for this project. I also revised and approved the final version of the drafted article.

Dense Sampling of Bird Diversity Increases Power of Comparative Genomics Feng S., Stiller J., Deng Y., Armstrong J., Fang Q., Reeve A. H., Xie D., Chen G., Guo C., Faircloth B. C., Petersen B., Wang Z., Zhou Q., Diekhans M., Chen W., Andreu-Sánchez S., Margaryan A., Howard J. T., **Pacheco G.**, Sinding M. S., Puetz L., Cavill E., Ribeiro Â. M., Fjeldså J., Hosner P. A., Brumfield R. T., Christidis L., Bertelsen M. F., Tietze D. T., Robertson B. C., Song G., Borgia G., Claramunt S., Lovette I. J., Cowen S. J., Njoroge P., Dumbacher J. P., Ryder O. A., Fuchs J., Bunce M., Burt D. W., Cracraft J., Meng G., Hackett S. J., Ryan P. G., Jønsson K. A., Jamieson I. G., da Fonseca R. R., Braun E. L., Houde P., Mirarab S., Suh A., Stervander M., Hansson B., Sigeman H., Ponnikas S., Frandsen P. B., Van der Zwan H., Balakrishnan C. N., Clark A. G., Fitzpatrick J. W., Bowman R., Chen N., Cloutier A., Sackton T. B., Foote D. J., Shakya S. B., Sheldon F. H., Vignal A., Soares A. E. R., Shapiro B., González-Solís J., Ferrer-Obiol J., Rozas J., Riutort M., Tigano A., Friesen V., Dalén L., Urrutia A. O., Székely T., Liu Y., Campana M. G., Corvelob A., Fleischer R. C., Rutherford K. M., Gemmell N. J., Dussex N., Mouritsen H., Thiele N., Delmore K., Liedvogel M., Franke A., Hoepfner M. P., Krone O., Fudickar A. M., Milá B., Ketterson E. D., Fidler A. E., Friis G., Parody-Merino Á. M., Battley P. F., Cox M. P., Lima N. C. B., Prosdociami F., Parchman T. L., Schlinger B. A., Loiselle B. A., Blake J. G., Lim H. C., Day L. B., Fuxjager M. J., Baldwin M. W., Braun M. J., Wirthlin M., Dikow R. B., Ryder T. B., Camenisch G., Keller L. F., DaCosta J. M., Hauber M. E., Louder M. I. M., Witt C. C., McGuire J. A., Mudge J., Megna L. C., Carling M. D., Wang B., Taylor S. A., Del-Rio G., Aleixo A., Vasconcelos A. T. R., Mello C. V., Weir J. T., Haussler D., Li Q., Yang H., Wang J., Lei F., Rahbek C., Gilbert M. T. P., Gary R. Graves, Jarvis E. D., Paten B. & Zhang G. *Nature* / Vol. 587, pp. 252–257 • 2020

ROLE: Acting as the main responsible person for this large-scale genomic project in Copenhagen, I performed a massive amount of lab work for this study. Moreover, I also contributed to the drafting of this article and approved its final version.

Phylogeny of Neotropical Seirinae (Collembola, Entomobryidae) Based on Mitochondrial Genomes Nerivania G., **Pacheco G.**, Shanlin L., Cipola N., Berbel-Filho W., Feng Z., Gilbert M. T. P. & Bellini B. *Zoologica Scripta* Issue / 0, pp. 1–11 • 2020

ROLE: I was involved in this project since its conception, namely in securing a visiting PhD scholarship to the first author of this study ([Dr. Nerivania Godeiro](#)), who I helped to train in molecular techniques at our labs in Copenhagen. Then, I generated together with Neri part of the data that was used in this project. I also contributed to the article writing process and approved its final version.

Darwin's Fancy Revised: An Updated Understanding of the Genomic Constitution of Pigeon Breeds **Pacheco G.**, van Grouw H., Shapiro M. D., Gilbert M. T. P. & Vieira F. G. *Genome Biology and Evolution* / Vol. 12, Issue 3, pp. 136–150 • 2020

ROLE: This was one of the main articles that composed my PhD thesis, thus I acted as the leader author of this study from its commencement until its end.

Evolutionary History, Genomic Adaptation to Toxic Diet and Extinction of the Carolina Parakeet Gelabert P., Sandoval-Velasco M., Serres A., Renom P., Margaryan A., de-Dios T., Fang Q., Feng S., Mañosa S., **Pacheco G.**, Ferrando-Bernal M., Shi G., Hao F., Chen X., Stiller J., Petersen B., Navarro A., Marquès-Bonet T., Deng Y., Dalén L., Zhang G., Antunes A., Gilbert M. T. P. & Lalueza-Fox C. *Current Biology* / Vol. 30, pp. 1–7 • 2019

ROLE: I performed crucial lab work for this project, such as DNA extractions and molecular quality checks. Naturally, I also contributed to the article writing process and approved its final version together with all other authors.

The Discovery of *Lepidosira* Schött 1925 (Collembola, Entomobryidae) in Neotropical Region and Its Systematic Position Among the Entomobryinae Nunes R. C., Godeiro, N. N., **Pacheco G.**, Liu S., Gilbert M. T. P., Alvarez-Valin F., Zhang F. & Bellini B. C. *Zoologica Scripta* / Vol. 48, Issue 6, pp. 783-800 • 2019

ROLE: This was a side project that resulted from Neri's visit to Copenhagen (see article 2), thus my role was the same here.

High-coverage Genomes to Elucidate the Evolution of Penguins Pan H., Cole T. L., Bi X., Fang M., Zhou C., Yang Z., Hart T., Bouzat J. L., Argilla L. S., Bertelsen M. F., Boersma P. D., Bost C., Cherel Y., Dann P., Fiddaman S. R., Howard P., Labuschagne K., Mattern T., Miller G., Parker P., Phillips R. A., Quillfeldt P., Ryan P. G., Taylor H., Thompson D. R., Young M. J., Ellegaard M. R., Gilbert M. T. P., Sinding M. S., **Pacheco G.**, Shepherd L. D., Tennyson A. J. D., Grosser S., Kay E., Nupen L. J., Ellenberg U., Houston D. M., Reeve A. H., Johnson K., Masello J. F., Stracke T., McKinlay B., Zhang D. X. & Zhang G. *GigaScience* Vol. 8, Issue 9, pp. 1-17 • 2019

ROLE: I performed crucial lab work for this project, such as sample acquisition, DNA extractions and molecular quality checks. I also contributed to the article writing process and approved its final version together with all other authors.

Killer Whale Genomes Reveal a Complex History of Recurrent Admixture and Vicariance Foote A. D., Morin P. A., Martin M. D., Gopalakrishnan S., Louis M., **Pacheco G.**, Robertson K. M., Sinding M. H. S., Sousa C. S., Amaral A. R., Baird R. W., Baker C. S., Balance L., Barlow J., Brownlow A., Collins T., Constantine R., Dabin W., Rosa L. D., Davison N. J., Durban J. W., Esteban R., Ferguson S. H., Forney K. A., Gerrodette T., Guinet C., Hanson M. B., Hoggard W., Kaschner K., Matthews C. J. D., Pitman R. L., Samarra F. I. P., de Stephanis R., Tavares S., Tixier P., Totterdell J. A., Wade P., M. Gilbert M. T. P., Wolf J. B. W. & Excoffier L. *Molecular Ecology* / Vol. 28, Issue 14, pp. 3427-3444 • 2019

ROLE: I performed crucial lab work for this project, such as sample acquisition, DNA extractions and molecular quality checks. I also received the leading author of this project (**Dr. Andrew Foote**) at our labs in Copenhagen and introduced him to some of the modern techniques that were used in this study. I also contributed to the article writing process and approved its final version together with all other authors.

Hologenomic Adaptations Underlying the Evolution of Sanguivory in the Common Vampire Bat Mendoza M. L. Z., Xiong Z., Escalera-Zamudio M., Runge A. K., Thézé J., Streicker D., Frank H. K., Loza-Rubio E., Liu S., Ryder O. A., Castruita J. A. S., Katzourakis A., **Pacheco G.**, Taboada B., Löber U., Pybus O. G., Li Y., Rojas-Anaya E., Bohmann K., Baez A. C., Arias C. F., Liu S., Greenwood A. D., Bertelsen M. F., White N. E., Bunce M., Zhang G., Sicheritz-Pontén T. & Gilbert, M. T. *Nature Ecology & Evolution* / Vol. 2, pp. 659-668 • 2018

ROLE: I performed crucial lab work for this project, such as DNA extractions, molecular quality checks and PCR experiments. I also contributed to the article writing process and helped its main author to finish up its final draft version based on inputs from all other collaborators.

Genomic Population Structure of Freshwater-resident and Anadromous Ide (*Leuciscus idus*) in North-western Europe Skovrind M., Olsen M. T., Vieira F. G., **Pacheco G.**, Carl H., Gilbert M. T. & Møller P. R. *Ecology and Evolution* Vol. 6, Issue 4, pp. 1064-1074 • 2016

ROLE: I performed crucial lab work for this project, such as DNA extractions and molecular quality checks. But most importantly, I introduced the main author of this study (**Dr. Mikkel Skovrind**) to the modern sequencing method that was used in this project. I also contributed to the article writing process and approved its final version.

Padrões Citogenéticos de Duas Espécies de Ciclídeos de Bacias do Semi-árido do Brasil: *Crenicichla menezesi* e *Cichlasoma orientale* Molina, W. F., **Pacheco, G. A.** & Berbel Filho, W. M. *Biota Amazônia* • 2014

ROLE: I conducted many of the experiments for this project and also wrote an initial drafted article version.

Submitted / Under Review

Additive and Non-additive Epigenetic Signatures of Hybridisation Between Fish Species with Different Mating Systems

Berbel-Filho W. M., Tatarenkov A., **Pacheco G.**, Espirito-Santo H. M. V., Lira M. G., de Leaniz C. G., Avise J. C., Lima S. M. Q., Rodríguez-López C. M. & Consuegra S. / Under revision in *Evolution* (**First Round of Revision**).

ROLE: I conducted several bioinformatic analyses for this project and also contributed to the discussion of the results and the writing of the drafted article.

Conservation Genomics of the Endangered Seychelles Magpie Robin (*Copsychus sechellarum*): A Unique Insight into the History of a Precious Endemic Bird

Cavill E., Gopalakrishnan S., Puetz L., Ribeiro Â., Mak S., da Fonseca R., **Pacheco G.**, Dunlop B., Accouche W., Shah N., Zora A., Calabrese L., Genner M., Jones G., Guo C., Zhang G. & Gilbert, M. T. P. / Under revision in *IBIS* (**Second Round of Revision**).

ROLE: I performed crucial lab work for this project, such as DNA extractions, molecular quality checks and PCR experiments. I also contributed to the article writing process and helped its main author to finish up its final draft version based on inputs from all other collaborators.

In Preparation

Genomic Insights into the Ubiquitous Feral Pigeon's Formation **Pacheco G.**, Vieira F. G., Martin M. D., Olsen M. T., Hulva P., Raso

T. deF., Njoroge P., Salaberria C., López-Rull I., Lalueza-Fox C., Ramírez O., Ávila-Arcos M. C., Escobar P. R., Faria R., Carneiro M., Sotelo G., Danielsen J., Haddad N., Khoury F., Dor R., Halajian A., Arias M. B., Krone O., Auls S., Seneviratne S. S., Mathiaparanam K., Bunce M., Coghlan M. L., Fjeldså J. & Gilbert M. T. P.

ROLE: This was one of the main articles that composed my PhD thesis, thus I acted as the leader author of this study from its commencement until now that we are close to submitting it to publication.

Genomic Variation Among European Perch *Perca fluviatilis* Driven by Differentiated Habitat and Selection Skovrind M.,

Pacheco G., Olsen M. T., Fietz K., Christensen E. F. A., Kragh M. A., Vieira F. G., Carl H., Gilbert M. T. P. & Møller P. R.

ROLE: I conducted several bioinformatic analyses for this project and also contributed to the discussion of the results as well as to the writing of the article.

Evolutionary Genomics of the Rarest Mammal in the World, the Microendemic *Cavia intermedia* (Caviidae, Mammalia)

Escalona M. A. R., de Manuel M., Gopalakrishnan S., **Pacheco G.**, Barreiro F. S., Ciucani M. M., Sinding M.-H. S., Margaryan A., Petersen B., Furnari N., Gava A., Cherem J., Salvador C. H., Dalén L., Gilbert M. T. P. & Bonatto S. L.

ROLE: During his visit at our labs in Copenhagen, was responsible to introduce the main author of this study (Dr. Manuel Escalona) to the sequencing techniques used in this project. Thus, together with Manuel, I carried out wet lab work for this project as well as contributed to some of the analyses and rationale applied to this project.

I am also involved in several other genomic projects – from birds to snakes, which will certainly be published in due time.