

Curriculum Vitae

Name, first name and title Dr Damien D. Hinsinger

Place and date of birth Wissembourg (France), 23/07/1983

Nationality French

E-mail damien.hinsinger@yahoo.com

Personal webpage <http://www.asianfagaceae.com/actg/damien/>

Research activity, education and formation

- 01/12/2019 - Post-doc; Genoscope, Evry, France: Genomics of planktonic Eukaryotes.
- 01/02/2015 - Post-doc; Guangxi University, Nanning, China: Phylogenomics of tropical trees, with a focus on *Castanopsis* (Fagaceae).
31/07/2019
- 14/07/2014 - Training in Genomic analyses, Queen Mary University, London. (FRAXBACK
19/07/2014 European COST funding).
- 06/01/2014 - Workshop; MPS with NGS for phylogeography and phylogenetics, Yale University,
10/01/2014 New Haven, USA.
- 01/09/2013 - Post-doc; CNRS: The genomic diversity of Mediterranean ashes.
31/08/2014
- 04/07/2013 Workshop: BEAST 2 software package, Muséum National d'Histoire Naturelle, Paris.
- 01/09/2010 - Teaching and Research Assistant; Université de Versailles Saint-Quentin en
31/08/2011 Yvelines: The genetic diversity in *Ramonda*, an endemic species in the Balkans.
- 01/11/2006 - Ph.D in Forestry Sciences: Diversity and Evolution of the genus *Fraxinus*, Ecole
29/06/2010 Nationale du Génie Rural (ENGREF), Paris, and Université Laval, Québec (joint thesis supervision).
- 01/09/2009 - Teaching and Research Assistant; Université Paris-Sud: Bioinformatics in biology
31/08/2010
- 04/09/2006 - "Santo 2006 Biodiversity Survey": Main marine fishes and parasites.
27/10/2006
- 01/09/2004 - Master in Life and Health Sciences, speciality "Interactions and Adaptations
31/08/2006 Biology", Université de Nice-Sophia-Antipolis, Nice, France.
- 02/01/2006 - Internship; Molecular phylogeny of serranids, Muséum National d'Histoire
13/07/2006 Naturelle, Paris.
- 03/01/2005 - Internship; Systematic parasitology of Epinephelinae, IRD centre Noumea, New-
24/06/2005 Calédonia.
- 05/07/2004 - Internship; Molecular techniques, UNSA, Nice.
27/08/2004
- 01/09/2003 - Licence in Organisms Biology, Université de Nice-Sophia-Antipolis, Nice, France.
31/08/2004
- 01/11/2003 - Internship; Biometry of algae, UNSA, Nice.
25/06/2004

Research skills

- Taxonomy :** Phylogeny and taxonomy of Fagaceae and Oleaceae, taxonomy and systematics, phylogeny of Serranids and Antarctic fishes, species description, DNA barcoding.
- Experiment:** DNA extraction, PCR, AFLP, genotyping, sequencing and other common methods of laboratory, development of new markers and primers, NGS libraries construction

(Illumina, Nanopore, MIGseq).

Data analysis: Plastomes reconstruction, repeats and SSRs analyses, MIGseq experiments, phylogenetic reconstruction and dating, barcoding and species delimitation, population genetics, phylogeographical reconstruction, character evolution, morphometry, SNP detection, comparative genomic analyses.

Informatics: Mac, windows and UNIX Operating System, phylogenetic and dating analyses (PAUP, MrBayes, BEAST and *BEAST, PHYML, PAML, MEGA, Bioedit, Mesquite, SplitsTree, R, Structure a.o.), comparative analyses (BISSE, MultiMedusa, BATS a.o.), programming language (bash, R, python and algorithmic), GIS software (for plotting diversity data).

Complementary skills

Language Langage: French (mothertong), english (fluent)
Cultural aspects knowledge and understanding of Asian cultures (4 years of Postdoc, with sampling and collaborations in Asia – PR China)
Others Grant writing, mentoring of PhD and Master students, sequencing projects planning and management

Grants & Scholarships

2019 Systematics Research Fund, Linnean Society of London and the Systematics Association (1,000 €)
2018 International Oaks Society (IOS) 9th conference (UC Davis, California, USA) travel grant (450 €)
2016-2018 Guangxi Province PostDoctoral Grant (6,600 €)
2016-2018 Chinese National Postdoctoral Foundation, Special Grant (20,000 €)
2015-2017 Chinese National Postdoctoral Foundation, Second Level Grant (7,000 €)
2015-2017 Guangxi Province PostDoctoral Fellowship Starting Grant (4,000 €)
July 2014 FRAXBACK European COST STSM (Short Term Scientific Mission) – Training in Genomic analyses.
2008 LAVOISIER scholarship ; Ministère des Affaires Etrangères et Européennes – 1 year
2006-2009 Scholarship; Ministère de l'enseignement, de la recherche et des technologies – 3 years
2005-2006 Master 2 Merit scholarship – 1 year

Teaching

2016 & 2017: Introductory course: Evolution, Phylogenetics and Genomics; Guangxi University, Nanning
2016: Phylogenetic reconstruction and evolution of traits, Guangxi University, Nanning
2014: Genomic (experimental design); U.P.M.C., Paris
2011: Ecology; Université de Versailles-Saint-Quentin-en-Yvelines
2011: Biodiversity and Phylogeny; Université de Versailles-Saint-Quentin-en-Yvelines
2011: Botany ; Université de Versailles-Saint-Quentin-en-Yvelines
2010: General Biology; Université de Versailles-Saint-Quentin-en-Yvelines
2010: Computing for Biology; Université Paris-Sud
2009: Genomic Sequence Analysis; Université Paris-Sud

Mentoring

- 2017-2020: Angelo Carrion: Development of bioinformatic tools for phylogenomics of tropical trees.
- 2016-2020: Tijana Cvetkovic: Genomic diversity and evolution of the major timber tree family Dipterocarpaceae.
- 2016-2019: XiJian Liang: Genomic diversity of chinese Neolitsea (Lauraceae).
2017: Laura Muller: Analyses of genomic data and plastome assemblies.
- 2007: Mariangela Arca: Evaluation of a newly proposed DNA barcode in *F. angustifolia* / *F. excelsior* species complex, and in the entire genus *Fraxinus*.

Publications

Peer-reviewed

- Strijk JS, Thi Bin H, Van Ngoc N, Pereira, J. T., Slik JWF, Sukri RS, Suyama Y, Tagane S, Wieringa JJ, Yahara T, **Hinsinger DD**. Museomics of a historical floristic exchange: Divergence of Stone Oaks across Wallacea. *PLOS ONE*, accepted pending revision.
- Carrion AD, **Hinsinger DD***, Strijk JS*. (2020) ECuADOR - Easy Curation of Angiosperm Duplicated Organellar Regions, a software tool for cleaning and curating plastomes obtained from next generation sequencing pipelines. *PeerJ*, 8: e8699.
- Carrion AD, **Hinsinger DD**, Strijk JS (2020). Genomics of the critically endangered monotypic genus *Sinopora*: the plastome of *S. hongkongensis* (Lauraceae). *Mitochondrial DNA part B*, 5(1): 379-381.
- Strijk JS*, **Hinsinger DD***, Zhang FP, Cao K. (2019) *Trochodendron aralioides*, the first chromosome-level draft genome in Trochodendrales and a valuable resource for basal eudicot research. *GigaScience*, 8:1-9.
- Hinsinger DD**, Strijk JS (2019). Plastome of *Quercus xanthoclada* and comparison of genomic diversity among selected *Quercus* species using genome skimming. *PhytoKeys*, 132: 75-89
- Cvetkovic T*, **Hinsinger DD***, Strijk JS* (2019). Exploring evolution and diversity of Chinese Dipterocarpaceae using next-generation sequencing. *Scientific Reports* 9: 11639.
- Liang XJ, **Hinsinger DD**, Elias, RB, Strijk JS (2019) The plastome sequence of *Laurus azorica* (Seub.) Franco, an endemic tree species of the Azores islands. *Mitochondrial DNA part B*, 4(1), 363-365.
- Xu LM, **Hinsinger DD** and Jiang GF (2018) The complete mitochondrial genome of the Basidiomycete fungus *Pleurotus cornucopiae* (Paulet) Rolland. *Mitochondrial DNA: part B*, 3(1), 73-75.
- Yu TH, **Hinsinger DD**, Strijk JS and Kim Shan Wee A (2018) The first complete chloroplast genome of a major mangrove species *Sonneratia alba* Sm and its implications on conservation efforts. *Mitochondrial DNA: part B*, 3(2), 500-502.
- Lei JY, **Hinsinger DD**, Jiang GF (2018) Characterization of the complete chloroplast genome of endangered Cycads *Zamia fischeri* Miq. *Mitochondrial DNA: part B*, 3(2): 1059-1061.
- Cvetkovic T, **Hinsinger DD**, Strijk JS (2017) The first complete chloroplast sequence of a major tropical timber tree in the Meranti family: *Vatica odorata* (Dipterocarpaceae). *Mitochondrial DNA: part B*, 2(1): 52-53.
- Hinsinger DD**, Strijk JS (2017) The chloroplast genome sequence of *Michelia alba* (Magnoliaceae), an ornamental tropical tree species. *Mitochondrial DNA: part B*, 2(1): 9-10.
- Xu LM, **Hinsinger DD** and Jiang GF (2017) The complete mitochondrial genome of the *Agrocybe aegerita*, an edible mushroom. *Mitochondrial DNA: part B*, 2(2), 791-792.
- Hinsinger DD**, Strijk JS (2016) Toward phylogenomics of Lauraceae: The complete chloroplast genome sequence of *Litsea glutinosa* (Lauraceae), an invasive tree species on Indian and Pacific Ocean islands. *Plant Gene*, 9: 71-79.
- Jiang GF*, **Hinsinger DD***, Strijk JS (2016) Comparison of intraspecific, interspecific and intergeneric chloroplast diversity in Cycads. *Scientific reports*, 6, 31473.

- Hinsinger DD**, Debruyne R, Denys G, Menneson M, Utge J, Thomas M, Dettai A (2015) Fishing for barcodes in the Torrent: from COI to complete mitogenomes on NGS platforms. *DNA barcodes*, 3(1), 170-186.
- Hinsinger DD**, Strijk JS (2015) Complete chloroplast genome sequence of *Castanopsis concinna* (Fagaceae), a threatened species from Hong-Kong and southern China. *Mitochondrial DNA part A*, 28(1), 65-66.
- Hinsinger DD**, Gaudeul M, Couloux A, Bousquet J, Frascaria-Lacoste N (2014) The phylogeography of Eurasian *Fraxinus* species reveals ancient transcontinental reticulation. *Molecular Phylogenetics and Evolution* 77: 223-237.
- Schoelincq C, **Hinsinger DD**, Dettai A, Couloux A, Justine JL (2014). A phylogenetic re-analysis of groupers with applications for Ciguatera fish poisoning. *PLoS one* 9(8): e98198.
- Hinsinger DD**, Basak J, Gaudeul M, Cruaud C, Bertolino P, Frascaria-Lacoste N, Bousquet J (2013) The phylogeny and biogeographic history of ashes (*Fraxinus*, Oleaceae) highlight the roles of migration and vicariance in the diversification of temperate trees. *PLoS one* 8(11): e80431.
- Arca M*, **Hinsinger DD***, Tillier A, Couloux A, Frascaria-Lacoste N (2012) Deciduous trees and the application of universal DNA barcodes: a case study on the circumpolar *Fraxinus*, *PLoS one* 7(3): e34089. doi:10.1371/journal.pone.0034089.
- Lautrédou AC, **Hinsinger DD**, Gallut C, Cheng C, Cruaud C, Lecointre G, Dettai A (2012). Phylogenetics footprints for Antarctic radiations: the example of Trematominae (Notothenioidei, Teleostei), *Molecular Phylogenetics & Evolution* 65(1): 87-101.
- Hinsinger DD** & Justine JL (2006) *Pseudorhabdosynochus venus* n. sp. (Monogenea, Diplectanidae) from *Epinephelus howlandi* (Perciformes: Serranidae) off New Caledonia, *Systematic Parasitology*, 63 (2) : 153-158.
- Hinsinger DD** & Justine JL (2006) The “*Pseudorhabdosynochus cupatus* group” (Monogenea, Diplectanidae) in *Epinephelus fasciatus*, *E. howlandi*, *E. rivulatus* and *E. merra* (Perciformes: Serranidae) off New Caledonia, with descriptions of *Pseudorhabdosynochus cyathus* n. sp. and *P. calathus* n. sp., *Systematic Parasitology*, 64 (2): 69-90.

Submitted and in review

- Colin O, **Hinsinger DD**, Strijk JS. *Mahonia lancasteri* O. Colin (Berberidaceae), a new species from Sichuan, China. *Phytotaxa*, in review.
- Areces-Berazain F, Wang Y, **Hinsinger DD**, Strijk JS. Comparative analysis of genomic diversity in maples (*Acer*, Sapindaceae). *Scientific Reports*, in review.

Other publications

- Hinsinger DD** & Strijk JS (2019) Combining molecular data to reconstruct the evolution of oaks, Proceedings of the 9th conference of the International Oaks Society.
- Strijk JS & **Hinsinger DD** (2019) Oaks of Vietnam : Genomic diversity and evolution, Proceedings of the 9th conference of the International Oaks Society.
- Hinsinger DD** (2019) *Trigonobalanus doichangensis*. The IUCN Red List of Threatened Species 2019: e.T31984A2808014. <http://dx.doi.org/10.2305/IUCN.UK.2019-2.RLTS.T31984A2808014.en>.
- Hinsinger DD** & Nguyen MC (2019) *Trigonobalanus verticillata*. The IUCN Red List of Threatened Species 2019: e.T191470A1984594. <https://dx.doi.org/10.2305/IUCN.UK.2019-3.RLTS.T191470A1984594.en>.

Selected oral communications

- Hinsinger DD**, Strijk JS. Combining molecular data to reconstruct the evolution of oaks, 9th International Oaks Society (IOS) conference, Davis, USA , October 22 - 24, 2018.
- Hinsinger DD**, Strijk JS. What shapes tropic al trees diversity? Specific and common factors driving diversity gradient in oaks, Southeast Asian Gateway Evolution (SAGE 2017), Bogor, Indonesia , August 28 - September 1, 2017.

Hinsinger DD, Strijk JS. Phylogenomics in tropical Fagaceae: an example from *Castanopsis* (D. Don) Spach, Genomics and Forest Tree Genetics IUFRO meeting, Arcachon, France, May 30 - June 5, 2016.

Hinsinger DD, Frascaria-Lacoste N, Fernandez-Manjarres J. Next-Generation sequencing identified thousands of SNPs for assessing hybridization between common and narrow-leaved ash, FRAXBACK COST meeting, Palanga, Lithuania, September 15-18, 2014.

Hinsinger DD. Une phylogénie des Epinephelinae de l'Indo-Pacifique. The Second International Symposium on Groupers of the Mediterranean Sea, Nice, France, May 10-13, 2007.

I have contributed to **17 posters** at **14 international conferences**.

Major research projects

- Metagenomics and Evolution of planktonic Eukaryotes

This project is based on the extensive sampling and sequencing data from the TARA campaigns, and will use metagenomic approaches to infer ecological and evolutionary processes occurring in oceanic plankton. Using recently assembled SAG (Single cell Assembled Genome) and MAG (Metagenomic Assembled Genome) sequences from plankton, I will build evolutionary hypotheses (i.e. phylogenies) used to explore the genome architecture, as well as evolution of gene functions in a highly connected environment.

- Genomic diversity, evolution and diversification in tropical trees

This project focused on the comparison of diversification and biogeography of speciose tropical families (e.g. Fagaceae, cycads, maples – *Acer* - and Dipterocarpaceae), based on genomic analyses. After assembling plastomes and/or MIGseq datasets, as well as phylogenetic reconstruction and evolutionary inference, I found that Cenozoic climate changes had major impact on the diversification of these families, and that they drove their biogeographic spread. These results were published in *Scientific Reports* and *PhytoKeys* and are submitted to *Journal of Biogeography*, *PloS one* and *Scientific Reports*.

- Resolving basal lineages evolution by phylogenomics

In this project, I focused on two difficult nodes of angiosperms evolution, namely the relationships among the main angiosperms lineages, and the position of Trochodendrales in basal eudicots. Using complete nuclear genome data I generated coupled with comparative genomics analyses, I found that the lack of support found in topologies are due to old incomplete lineage sorting, with conflicting phylogenetic signals in genes clustered along the chromosomes/scaffolds. These results are *in press* and accepted in *Gigascience*.

Major collaborations

- Whittemore A. (National Arboretum, USA), Hardy S. (New York Bot. Garden, USA) and others, population genomics of american ash trees.
- Strijk, J.S., Jiang, G.F., Areces-Berazain, F. and others (Guangxi University, PR China), tropical tree genomics.
- Robert, T., Nadot S and others (Université Paris-Saclay, France), Genome evolution in endemics species from the Kerguelen islands (Southern Ocean).

Other merits

In the last 10 years the I have presented my research results by participating in 16 conferences in Austria, France, Canada, China, Spain, United Kingdom, PR Lao, Indonesia and USA. In the last 10

years I have participated in 13 research projects, 6 French funded, 1 EU funded and 6 PR China funded.

- Organization of scientific events:

- Conservation of Fagaceae in Indochina Workshop, PTK Bot. Garden (Luang Prabang, PR Laos), September 2018. Trainer for the Evolution and Biogeography of Fagaceae.
- European Conference of Tropical Ecology (Paris): the symposium “Tropical trees ecology & evolution”, March 2018. Co-organizer.
- “Chlorothon 2 – intensive workshop on chloroplast genome assembly” (GXU, Nanning, PR China), January 2018. Co-organizer.
- “Chlorothon – intensive workshop on chloroplast genome assembly” (GXU, Nanning, PR China), March 2017. Co-organizer.
- « Le Petit Pois Dérivé », 36ème Réunion du Groupe de Biologie et de Génétique des Populations, Orsay, France, August 25-28, 2014. Member of the scientific organization committee.

- Academic referee for scientific journals: *Journal of Systematics and Evolution*, *International Journal of Plants Sciences*, *Botany Letters*, *Genome*, *Biomedical and Environmental Sciences*, *Turkish Journal of Botany*, *Journal of Agricultural Science and Technology*, *Conservation Genetics*, *Plant Systematics and Evolution*, *PLoS one*, *Molecular Ecology Resources*, *PhytoKeys* and *BMC Evolutionary Biology*.

- Member of the European Society for Evolutionary Biology (ESEB), member of the International Oaks Society (IOS), member of The Maple Society (TMS), member of The Systematics Association, member of the ATBC (Association for Tropical Biology and Conservation).

- Qualified for a lecturer position in ‘Population Biology and Ecology’ and ‘Organisms Biology’ at French Universities and at National Museum of Natural History.

- Vulgarization of Science:

- “Life in water” Scientific tutoring, Muséum National d’Histoire Naturelle, Paris. Definition and setting-up of a scientific project with a schoolteacher, Feb-May 2007.
- “Ethical concerns about complete genome sequence” conference and debate in Lycée Saint-Exupéry, Montigny le Bretonneux, 11th and 12th grades, 2009, March.
- “Discovering the lab”, visit to the laboratory Ecologie, Systématique et Evolution, 12th grade from the Lycée Saint-Exupéry, Montigny le Bretonneux, 2010, April.
- Scientific contribution to the exhibition « Arbre, regards croisés », September, 8-27, 2010, Senate orangery, Paris. Popularization poster: the evolution of the genus *Fraxinus*.