

## - Curriculum Vitae -

**Raphaël Leblois**

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### **PRESENT POSITION**

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Sept 2010 – Today **Researcher (CR1)** at the Center for Biology and Management of Populations, National Institute for Agronomical Research (CBGP - INRA), Montpellier, France

### **EDUCATION & RESEARCH TRAININGS**

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2006-2010

**Assistant Professor (« Maitre de conférence »)** at the National Museum of Natural History of Paris (MNHN).

2005-2006

**PostDoc (6 months):** « *Multilocus genetic analyses and demographic inferences with applications to human populations from Central Asia* » with Pr. Evelyne Heyer et Dr. Renaud Vitalis, Musée de l'Homme - MNHN, Paris, France.

2004-2005

**PostDoc, Lavoisier grant (1 year):** « *Bottleneck detection and inference of the number of founding individuals from SNPs markers* », with Pr. Montgomery Slatkin, University of California, Berkeley, United-States.

2000-2004

**PhD in Integrative Biology (3 ½ years):** « *Inference of dispersal parameters from genetic data in subdivided populations* » under the supervision of Dr. François Rousset and Dr. Arnaud Estoup. Montpellier Supagro – University of Montpellier II, France.

1999-2000

**MSc in Evolutionary Biology and Ecology, 6 months project:** « *Simulation study of the influence of mutational and demographic factors on the inference of demographic parameters from individual microsatellite genotypes* » under the supervision of Dr. François Rousset et Dr. Arnaud Estoup. Montpellier Supagro – University of Montpellier II.

### **LANGUAGES**

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FRENCH: MOTHER LANGUAGE

English: Read, written and spoken.

### **TECHNICAL AND PRACTICAL SKILLS**

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**Statistical and computing tools:** population genetic data analyse, advanced programming in C, C++, R and Mathematica (Windows, Linux, Mac).

**Molecular techniques:** DNA extractions, PCR, microsatellites development and genotyping.

**Fieldwork:** amphibians/reptiles/insects/trees sampling.

## EDITORIAL ACTIVITIES AND SCIENTIFIC EXPERTISE

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Referee for *Cladistic*, *Conservation Biology*, *Ecography*, *Ecology Letters*, *Evolutionary Applications*, *Evolutionary Ecology Research*, *Forest Ecology and Management*, *Genetics*, *Human Biology*, *Mitochondrial DNA*, *Molecular Ecology*, and *Molecular Ecology Resources*.

Expertise in theoretical and applied population genetics, conservation genetics, inference of dispersal, modelling in population genetics, coalescent theory.

## FUNDING

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- 2010-2014: **ANR (french national agency for research funding)**, with S. Planes et al., “**IM-MODEL@CORALFISH**: *An isolation-migration model of the history of coral reef fish communities: theory and data*”. 500 k€
- 2010-2014: **ANR**, with C. Denys et al., “**MOHMIE: Modern Human installation in Morocco** *Influence on the small terrestrial vertebrate biodiversity and its Evolution*”. 809 k€
- 2009-2013: **ANR**, with J. -M. Cornuet et al., “**EMILE: Inference methods and software’s for Evolution**”. 372 k€
- 2008-2011: **CNRS Amazonia**, with H. Fréville and C. Scotti-Saintagne, “**CLIPS: Past climate change and ecological specialization in tropical species: input from population genetic approaches**”. 100 k€
- 2008-2010: **ANR Biodiversity**, with P. Grandcolas et al., “**BioNeoCal: Endemism in New Caledonia: phylogenetic and population study of its emergence**”. 940 k€

## MAIN CURRENT RESEARCH PROJECTS

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Inference of demographic parameters using importance-sampling algorithms under various demographic models: Isolation by distance, Isolation with migration, Single population with variable size: collaboration with F. Rousset (ISEM, Montpellier), R. Vitalis (CBGP, Montpellier), M. Gautier (CBGP, Montpellier), M. Navascues (CBGP, Montpellier) and C. Reddy Beeravolu (Post-doc ANR, CBGP - EPHE, Montpellier).

Inference of sex-specific dispersal under isolation by distance models using Approximate Bayesian Computations: collaboration with R. Vitalis (CBGP, Montpellier).

Extending population genetics tools to study recent divergence between closely related species: collaboration with M. Navascues (CBGP, Montpellier), P. Grandcolas and R. Nattier (MNHN, Paris).

DNA barcoding using coalescent based methods: collaboration with O. David, C. Laredo.

## PUBLICATIONS

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- [26] Rousset F., R. Leblois, **2011**. Likelihood-based inferences under a coalescent model of isolation by distance: two-dimensional habitats and confidence intervals. Submitted.
- [25] Lalis A.\*, R. Leblois\*, E. Lecompte, C. Denys, J. Ter Meulen, T. Wirth. **2011**. Guns, germs and rats: Impact of human conflicts on Lassa virus. Submitted. \* co-first authors.
- [24] David O., C. Laredo, R. Leblois, B. Shaeffer, N. Vergne. **2011**. Coalescent-based DNA barcoding: multilocus analysis and robustness. Submitted. (Author list is alphabetical).
- [23] Deu, M., F. Sagnard, D. Dembélé, R. Leblois, L. Touré, M. Diakitè, C. Calatayud, M. Vaksman, S. Bouchet, Y. Mallé, S. Togola, P. Traoré. **2011**. Genetic diversity, structure, gene flow and

evolutionary relationships within the *Sorghum bicolor* wild-weedy-crop complex in a western African region. *Theoretical Applied Genetics*, DOI 10.1007/s00122-011-1662-0.

- [22] Leblois R\*, K. Kuhls\*, O. Francois, G. Schöniar, T. Wirth. **2011**. Guns, germs and dogs: On the origin of *Leishmania chagasi*. *Infections, Genetics and Evolution* **188**: 165-179. \* co-first authors.
- [21] Girod C., R. Vitalis, R. Leblois, H. Fréville. **2011**. Inferring population decline and expansion from microsatellite data: a simulation-based evaluation of the MSVAR method. *Genetics* **188**: 165-179.
- [20] Morelli G., Y. J. Song, C. J. Mazzoni, M. Eppinger, P. Roumagnac, D. M. Wagner, M. Feldkamp, B. Kusecek, A. J. Vogler, Y. J. Li, Y. J. Cui, N. R. Thomson, T. Jombart, R. Leblois, P. Lichtner, L. Rahalison, J. M. Petersen, F. Balloux, P. Keim, T. Wirth, J. Ravel, R. F. Yang, E. Carniel, M. Achtman. **2010**. *Yersinia pestis* genome sequencing identifies patterns of global phylogenetic diversity. *Nature Genetics* **42**: 1140.
- [19] Verdu P., R. Leblois, A. Froment, S. Thery, S. Bahuchet, F. Rousset, E. Heyer, R. Vitalis. **2010**. Limited dispersal in mobile hunter-gatherer Baka Pygmies. *Biology Letters* **6**: 858-861.
- [18] Nubel U., J. Dordel, K. Kurt, B. Strommenger, H. Westh, S. K. Shukla, H. Zemlickova, R. Leblois, T. Wirth, T. Jombart, F. Balloux, W. Witte. **2010**. A Timescale for Evolution, Population Expansion, and Spatial Spread of an Emerging Clone of Methicillin-Resistant *Staphylococcus aureus*. *Plos Pathogens* **6**: e1000855.
- [17] Alberto F., P. T. Raimondi, D. C. Reed, N. C. Coelho, R. Leblois, A. Whitmer, E. A. Serrão. **2010**. Habitat continuity and geographic distance predict population genetic differentiation in giant kelp. *Ecology* **91**: 49-56.
- [16] Boisselier-Dubayle M. -C., R. Leblois, M. I. Khodabux, S. Samadi, J. Lambourdière, C. Sarthou. **2010**. Genetic structure of a xerophilous bromeliad in a fragmented habitat and the forest refuge hypothesis: *Pitcairnia geyskeysii* on inselbergs in French Guyana. In Press for *Ecography*.
- [15] Guillot G., R. Leblois, A. Coulon, A. C. Frantz. **2009**. Statistical methods in spatial genetics. *Molecular Ecology* **18**: 4734-4756.
- [14] Austerlitz F., O. David, B. Schaeffer, K. Bleakley, M. Olteanu, R. Leblois, M. Veuille, C. Laredo. **2009**. Comparing phylogenetic and statistical classification methods for DNA barcoding. *BMC Bioinformatics* **10**: Suppl. 14: S10.
- [13] Leblois, R., A. Estoup, F. Rousset. **2009**. IBDSim: a computer package for coalescent simulations under isolation by distance with temporal and spatial heterogeneities. *Molecular Ecology Resources* **9**: 107–109.
- [12] Frezal L., R. Leblois. **2008**. 4 years of DNA barcoding: current advances and prospects. *Infection, Genetics & Evolution* **8**: 727–736.
- [11] Rousset, F., R. Leblois. **2007**. Likelihood and approximate likelihood analyses of genetic structure in a linear habitat: performance and robustness to model mis-specification. *Molecular Biology and Evolution*. **24**:2730–2745.
- [10] Leblois, R., M. Slatkin. **2007**. Estimating the number of founder lineages from haplotypes of closely linked SNPs. *Molecular Ecology* **16**, 2237-2245.
- [9] Watts P.C., F. Rousset, I.J. Saccheri, R. Leblois, S.J. Kemp, D.J. Thompson. **2007**. Compatibility of genetic and demographic estimates of ‘neighborhood size’ in insect populations: analysis of *Coenagrion mercuriale* (Odonata: Zygoptera) using an improved estimator of genetic divergence. *Molecular Ecology* **16**, 737–751.
- [8] Leblois, R., Estoup, A., Streiff, R. **2006**. Habitat contraction and reduction in population size: Does isolation by distance matter? *Molecular Ecology* **15**, 3601–3615.

- [7] De Iorio M., Griffiths R., Leblois R., Rousset F. **2005**. Stepwise mutation likelihood computation by sequential importance sampling in subdivided population models. *Theoretical Population Biology* **68**: 41-53. (Author list is alphabetical).
- [6] Leblois R., Rousset F., Estoup A. **2004**. Influence of spatial and temporal heterogeneities on the estimation of demographic parameters in a continuous population from microsatellite data. *Genetics* **166**: 1081-1092
- [5] Brouat C., Sennedot F., Audiot P., Leblois R., Rasplus J. -Y. **2003**. Fine-scale genetic structure of two carabid species with contrasted levels of habitat specialization. *Molecular Ecology* **12**: 1731 - 1745.
- [4] Leblois R., Estoup A. 2003. Invited commentary on the article by Wilson IJ, Weale ME, Balding DJ (2003): Inferences from DNA data: population histories, evolutionary processes, and forensic match probabilities, *Journal of the Royal Statistical Society A* **166**: 1-33.
- [3] Leblois R., Estoup A., Rousset F. 2003. Influence of mutational and sampling factors on the estimation of demographic parameters in a continuous population under isolation by distance. *Molecular Biology and Evolution*. **20**: 491-502
- [2] Tikel D., Peatkau D., Cortinas N., Leblois R., Moritz C., Estoup A. 2000. Microsatellite loci in the invasive toad species *Bufo marinus*. *Molecular Ecology* **9**: 1927-1929.
- [1] Leblois R., Rousset F., Tikel D., Moritz C., Estoup A. 2000. Absence of evidence for isolation by distance in an expanding cane toad (*Bufo marinus*) population: an individual-based analysis of microsatellite genotypes. *Molecular Ecology* **9**: 1905-1909.

#### **PUBLICATIONS IN PREPARATION**

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- Leblois R., F. Bertaux, J. Néron, R. Vitalis, F. Rousset. Importance sampling on populations with varying size : inference of bottlenecks and expansions. In prep.
- Lalis A., R. Leblois, M.-C. Boisselier-Dubayle, C. Denys. Genetic structure and dispersal of *Mastomys* species in Guinea. In prep.
- Leblois R., C. Reddy Beeravolu, R. Vitalis, F. Rousset. Importance sampling on Isolation with Migration models. Work in progress.
- Vitalis R., R. Leblois. IBDSex : a coalescent-based computer program to simulate sex-specific gene genealogies under isolation by distance. Work in progress.

#### **ACADEMIC PUBLICATIONS**

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- Leblois, R. 2004. Estimation de paramètres de dispersion en populations structurées à partir de données génétiques. Thèse de doctorat de l'Agro-M (ENSA-Montpellier), 233 pp.
- Leblois, R. 2000. Etude par simulation de l'influence de facteurs mutationnels et démographiques sur l'estimation de paramètres démographiques à partir de génotypes individuels. Diplôme d'Etudes Approfondies (DEA Biologie de l'Evolution et Ecologie, Agro-M et Université Montpellier II). 30pp.

#### **TEACHING**

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- 2006-Today: 50h per year of population genetic teaching: population genetic data analysis, inference of demographic parameters, coalescent theory and DNA Barcoding (Master and PhD courses at the University of Montpellier II, MNHN, Ecole Normale Supérieure de Paris, Université Paris VII, EPHE and Université Lille I).

2007-Today: co-organisation, with R. Vitalis, of one week course for PhD students: “Data analyses in population genetics” (European Master MEME, University Montpellier II).

2006-2010: co-organisation, with R. Vitalis and E. Heyer, of one week course for Master students (Ecole Doctorale ParisVI-ParisVII-MNHN): “Molecular population genetics and coalescent theory”

#### **COLLECTIVE AND ADMINISTRATIVE ACTIVITIES**

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2008-2010: Internal seminar organisations at the “Origine, Structure and Evolution of biodiversity” lab (OSEB, MNHN, UMR 7205).

2008-2010: Scientific manager of the Museum computer cluster (76 nodes, MNHN, UMS 2700).

2006-2010: participation to the DNA Barcoding initiative to develop DNA barcoding in France.

2006-Today: members of various PhD supervision comities: Anne-Laure Ferchaud (EPHE, Montpellier 2008, 2010), Christophe Girod (MNHN Paris, 2008, 2009), Camille Roux (Université Lille I, 2008), Romain Nattier (MNHN Paris, 2008, 2009), Erhan Yalcindag (Université Montpellier II, 2009), Stéfanie Wagner (INRA Bordeaux – Munich University, 2011).

2006: member of the organizing comity for the international meeting “DNA sampling: Strategy & Design” at the MNHN (March 15th-16th 2007)