

Scientific CV

Name Frederik Van den Broeck
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Research focus

Exploring genomic data to understand the evolution, adaptation and biology of eukaryote parasites, providing insights into disease origin and spread, within the context of biomedical relevance and public health.

Expertise

I have a strong expertise in analysing and biologically interpreting a wide array of genetic data, ranging from microsatellites to whole genome and transcriptome sequencing data that have been generated by Illumina, Nanopore or PacBio sequencing technologies. To this end, I'm used to work and write customized scripts in R, the Unix shell and python to do upstream bio-informatic analyses (e.g. *de novo* genome assembly, mapping, variant (SNP/indel/CNV) calling, somy estimation, ...) and downstream population genomic and phylogenomic analyses (e.g. SNP and haplotype-based population structure inference, haplotype network analyses, ...).

Education and research career

Current	Senior post-doctoral fellow, Rega Institute, University of Leuven (KUL) & Antwerp Institute of Tropical Medicine (ITM) Supervisors: Prof. Philippe Lemey & Prof. Jean-Claude Dujardin Focus: Viral phylodynamics as a lens on protozoa evolution Funding: Research Foundation Flanders (FWO)
2018-2019	Visiting scientist, Wellcome Sanger Institute, Hinxton, United Kingdom Supervisors: Dr. Matthew Berriman & Dr. James Cotton Focus: Speciation genomics of Neotropical Leishmania parasites Funding: Research Foundation Flanders (FWO)
2014-2019	Post-doctoral fellow, ITM Supervisors: Prof. Jean-Claude Dujardin & Prof. Jan Van Den Abbeele Focus: Population genomics of Leishmania and Trypanosoma parasites Funding: Assistant Academic Track Mandate + ITM core funding
2009-2014	PhD student, KUL Supervisors: Dr. Tine Huyse and Prof. Katja Polman Focus: Population genetics of Schistosoma mansoni in Senegal. Funding: VLADOC PhD fellow
2007-2009	Masters in Evolutionary Biology & Molecular Biology, KUL. <i>Cum laude.</i>
2007-2008	Erasmus program. University of Montpellier III, France. <i>Cum laude.</i>
2003-2007	Bachelor in Biology, KUL. <i>Cum laude.</i>

Additional courses

2015	Workshop Molecular Evolution and Phylogenetics. Czech Republic.
2013	Linux for bioinformatics. VIB Bioinformatics Workshop. Meeting Skills Training. Arenberg Doctoral School.
2012	Introduction to Perl programming. VIB Bioinformatics Workshop.
2011	Basics of NGS data analysis. VIB Bioinformatics Workshop. European Summer Institute in Statistical Genetics. University of Washington. Mixed and Multilevel Models. KUL.
2005	Diagnostics of human African Trypanosomiasis. ITM.

Successful grant writing

Attracted 15+ grants:

- 2 research grants as Principal Investigator:
 - 2017. ITM Pump Priming Project. €90000. Title: “*The RNA editing space of the neglected genome in the major livestock African trypanosome parasite Trypanosoma congolense*”
 - 2016. FWO Research Grant. €29000. Title: “*Kinetoplast genomics for the fine-scale study of hybrid zones in eukaryote parasites*”
- 2 research grants as collaborator:
 - 2018. ITM-SOFI MADLEI. €999814. Title: “*Aneuploidy and mosaicism: a strategy for early adaptation to drug pressure in Leishmania*”
 - 2018. ITM-SOFI CHARHAT-DRC. €983673. Title: “*Cryptic human and animal reservoirs compromise the sustained elimination of gambiense-human African trypanosomiasis in the Democratic Republic of the Congo*”
- 3 fellowships:
 - 2019. FWO senior postdoc mandate. 3 year postdoctoral Fellowship. Title: “*Calibrating the recent evolution of protozoan pathogens using viral evolutionary timescales*”.
 - 2015. ITM-AAP KINUGEN. 3 year postdoctoral Fellowship. Title: “*Kinetoplast and nuclear genomics for the fine-scale study of hybridization and drug resistance in Trypanosomatid parasites*”
 - 2010. VLADOC. 3 year PhD Fellowship. Title: “*Evolutionary potential of the human parasite Schistosoma mansoni in a changing world*”
- 8+ travel grants (for research visits, fieldwork and conferences)

Reviewer and editor for peer reviewed journals or conferences

Handled 87 papers as editor

- Infection, Genetics and Evolution (2014-2016)

Handled 15 papers as reviewer

- Nature Communications (1 paper)
- Molecular Ecology (2 papers)
- Evolutionary Applications (1 paper)
- Heredity (1 paper)
- BMC genomics (1 paper)
- Genome Biology and Evolution (1 paper)
- Parasite and Vectors (2 papers)
- PLOS Neglected Tropical Diseases (4 papers)
- Infection, Genetics and Evolution (1 paper)
- Memórias do Instituto Oswaldo Cruz (1 paper)

Twice member of the Scientific Committee of the 13th International Meeting on Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases. 2016 and 2018.

Mobility: experience in the south

- 2009-2014** Organized five missions for sampling *Schistosoma* parasites, Senegal.
2010 Boyekoli Ebale Congo Expedition, Democratic Republic of Congo.

Mobility: research visits

Visited 4 laboratories

- 2016 - 2018. Wellcome Trust Sanger Institute, Hinxton, UK
- 2017. London School of Hygiene and Tropical Medicine, London, UK
- 2013. University of Perpignan, Perpignan, FR
- 2010. Natural History Museum, London, UK

Teaching and supervision

Instructor

- Molecular Data in Infectious Diseases Workshop. ITM (2018-2019).
- Ecological and Evolutionary Genomics Course. University of Leuven (2017-2019).
- Molecular epidemiology Course. University of Antwerp (2017-2019).
- Applied Molecular Epidemiology of Infectious Diseases Workshop. ITM (2016).
- Marine Ecological and Environmental Genomics Workshop. Roscoff, France (2015).

Teaching assistant

- Bio-informatics & Quantitative Genetics. University of Leuven (2013, 2014).
- Ecology. University of Leuven (2012-2013).

Supervised 1 PhD student, 8 master students and 1 bachelor student

Presentations

Invited 3 times at an international meeting or a seminar

- Plenary Speaker at MEEGID XIV, Sitges, Spain (2018)
- Departmental seminar at the London School of Hygiene and Tropical Medicine (2018)
- Seminar at the BIOMedical Informatics research Network Antwerp (2019)

Presented 13 times at international meetings

- 8 oral presentations at the Trypanosomatid Parasites Meeting, the British Society of Parasitology Meeting (BSP), Belgian Society for Parasitology and Protistology (BSPP), Molecular epidemiology, evolution and genetics of infectious diseases (MEEGID), Population Genetics Group Meeting (POPGROUP).
- 5 poster presentations at BSP, Animal Genetics and Diseases (AGD), Infectious Diseases Genomics (IDG), World Congress on Leishmaniasis (WORDLEISH)

Publications

H-index: 12

Published 20 peer-reviewed (A1) papers, and 1 paper is submitted to BIORXIV

- 8 papers in key author positions (5 as 1st author, 1 as shared 1st author and 2 as last author)
- 5 papers as second author
- 7 papers with impact factor > 6, incl. 2 papers with impact factor > 10
- 12 papers without my PhD supervisor

Below you can find a full list of my publications:

- [21] **Van den Broeck F**, Savill N, Imamura H, Sanders M, Maes I, Cooper S, Mateus D, Jara M, Adai V, Arevalo J, Llanos-Cuentas A, Garcia L, Cupolillo E, Miles M, Berriman M, Schnauffer A, Cotton J, Dujardin JC. Ecological divergence and hybridization of Neotropical *Leishmania* parasites. BIORXIV. 2019. <https://doi.org/10.1101/824912>
- [20] Domagalska M, Imamura H, Sander M, **Van den Broeck F**, Bhattarai N, Vanaerschot M, Maes I, D'Haenens E, Rai K, Rijal S, Berriman M, Cotton J, Dujardin JC. Genomes of *Leishmania* parasites directly sequenced from patients with visceral leishmaniasis in the Indian subcontinent. PLOS NEGLECTED TROPICAL DISEASES. 2019. In press.
- [19] Schwabl P, Imamura H, **Van den Broeck F**, Costales JA, Maiguashca-Sánchez J, Miles MA, Andersson B, Grijalva MJ, Llewellyn MS. Meiotic sex in Chagas disease parasite *Trypanosoma cruzi*. NATURE COMMUNICATIONS. 2019. 10(1): 3972.
- [19] **Van den Broeck F**, Tavernier LJM, Vermeiren L, Dujardin JC, Van Den Abbeele J. Mito-nuclear genomics challenges the theory of clonality in *Trypanosoma congolense*. Reply to Tibayrenc and Ayala. MOLECULAR ECOLOGY. 2018. 27: 3425-3431.
- [18] Boon N, **Van den Broeck F**, Faye D, Volckaert FAM, Mboup S, Polman K, Huyse T. Barcoding hybrids: heterogeneous distribution of *Schistosoma haematobium* × *Schistosoma bovis* hybrids across the Senegal River Basin. PARASITOLOGY. 2018. 145 (5): 634-645.
- [17] Huyse T, Boon N, **Van den Broeck F**, Mbow M, Chaturvedi A, Meurs L, Volckaert F, Polman K. Evolutionary epidemiology of schistosomiasis: linking parasite genetics with disease phenotype in humans. INTERNATIONAL JOURNAL OF PARASITOLOGY. 2018. 48 (2): 107-115.
- [16] Tihon E, Imamura H, **Van den Broeck F**, Vermeiren L, Dujardin JC & Van Den Abbeele J. Genomic analysis of Isometamidium Chloride resistance in *Trypanosoma congolense*. INTERNATIONAL JOURNAL OF PARASITOLOGY: DRUGS AND DRUG RESISTANCE. 2017. 7 (3): 350-361.
- [15] Tihon E, Imamura H, Dujardin JC, Van Den Abbeele J & **Van den Broeck F**. Discovery and genomic analyses of hybridization between divergent lineages of *Trypanosoma congolense*, causative agent of Animal African Trypanosomiasis. MOLECULAR ECOLOGY. 2017. 26 (23): 6524–6538.
- [14] Cuypers B, **Van den Broeck F**, Van Reet N, Meehan C, Cauchard J, Wilkes JM, Claes F, Goddeeris B, Hadush B, Dujardin JC, Laukens K, Büscher P & Deborggraeve S. Genome-wide SNP analysis reveals distinct origins of *Trypanosoma evansi* and *Trypanosoma equiperdum*. GENOME BIOLOGY AND EVOLUTION. 2017. 9 (8): 1990–1997.
- [13] Zein Eddine R, Djuikwo-Teukeng F, Dar Y, Dreyfuss G & **Van den Broeck F**. Population genetics of the *Schistosoma* snail host *Bulinus truncatus* in Egypt. ACTA TROPICA. 2017. 172: 36-43.
- [12] Cuypers B, Lecordier L, Meehan C, **Van den Broeck F**, Imamura H, Büscher P, Dujardin JC, Laukens K, Schnauffer A, Deward C, Lewis M, Balmer O, Azurag T, Kjei-Faried S, Oheneh SA, Duahi B, Homiahi P, Mensah EK, Anleah F, Franco JR, Pays E & Deborggraeve S. Novel Apolipoprotein L-I Variant Associated with Increased Susceptibility to Trypanosome Infection. MBIO. 2016. 7 (2): e02198-15.
- [11] Imamura H, Downing T, **Van den Broeck F**, Sanders MJ, Rijal S, Sundar S, Mannaert A, Vanaerschot M, Berg M, De Muylder G, Dumetz F, Cuypers B, Maes I, Domagalska M, Decuypere S, Rai K, Uranw S, Bhattarai NR, Khanal B, Prajapati VK, Sharma S, Stark O, Schöniar G7, De Koning HP, Settimo L, Vanhollebeke B, Roy S, Ostyn B, Boelaert M, Maes L, Berriman M, Dujardin JC & Cotton JA. Evolutionary genomics of epidemic visceral leishmaniasis in the Indian subcontinent. ELIFE. 2016. 5: e12613.
- [10] **Van den Broeck F**, Maes G, Larmuseau M, Rollinson D, Sy I, Faye D, Volckaert F, Polman K & Huyse T. Reconstructing colonization dynamics of the human parasite *Schistosoma mansoni* following anthropogenic environmental changes in Northwest Senegal. PLOS NEGLECTED TROPICAL DISEASES. 2015. 9 (8): e0003998.

- [9] **Van den Broeck F**, Meurs L, Raeymaekers JAM, Boon N, Tandakha N, Volckaert FAM, Polman K & Huyse T. Inbreeding within human *Schistosoma mansoni*: do host-specific factors shape the genetic composition of parasite populations? HEREDITY. 2014. 113: 32-41.
- [8] Vanaerschot M, Huijben S, **Van den Broeck F** & Dujardin JC. Drug resistance in vector-borne parasites: multiple actors and scenarios for an evolutionary arms race. FEMS MICROBIOLOGY REVIEWS. 2014. 38 (1): 41-55.
- [7] Huyse T, **Van den Broeck F**, Jombart T, Webster B, Diaw O, Volckaert F, Balloux F, Rollinson D & Polman K. Regular treatments of praziquantel do not impact on the genetic make-up of *S. mansoni* in northern Senegal: evidence for drug tolerance? INFECTION GENETICS AND EVOLUTION. 2013. 18: 100-105.
- [6] Huyse T, **Van den Broeck F**, Hellemans B, Volckaert F, Polman K. Hybridization between the two major African schistosome species of humans. INTERNATIONAL JOURNAL OF PARASITOLOGY. 2013. 43: 687-689.
- [5] De Waele V, **Van den Broeck F**, Huyse T, McGrath G, Higgins I, Speybroeck N, Berzano M, Raleigh P, Mulcahy GM & Murphy TM. Panmictic structure of the *Cryptosporidium parvum* population in Irish calves: influence of prevalence and host movement. APPLIED AND ENVIRONMENTAL MICROBIOLOGY. 2013. 79 (8): 2534-2541.
- [4] Meurs L, Mbow M, Boon N, **Van den Broeck F**, Vereecken K, Dièye TN, Abatih E, Huyse T, Mboup S, Polman K. Micro-geographical heterogeneity in *Schistosoma mansoni* and *S. haematobium* infection and morbidity in a co-endemic community in Northern Senegal. PLOS NEGLECTED TROPICAL DISEASES. 2013. 7 (12): e2608.
- [3] Raeymaekers JAM, Lens L, **Van den Broeck F**, Van Dongen S & Volckaert FAM. Quantifying population structure on short timescales. MOLECULAR ECOLOGY. 2012. 21 (14): 3458-73
- [2] Adaui V, Maes I, Huyse T, **Van den Broeck F**, Talledo M, Kuhls K, De Doncker S, Maes L, Llanos-Cuentas A, Schönian G, Arevalo J & Dujardin JC. Multilocus genotyping reveals a polyphyletic pattern among naturally antimony-resistant *Leishmania braziliensis* isolates from Peru. INFECTION GENETICS AND EVOLUTION. 2011. 11 (8): 1873-1880.
- [1] **Van den Broeck F**, Geldof S, Polman K, Volckaert FAM & Huyse T. Optimal sample storage and extraction protocols for reliable multilocus genotyping of the human parasite *Schistosoma mansoni*. INFECTION GENETICS AND EVOLUTION. 2011. 11 (6): 1413-1418.