

Curriculum Vitae

Personal information

First name / Family name	Julie Ferreira de Carvalho		
Address(es)	Juliana van Stolberglaan 207, 6713PH Ede, The Netherlands		
Telephone	+31 (0)3 17 47 34 00		
Mobile	+33 (0)6 82 04 95 26		
E-mail	Julie.ferreira.carvalho@gmail.com		
Nationality	French		
Date of birth	25/10/1985		
Gender	Female		

Personal statement

After a successful PhD thesis with no revision and a 4-year post-doctoral fellowship in Wageningen (NL), I have become a recognized and independent evolutionary biologist working at the interface of molecular ecology and genome evolution. Since 2009, I gained international experience in gene expression evolution in polyploid plant genomes (using RNA Seq), in characterising and understanding the role of transposable elements on genome evolution and gene expression, as well as on epigenetic inheritance and regulation in plants. Also, I am leading a consortium (of 3 academic groups and 1 private company) to develop and publish the first complete annotated genome of the common dandelion. I have contributed to 8 international publications (including 4 as a first author), one book chapter and 3 peer-reviewed proceedings in major journals in the field of evolutionary biology, genomics, ecology and plant science. I have decided to return to my home country and more specifically I want to integrate INRA and the research group IGEPP (Rennes). I believe my current knowledge and skills will be transferable and valuable to the hosting laboratory. I have complimentary expertise with members of the host team and particularly efficient and original integrative research can be achieved. This genuine mobility will not only allow me to bring and transfer conceptual knowledge but also to improve and implement cutting-edge methods in epigenetics and functional genomics, reinforcing the scientific potential and competitiveness of the research group. I will also be able to broaden my skills on structural evolution and acquire additional expertise in plant breeding, metabolomics, cytogenetics and bioinformatics. It will also be an excellent opportunity for me to develop my partnership towards the private sector by interacting regularly with breeding companies. Ultimately, this AgreenSkills+ mobility grant will put me on track to obtain a permanent academic position at INRA.

Education and training

Location and dates	October 2009 – December 2012 Rennes, France.
Title of qualification awarded	Ph.D. Cum Laude in Plant Genomics and Ecology Thesis examining committee (external members): Dr. Boulos Chalhoub (URGV, Evry, France) Dr. Angélique d’Hont (CIRAD, Montpellier, France)

	Dr. Anne-Marie Chèvre (IGEPP, Le Rheu, France) Prof. Jonathan Wendel (Iowa State University, USA)
Principal subjects/occupational skills covered	<p>PhD thesis on genome evolution of polyploid <i>Spartina</i> species invading salt-marshes: contribution of Next-Generation Sequencing technologies.</p> <p><u>Abstract:</u> <i>Spartina</i> species play an important ecological role on salt marshes. They represent an excellent system to study the ecological consequences of hybrid and polyploid speciation in biological invasion contexts. During my PhD, I examined the effects of hybridization between the hexaploid native American species <i>Spartina alterniflora</i> and the European species <i>S. maritima</i>, that gave rise to two F1 hybrids (<i>S. x townsendii</i> in England et <i>S. x neyrautii</i> in France) and the new invasive allododecaploid species (<i>S. anglica</i>). Next generation sequencing technologies offer new perspectives to explore these previously poorly known genomes. The assembly of a reference transcriptome allowed annotation of 16,753 genes in hexaploid <i>Spartina</i> and identification of ecologically and evolutionary important genes. Expression levels of a subset of these genes were analyzed by quantitative PCR in <i>Spartina</i> natural populations. The results indicate homogenous intrapopulation expression but extreme variability between species. The European <i>S. maritima</i> benefited from genomic resource development through a BAC library and one pyrosequencing run. Our analyses estimated the relative proportions of repetitive sequences as about 30% and have identified the main transposable element families. Data generated were also compared to closely related sequenced species and provided the first insights into the evolution of <i>Spartina</i> genomes in the Poaceae family.</p> <p><u>General approaches and techniques practiced:</u></p> <p>Field trips and population sampling DNA and RNA extractions, cDNA synthesis, NGS library prep, Cloning Quantification by RT-PCR (SybrGreen method) Genome and transcriptome large-scale sequence analyses (from Roche-454 pyrosequencer): sequence assembly, annotation, comparative analyses Bioinformatic softwares and analyses: Primer Express, Primer3, Mega, BioEdit, Geneious, Blast, Mafft, Mira, Newbler, Tablet. Use of bioinformatics SGE platform, work under UNIX, work with large genomic databases and basic knowledge of Python language. Statistical analyses (R software)</p>
Name of Institute	UMR ECOBIO, CNRS-University of Rennes 1

Location and dates	September 2007 – August 2009 Rennes, France.
Title of qualification awarded	Master in Functional, Behavioural and Evolutionary Ecology with first class honours
Principal subjects/occupational skills covered	<p>Title of the Master thesis 2 (8 months): Quantitative study of mitochondrial heteroplasmy in <i>Globodera pallida</i>. Bio3P-Nematology lab, INRA Le Rheu, under supervision of Dr. Eric Petit.</p> <p><u>Abstract:</u> This work underlines the extreme variability of mitochondrial haplotypes in the nematode <i>G. pallida</i>. Peruvian populations are divided into five clades derived from a single ancestral population restricted in the South of Peru. The haplotype quantifications bring to light a South to North phylogeographical gradient with five well-supported clades. Moreover, mitochondrial heteroplasmy detected within a cyst provided new hypotheses regarding heredity of the mitochondrial genome. Indeed, mutations, recombination, biparental and/or multiple paternal transmission potentially generate heteroplasmy whereas</p>



	<p>positive selection contributes to sequence retention in populations.</p> <p><u>General approaches and techniques:</u> DNA extraction, PCR, cloning, RT-PCR Set up (TaqMan method) Statistical analyses (R software)</p> <p>Title of the Master thesis 1 (4 months): Role and influence of oilseed rape fields on different pollinator groups (solitary and domestic bees, bubblebees and hoverflies) and different landscape structures. Team Landscape, Climate Change-Biodiversity, UMR ECOBIO 6553, University of Rennes 1, under the supervision of Dr. Françoise Burel and Dr. Violette Leféon.</p> <p><u>General approaches and techniques:</u> Field collections and sampling of pollinators, taxonomy Geographical analyses (SIG) Statistical analyses (R software)</p>
Name of Institute	University of Rennes 1

Work experience

Location and dates	February 2016-Present, Wageningen, The Netherlands
Occupation or position held	Guest Researcher
Main activities and responsibilities	Project leader on <i>Taraxacum officinale</i> genome assembly and annotation, effects of apomixis on genome dynamic and evolution. I am coordinating a consortium of 3 public research institutes (NIOO-KNAW, Biosystematics and BioScience, Wageningen) and one private company (KeyGene) to publish the first reference genome for the common dandelion (<i>Taraxacum officinale</i>) and elucidate genome dynamics under asexual reproduction.
Name of employer	Prof Eric Schranz , Biosystematics group, Wageningen University, The Netherlands.

Location and dates	April 2013-Present, Wageningen, The Netherlands
Occupation or position held	Postdoctoral fellow
Main activities and responsibilities	Project leader on the (epi)genomic footprints associated with asexual evolution. I have introduced novel research topics to my current group, notably on transposable element evolutionary dynamics and its impact on gene expression and genome structure. This research line is now well integrated into the group and part of a pending ERC proposal. I have supervised five Msc students. I trained these students but also PhDs and technicians in cutting-edge molecular techniques (bisulfite treatment, Epi-GBS), as well as high-throughput sequence analyses (Illumina and PacBio). I also participated in grant application writing (as PI for some of them) for travel funds from French Genetic Society, Dutch Ecological Organization, Hubert Curien or collaborative programs such as ITN and ERC European proposals on Ecological Epigenetic.
Name of employer	Dr Koen Verhoeven , Terrestrial Ecology Department, Netherlands Institute of Ecology (NIOO-KNAW), The Netherlands. Prof Wim van der Putten , Head of the Terrestrial Ecology Department, Netherlands Institute of Ecology (NIOO-KNAW) and Nematology Laboratory, Wageningen University, The Netherlands.

Location and dates	October 2009 – June 2012 Rennes, France.
Occupation or position held	Teaching assistant
Main activities and responsibilities	During 3 years, I taught undergraduate practical classes and lectures (with a total of 192h in French and English) in Nutrition and Reproduction, Plant Biology, Evolutionary Biology, Phylogenetic, Biosystematics and Biotic Interactions in Angiosperms.
Name of employer	University of Rennes 1, France.

Location and dates	June – August 2008
Occupation or position held	Research assistant in Entomology
Main activities and responsibilities	Taxonomic identification of pollinators, preparation and storage of specimen.

Name of employer	Dr Violette Leféon, UMR ECOBIO, CNRS-University of Rennes 1, France.
------------------	--

Languages

Mother tongue(s)	French				
Other language(s)	Understanding		Speaking		Writing
European level (*)	Listening	Reading	Spoken interaction	Spoken production	
English	C2	C2	C2	C2	C2
Spanish	B1	B2	B1	B1	A2
Dutch	A1	A1	A1	A1	A1
(*) Common European Framework of Reference for Languages http://europass.cedefop.europa.eu/en/resources/european-language-levels-cefr					

Academic Record

Publications	<p>Accepted, in press and published articles / papers:</p> <ol style="list-style-type: none"> Ferreira de Carvalho J., de Jager V., van Gorp T., Wagemaker N. and K.J.F. Verhoeven. Recent and dynamic transposable elements contribute to genomic divergence under asexuality. <i>Accepted in BMC Genomics</i> (IF=3.99). Boutte J., Ferreira de Carvalho J., Ainouche M. and Salmon A. Reference transcriptomes and detection of duplicated copies in hexaploid parents, hybrids and allododecaploid <i>Spartina</i> species (Poaceae). <i>Accepted in Genome Biology and Evolution</i> (IF=4.10). Huska D., Leitch I., Ferreira de Carvalho J., Leitch A., Salmon A., Ainouche M. and A. Kovarik (2016). Persistence, dispersal and genetic evolution of recently formed <i>Spartina</i> homoploid hybrids and allopolyploids in Southern England. <i>Biological Invasions</i> 18(8):2137-51. (IF=2.59) Ferreira de Carvalho J., Oplaat C., Pappas N., Derks M., de Ridder D. and K.J.F. Verhoeven (2016). Heritable gene expression differences between apomictic clone members in <i>Taraxacum officinale</i>: Insights into early stages of evolutionary divergence in asexual plants. <i>BMC Genomics</i>. 17: 203. (IF=3.99) Boutte J., Aliaga B., Lima O., Ferreira de Carvalho J., Ainouche A., Macas J., Rousseau-Gueutin M., Coriton O., Ainouche M. and A. Salmon (2015). Haplotype Detection from Next Generation Sequencing in High Ploidy-Level Species: 45S rDNA Gene Copies in the Hexaploid <i>Spartina maritima</i>. <i>G3</i> 6(1):29-40. (IF=3.20, 2 citations) Guillaume M., Rousseau-Gueutin M., Cordonnier S., Lima O., Michon-Coudouel S., Naquin D., Ferreira de Carvalho J., Ainouche M., Salmon A. and A. Ainouche (2014). The first complete chloroplast genome of Genistoid legume <i>Lupinus luteus</i>: Evidence for a novel major lineage-specific rearrangement and new insights regarding plastome evolution in the legume family. <i>Annals of Botany</i> 113 (7): 1197-1210. (IF=3.65, 11 citations) Ferreira de Carvalho J., Poulain J., Da Silva C., Wincker P., Michon-Coudouel S., Dheilly A., Naquin D., Boutte J., Salmon A. and M. Ainouche (2013a). Transcriptome de novo assembly from Next-Generation Sequencing and comparative analyses in the hexaploid salt marsh species <i>Spartina maritima</i> and <i>Spartina alterniflora</i> (Poaceae). <i>Heredity</i> 110: 181-93. (IF=3.80, 24 citations) Ferreira de Carvalho J., Chelaifa H., Mangenot S., Couloux A., Wincker P., Bellec A., Fourment J., Berges H., Salmon A. and M. Ainouche (2013b). Exploring the
--------------	---

	<p>genome of the salt-marsh species <i>Spartina maritima</i> (Poaceae, Chloridoideae) through BAC End Sequence analysis. <i>Plant Molecular Biology</i> 83: 591-606. (IF=4.26, 7 citations)</p> <p>Submitted publications:</p> <p>9. Ferreira de Carvalho J., Boutte J., Bourdau P., Chelaifa H., Ainouche K., Salmon A. and M. Ainouche. Gene expression variation in natural populations of hexaploid (parents and hybrids) and allododecaploid <i>Spartina</i> species (Poaceae). <i>Plant Systematics and Evolution</i>.</p> <p>10. Verhoeven K.J.F, Verbon E., van Gorp T., Oplaat C., Ferreira de Carvalho J. et al. Parental jasmonic acid treatment affects offspring transcriptomes and leaf chemical profiles in dandelion. <i>New Phytologist</i>.</p>
<p>Presentations as invited speaker</p>	<p>SELECTED ORAL PRESENTATIONS</p> <p>-Ferreira de Carvalho J. and K. Verhoeven (2016). Dead-end trajectory of young triploid apomicts: Can transposable elements improve their adaptive potential? French annual meeting on Plant Genome Dynamic, Paris (France).</p> <p>-Ferreira de Carvalho J. and K. Verhoeven (2016). Dead-end trajectory of young triploid apomicts: Can transposable elements improve their adaptive potential? International Conference on Polyploidy, Hybridization and Biodiversity ICPHB, Rovinj (Croatia).</p> <p>-Ferreira de Carvalho J. and K. Verhoeven (2015). Transposable elements and methylation variation between apomictic clone members in <i>Taraxacum officinale</i>: Insights into early stages of genome evolution under asexuality. Plant Genome Evolution Conference, Amsterdam (The Netherlands).</p> <p>-Ferreira de Carvalho J. et al. (2014). Phenotypic, transcriptomic and epigenetic heritable variation within apomictic lineages of dandelion natural populations. Society of Molecular Biology and Evolution, San Juan (Puerto Rico).</p> <p>-Ferreira de Carvalho J. et al. (2012). Genome and Transcriptome analysis of the hexaploid <i>Spartina</i> species colonizing salt marshes using next generation sequencing. International Conference on Polyploidy, Hybridization and Biodiversity ICPHB 2012, Prague (Czech Republic).</p> <p>-Ferreira de Carvalho J., Salmon A. and M. Ainouche (2011). Genome evolution of <i>Spartina</i> hybrid and allopolyploid species invading salt marshes. Polyploidy and Cytogenetics workshop, London (England).</p> <p>-Ferreira de Carvalho J., Chelaifa H., Salmon A., Macas J. and M. Ainouche (2011). High-throughput genome and transcriptome sequencing in hexaploid and allo-dodecaploid <i>Spartina</i> species (Poaceae). French annual Polyploidy Meeting, Montpellier (France).</p> <p>INVITED PRESENTATION</p> <p>-Ferreira de Carvalho J. Genomic footprints of asexuality in dandelions. University of Neuchatel (Switzerland), November 2015. Invited by Dr C. Parisod.</p>
<p>Authored books or book chapter(s)</p>	<p>11. Ainouche M., Chelaifa H., Ferreira de Carvalho J., Bellot S., Ainouche A. and A. Salmon (2012). Polyploid evolution in <i>Spartina</i>: dealing with highly redundant genomes. In: Soltis PS, Soltis DE (Eds) <i>Polyploidy and Genome Evolution</i>, Springer Berlin Heidelberg. pp 225-244. (21 citations)</p>
<p>Participation in open calls for proposals as contributor or leader</p>	<p>2016 <i>Contributor</i> to an ERC proposal "Fixed yet flexible: epigenetic plasticity in asexual plant genomes" (Submitted).</p> <p>2013-2016 <i>Participant</i> of the NWO-VIDI project "Hereditary differences without genetic differences?" attributed to Dr Koen Verhoeven.</p>

	<p>2009-2012 Beneficiary of ARED Grant “EVOSPART: Study on Invasive Spartina in Brittany Salt-marshes” Principal investigator Prof Malika Ainouche, financed by the Regional Council of Brittany, France.</p> <p>2009-2010 Participant of the Project “GENOSPAR: Genomics of Spartina” Principal investigator Prof Malika Ainouche, financed by the Génoscope, France.</p>
Graduate teaching as lecturer or training coordinator	<p>Undergraduate and graduate classes total of 192h (in French and English) in Nutrition and Reproduction, Plant Biology, Evolutionary Biology, Phylogenetic, Biosystematics and Biotic Interactions in Angiosperms.</p> <p>2014-2018: Qualified to apply to a French lecturer position in Section 68 (Biology of Organisms).</p> <p>Supervisions of graduate students (M.Sc. theses):</p> <ul style="list-style-type: none"> -Sabrina Kalita (8 months, Erasmus+, University of Bremenhaven, Germany). -Alise Zvigule (6 months, University of Maastricht, NL). -Arnoud Witteveen (6 months, University of Wageningen, NL). -Kim Magnee (6 months, University of Wageningen, NL). -Nikolaos Pappas (6 months, University of Wageningen, NL). -Pierre Bourdaud (4 months, University of Rennes 1, France).
Awards and prizes, if any	<p>2012 Travel Award to the Plant and Animal Genome Meetings (San Diego, USA) financed by the French Society of Genetics.</p> <p>2010 Scholarship from VAS PhD School to attend the International European course on Comparative Genomics and Epigenomics at Ecole Normale Supérieure of Lyon, France</p> <p>2010 1st prize for the best oral and poster presentation at the PhD school (VAS) meeting, Rennes, France.</p>

Collaboration and Networking

Participation in collaborative projects funded by competitive programmes	<p>2011-2012 Participant of the BARRANDE project on “Evolution of repetitive sequences in the genome of Spartina species” Principal investigators Prof Ainouche and Dr Ales Kovarik, financed by the Hubert Curien Programme France-Czech Republic.</p>
Partnerships or experience with industry	<p>Collaborations and co-supervision of students with KeyGene company (Wageningen, NL) on the effects of apomixis in <i>Taraxacum officinale</i>.</p>
Membership of professional bodies and committees	<p>Committee member for Master’s thesis defenses (Wageningen University, NL)</p>

Research management, Technology transfer, and Communication

Team management	<p>Committee member of the scientific communication board (Department of Terrestrial Ecology, NIOO-KNAW)</p> <p>Committee member for hiring bioinformaticians (NIOO-KNAW)</p>
Other experience and skills relevant to the application	<p>Organisation of scientific meeting: International conference for PhD students “Ecology and Behavior”, 2-6 May 2011, Rennes (France).</p> <p>Participation in Scientific Open Days October 2013 and 2016 (Netherlands Institute of Ecology, Wageningen)</p> <p>Reviewer for several scientific journals</p>

Scientific References

Full name	Prof Malika Ainouche
Position	Group Leader
Institution	UMR ECOBIO 6553, University of Rennes 1 (France).
Email address	malika.ainouche@univ-rennes1.fr

Full name	Dr Koen Verhoeven
Position	Group leader
Institution	Terrestrial Ecology Department, Netherlands Institute of Ecology (NIOO-KNAW), Wageningen (NL).
Email address	k.verhoeven@nioo.knaw.nl

Full name	Prof Eric Schranz
Position	Group leader
Institution	Biosystematics, Plant Science Department, University of Wageningen (NL).
Email address	eric.schranz@wur.nl

How did you hear about AgreenSkills programmes?

	Professional network
--	----------------------