

# Giobbe Forni

Via Arienti 26, Bologna 40124 (Italy)

forni.giobbe@gmail.com

+39 3892907645

## RESEARCH EXPERIENCES

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October 2016 – November 2017 Postgraduate Internship

During the last year I have been working on the phylogeny of Phasmida. My first effort has been to develop new universal primers and to test the phylogenetic informativeness of different molecular markers relatively to this insect Order. During this period I have generated sequences of seven molecular markers for more than 200 species and I have applied a species delimitation approach to the *Candovia* genus. I have also been working on the mitogenomics and phylogenesis of reticulitermites.

October 2015 – May 2016 MSc Thesis

During six months abroad, at the University of Lleida, Spain, I applied CRISPR-Cas9 in rice to create two knockout callus lines relatively to the *OsAPL3* gene, a subunit of a key enzyme in the starch pathway. After the transformation, I screened the putative transgenic population and identified two candidate lines, from which I cloned and characterized frequency and structure of the targeted mutation.

## EDUCATION

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November 2017 PhD student  
University of Bologna, Bologna (Italy).

July 2016 MSc in Biodiversity and Evolution - 110 / 110 *cum laude*  
University of Bologna, Bologna (Italy).

March 2013 BSc in Biotechnology - 103 / 110  
University of Bologna, Bologna (Italy).

## ADDITIONAL COURSES

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February 2016 Bioinformatics Methods I  
Two month course taken through the on-line platform Coursera.

March 2017 Integrative Taxonomy and Taxonomic Expertise: DNA Barcodes in the Genomic Era  
Five day course at MNHN Muséum National d'Histoire Naturelle, Paris.

April 2016 Comparative methods in evolutionary biology  
Four days workshop at Stazione Anthon Dhorn, Naples.

November 2017 The Unix workbench

One month course taken through the on-line platform Coursera.

## SKILLS

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linguistic skills	Italian	native speaker
	English	C1
	Spanish	A2
informatics skills	Confortable using MacOSX, Windows, Linux and the Office and Adobe suites. Used to work on remote-access servers and in command-line environements. Good knowledge of on-line databases - such as NCBI and BOLD - and tools - such as CIPRES or Galaxy. Experience in many molecular phylogenesis tools such as Mega, Mesquite, PartitionFinder2, JmodelTest, MAFFT, T-Coffe, RAxML, Beast, Mr Bayes, Phyutility, GBLOCKS, PAML, and more. Knowledge in NGS data manipulation and tools such as SRA toolkit, fastQC, SAMtools, Bowtie, BLAST, Trinity.	
wet lab skills	CRISPR-Cas9, T7 and PCR-RE assays, PCR and electroforesis in agarose and acrylamide, degenerate primer design, molecular cloning and competent cell preparation, DNA and RNA extraction, qRT-PCR, biolistics and tissue culture, Sanger sequencing, HPLC, ELISA.	

## PAPERS AND POSTERS

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Bortesi, Luisa; Zhu, Changfu; Zischewski, Julia; Perez, Lucia; Bassié, Ludovic; Nadi, Riad; Forni, Giobbe; Lade, Sarah; Soto, Erika; Jin, Xin; Medina, Vicente; Villorbina, Gemma; Munoz, Pilar; Farré, Gemma; Fischer, Rainer; Twyman, Richard; Capell, Teresa; Christou, Paul; Schillberg, Stefan. ***Patterns of CRISPR/Cas9 activity in plants, animals and microbes.*** Plant Biotechnology Journal, 14(12), 2203–2216 (2016).

Nadi, Riad; Soto, Erika; Forni, Giobbe; Villorbina, Gemma; Farré, Gemma; Capell, Teresa; Zhu, Changfu ; Christou, Paul. ***Knocking out NDP-glucose-starch glucosyltransferase (Waxy) gene in Rice (Oryza sativa) using CRISPR/Cas9.*** VIII European Plant Science Retreat, Barcellona (2016).

Forni, Giobbe; Cussigh, Alex; Valero, Pablo; Seow-Choen, Francis; Costa von Sydow, Jane; Bresseel, Joachim; Constant, Jérôme; Gutiérrez, Yeisson; Kneubühler, Bruno; Ortiz, Antonio S.; Brock, Paul; Hennemann, Frank; Conle, Oskar; Mantovani, Barbara. ***Turning chaos into Order: the phylogeny of Phasmida.*** Evoluzione 2017 Congress (2017).