

# GABRIEL E. RECH, Ph.D. – Computational Biologist

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## EDUCATION

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- Ph.D. (Doctorate)** Jan. 2014  
University of Salamanca (Salamanca, Spain)  
*Ph.D. International Mention, Summa Cum Laude. Ph.D. Extraordinary Award.*
- Visiting Ph.D. Student** Sep. – Dec. 2012  
Computational Biochemistry Research Group.  
Swiss Federal Institute of Technology (ETH) (Zürich, Switzerland)
- Visiting Ph.D. Student** Sep. – Dec. 2011  
Centre for Bioinformatics and Computational Genetics.  
University of Adelaide (Adelaide, Australia)
- Master Agrobiotechnology** Jul. 2011  
University of Salamanca (Salamanca, Spain)
- Degree in Biological Sciences** (Equivalent to B.S.) Dec. 2008  
National University of Salta (Salta, Argentina)

## EXPERIENCE

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**Computational Scientist** Jul. 2022 – Present

**Bioinformatics Analyst II** Aug. 2020 – Jul. 2022

*The Jackson Laboratory for Genomic Medicine (Farmington, CT, USA)*

Supervisor: Chia-Lin Wei

- Design, develop, and execute computational approaches for R&D projects, including:
  - Structural variations at the single-cell level using long-read sequencing in cancer.
  - Long-read targeting sequencing with applications to genetic diagnostic and vector genomic integration.
  - Extrachromosomal circular DNA (ecDNA) in cancer cell lines using long-reads.
  - Cancer methylation signatures on cell-free DNA (cfDNA) from liquid biopsies.
- Lead computational analyses for long-read targeting sequencing operations.
- Organized the Computational Biology Sessions for the 2022 Long-Read Sequencing Workshop.

**Research Associate**

*Spanish National Research Council (CSIC) (Barcelona, Spain)*

Sep. 2016 – Aug. 2020

Supervisor: Josefa González

- Designed, developed, and executed scientific projects, including:
  - Population-scale whole-genome sequencing using short and long-reads (available at [NCBI \(PRINA559813\)](#)).
  - Transposable elements annotation, population dynamics and gene expression.
- Data management of several terabytes of omics data from different projects in the lab.
- Established successful collaborations with lab members and scientists across Europe and the US.
- Published 7 research articles, two of them as the first author in *PLoS Genetics* and *Nature Communications*.
- Shared and discussed results in webinars and research conferences.
- Mentored 2 grad students.

**Bioinformatician**

*Institute of Predictive and Personalized Medicine of Cancer (IMPPC) (Barcelona, Spain)*

Jan. 2014 – Aug. 2016

Supervisor: Lauro Sumoy

- Developed bioinformatics tools and pipelines for cancer multi-omics data analysis, including WGS, WES, RNA-Seq, and expression/methylation microarrays.
- Worked in collaboration with scientists from diverse backgrounds, including physicians.
- Performed experimental design and provided consultation for custom solutions to researchers and clinicians working on cancer-related omics projects.
- Worked closely with wet-lab technicians and scientists to refine experimental and analytical approaches.
- Data management of several terabytes of omics data generated at the Genomics and Bioinformatics Unit.

**Ph.D. Fellow, *University of Salamanca (Salamanca, Spain)***

**Sep. 2009 – Jan. 2014**

Supervisor: Michael R. Thon

- Used evolutionary genomics computational methods to identify pathogenicity-related genes in a plant pathogenic fungus, including whole-genome NGS data analysis, genome assembly, SNP calling, gene annotation, phylogenetic reconstruction and 3D protein reconstruction.
- Wrote scientific articles. Shared and discussed results in webinars and research conferences
- Established successful collaborations as a Visiting Ph.D. Student at the Swiss Federal Institute of Technology (ETH) in Zürich (Switzerland) and at the University of Adelaide (Australia).
- Awarded with the Ph.D. International Mention, the Summa Cum Laude (highest distinction), and the University's Ph.D. Extraordinary Award in Genetics.
- Published 6 research articles, two as first author and four collaborations.

## **TECHNICAL SKILLS**

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**Computing:** Administration and advanced command-line usage of Unix-based OS. Experience with high-performance computing (HPC) environments and cloud-based systems (AWS). Experience using containers (Docker and Singularity), workflow (Nextflow, Snakemake) and source code (Git) management systems.

**Programming:** Proficiency in Python (including BioPython, scipy), R (including Tidyverse), and bash.

**Statistics:** Parametric and non-parametric statistics, exploratory analysis (correlation, PCA, heatmap), linear regression.

**Sequencing:** short-read (Illumina) and long-read (Nanopore and PacBio) sequencing processing (WGS, WES, RNAseq, targeted sequence capture, shotgun genomics, bisulfite sequencing).

**Omics:** quality control, genome assembly and polishing, multiple sequence alignment, phylogenetic reconstruction, mapping and similarity search, variant calling, metagenomics, DNA methylation analysis, RNA-Seq, biological function prediction from gene lists and SNPs.

## **AWARDS and HONORS**

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**Marie Skłodowska-Curie Individual Fellowships (IF-GF). ChaConGen:** Exploring the role of host-parasite genotypes in the congenital transmission of Chagas disease: an emergent infectious disease in Europe. Call: H2020-MSCA-IF-2019. Grant Amount: €224,496. (**Declined by the beneficiary**). 2019

**Travel award.** Special Topic Networks (STN) from the European Society for Evolutionary Biology (ESEB). Groningen, The Netherlands. 2017

**PhD Extraordinary Award.** University of Salamanca, Spain. 2015

**PhD Suma Cum Laude.** University of Salamanca, Spain. 2014

**PhD International Mention.** University of Salamanca, Spain. 2014

**Four years PhD fellowship** (Formacion Personal Investigador, FPI) including financial support and education allowance. Spanish Government. University of Salamanca, Spain. 2009

**Four years PhD fellowship** (JAE) which supports outstanding graduate students with and excellent academic transcript. Spanish National Research Council (CSIC). (*Rejected for accepting the FPI*). 2009

**Travel Grant for advanced studies.** CAPACIT-AR del NOA Foundation. Salta, Argentina. 2008

**Fellowship for Advanced Students** (BIEA), Order: First Position. National University of Salta Research Council (CIUNSa). Salta, Argentina. 2008

## **PATENTS**

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- Methods and systems to identify genetic and epigenetic alterations in a target-specific manner. JAX internal IDs: D21-014: TARGET CAPTURE ULTRALONG-READ ANALYSIS. Temporal US Serial Number: 63/297,914.

## **PUBLICATIONS**

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1. Horváth, V., Guirao-Rico, S., Salces-Ortiz J., **Rech G.E.**, Green, L., Aprea, E., Rodeghiero, M., Anfora, G., J. González. *Gene expression differences consistent with water loss reduction underlie desiccation tolerance of natural Drosophila populations.* BMC Biol 21, 35 (2023) <https://doi.org/10.1186/s12915-023-01530-4>.
2. **Rech, G.E.**, Radfo, S., Guirao-Rico, S. L. Aguilera, V. Horvath, L. Green, H. Lindstadt, V. Jamilloux, H. Quesneville, J. González. *Population-scale long-read sequencing uncovers transposable elements associated with gene expression variation and adaptive signatures in Drosophila.* Nature Communications 13, 1948 (2022). <https://doi.org/10.1038/s41467-022-29518-8>.

3. Green, L., Coronado-Zamora, M., Radio, S.E., **Rech G.E.**, Salces-Ortiz, J. and González, J. *The genomic basis of copper tolerance in Drosophila is shaped by a complex interplay of regulatory and environmental factors*. BMC Biology 20, 275 (2022). <https://doi.org/10.1186/s12915-022-01479-w>.
4. Núñez-Álvarez, Y., Hurtado, H., Muñoz, M., García-Tuñón, I., **Rech, G.E.**, Pluvinet, R., Sumoy, L., Alberto M. Pendás, A.M., Peinado, M.A., Suelves, M. *Loss of HDAC11 accelerates skeletal muscle regeneration*. The FEBS Journal (2020). <https://doi.org/10.1111/febs.15468>.
5. Salces-Ortiz, J., Vargas-Chavez, C.A., Guio, L., **Rech, G. E.**, and González, J. *Transposable elements contribute to the genomic response to insecticides in Drosophila melanogaster*. Philosophical Transactions of the Royal Society B: Biological Sciences, 1795: 375 (2020). <https://doi.org/10.1098/rstb.2019.0341>.
6. **Rech, G. E.**, Bogaerts-Marquez, M., Barrón, M.G., Merenciano, M., Villanueva-Cañas, J.L., Horváth, V., Fiston-Lavier, A.S., Luyten I., Venkataram, S., Quesneville, H., Petrov, D.A. and J. González. *Stress response, behavior, and development are shaped by transposable element-induced mutations in Drosophila*. PLoS Genetics 15 (2): e1007900 (2019). <https://doi.org/10.1371/journal.pgen.1007900>.
7. Mateo, L., **Rech, G.** and González J. *Genome-wide patterns of local adaptation in Western European Drosophila melanogaster natural populations*. Scientific Reports, 8:16143 (2018). [doi: 10.1038/s41598-018-34267-0](https://doi.org/10.1038/s41598-018-34267-0).
8. Agostini, R., Postigo, A., Campos-Bermudez, V., Rius, S., **Rech G.E.** and Vargas, W. *Long-lasting primed state in maize plants. Salicylic acid and steroids signaling pathways as leading actors for the early activation of immune responses in silks*. Mol Plant Microb Interact., 32(1):95-106 (2018). [doi: 10.1094/MPMI-07-18-0208-R](https://doi.org/10.1094/MPMI-07-18-0208-R).
9. Villanueva-Cañas, J. L.\*, **Rech, G. E.\***, de Cara, M. A. R. and González, J. *Beyond SNPs: how to detect selection on transposable element insertions*. Methods Ecol Evol; 8: 728–737 (2017). [doi:10.1111/2041-210X.12781](https://doi.org/10.1111/2041-210X.12781).  
\*Authors contributed equally to this paper.
10. Saludes, V., Salvatierra, K., **Rech, G.**, Sumoy, L., Artacho A., Morillas, R.M., Berenguer, M., López-Labrador, F.X. and Martró, E. *Assessment of the Illumina MiSeq massively parallel sequencing platform for simultaneous analysis of Hepatitis C virus resistance to all direct-acting antivirals combination regimens*. Journal of Clinical Virology, Vol. 82, S15-S16 (2016). <https://doi.org/10.1016/j.jcv.2016.08.028>.
11. Vargas, W.A., Sanz-Martin, J.M., **Rech, G.E.**, Armijos-Jaramillo, V.D., Rivera, L.P., Echeverria, M.M., Díaz-Mínguez, J.M., Thon, M.R., and Sukno, S.A. *A fungal effector with host nuclear localization and DNA-binding properties is required for maize anthracnose development*. Molecular Plant-Microbe Interactions; 29(2): 83-95 (2016). <https://doi.org/10.1094/MPMI-09-15-0209-R>.
12. **Rech, G.E.**, Vilaplana, C., Velasco, J., Pluvinet, R., Comas, I., Sumoy, L. and Cardona, P.J. *Draft Genome Sequences of Mycobacterium sensu lato Type Strain DSM-45070 and the Nonpathogenic Strain Manresensis, Isolated from the Bank of the Cardener River in Manresa, Catalonia, Spain*. Genome Announcements; 3(1):e01485-14 (2015). [doi: 10.1128/genomeA.01485-14](https://doi.org/10.1128/genomeA.01485-14).
13. **Rech, G.E.**, José M. Sanz Martín, Serenella A. Sukno, Maria Anisimova and Michael R. Thon. *Natural Selection on Coding and Noncoding DNA Sequences Is Associated with Virulence Genes in a Plant Pathogenic Fungus*. Genome Biol and Evol; 6 (9): 2368-2379 (2014). <https://doi.org/10.1093/gbe/evu192>.
14. Baroncelli, R., Sanz-Martin, J.M., **Rech, G. E.**, Sukno, S.A., and Thon, M.R. 2014. *Draft Genome Sequence of Colletotrichum sublineola, a Destructive Pathogen of Cultivated Sorghum*. Genome Announcements; 2(3): e00540-14 (2014). [doi: 10.1128/genomeA.00540-14](https://doi.org/10.1128/genomeA.00540-14).
15. **Rech, G.E.**, Vargas, W.A., Sukno, S.A. and Thon, M.R. *Identification of positive selection in disease response genes within members of the Poaceae*. Plant Signaling & Behavior; 7(12):1667-75 (2012). <https://doi.org/10.4161/psb.22362>.
16. O'Connell R.J., Thon M.R., ..., **Rech G.**, ..., Schulze-Lefert P., Ma L.J. and Vaillancourt L.J. *Life-style transitions in plant pathogenic Colletotrichum fungi deciphered by genome and transcriptome analyses*. Nature Genetics; 44, 1060–1065 (2012). <https://doi.org/10.1038/ng.2372>.
17. Vargas, W.A., Sanz Martín, J.M., **Rech, G.E.**, Rivera, L.P., Benito, E.P., Díaz-Mínguez, J.M., Thon, M.R. and Sukno S.A. *Plant defense mechanisms are activated during biotrophic and necrotrophic development of Colletotrichum graminicola in maize*. Plant Physiology; 158(3):1342–1358 (2012). <https://doi.org/10.1104/pp.111.190397>
18. Mariotti, J. A., Machado Assefh, C.R., **Rech, G.**, Fontana, P.D., Collavino, N.G., Pocovi, M.I., Rago, A.M., Daz, M.E. *Avances en la investigación de la relación patógeno-hospedante y de la resistencia genética a enfermedades de la caña de azúcar en Argentina*. Journal of Basic & Applied Genetics; 22,1:14. ISSN: 1852-6233 (2011) ([link](#))
19. Pocovi, M. I.\*, **Rech, G. E.\***, Collavino, N. G., Caruso, G. B., Ríos, R. and Mariotti, J. A. *Molecular Diversity of Puccinia melanocephala Populations*. Journal of Phytopathology; 158: 769–775 (2010). <https://doi.org/10.1111/j.1439-0434.2010.01698.x>. \*Authors contributed equally to this paper.
20. Rago, A., Perez Gómez, S., Fontana, P.D., Fernández de Ullivarri, E., Sopena, R.A., Felipe, A., **Rech, G.**, Pocovi, M. *Diagnóstico de las enfermedades sistémicas que afectan la caña de azúcar*. In: Cultivos Industriales. Informe del Programa Nacional de Cultivos Industriales 1ªed. – Buenos Aires: Ed. INTA, pp. 52- 59 (2010). ([link](#))
21. Pocovi, M., Collavino, N.G., Caruso, G., Diaz, M., Locatelli, F., **Rech, G.**, Machado Assefh, C., Fernández, C., Rago, A.M., Ríos, R., Díaz, D., Pacheco, M.G., Mariotti, J.A., Canavides, A. *Variabilidad genética en caña de azúcar*. In: Cultivos Industriales. Avances 2006/2009. Informe del Programa Nacional de Cultivos Industriales 1ªed. – Buenos Aires: Ed. INTA, pp. 63-64 (2010). ([link](#))

## CONFERENCES

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1. **Rech G.E.**, R. Goldfeder, R. Maurya, A. V. Danilov and CL. Wei. *DNA methylation signatures in solid and liquid biopsies*. AGBT 2022, Orlando, FL, USA.
2. Horvath V., Salces-Ortiz J., **Rech G.E.**, Guirao S., González J. *Unravelling the transcriptomic and physiological bases of desiccation tolerance in natural European D. melanogaster populations*. 62nd Annual Drosophila Research Conference. Online, Apr. 2021.
3. Horvath V., Salces-Ortiz J., **Rech G.E.**, Guirao S., González J. *Characterizing the molecular basis of desiccation resistance in Drosophila melanogaster European populations and the role of transposable elements in this process*. European Society for Evolutionary Biology. Turku, Finland. Aug. 2019.
4. *Selected Talk: Unravelling transposable element diversity using long-read sequencing*. Genome Science Conference, Nottingham, UK. 5 Sep. 2018.
5. **Rech, G.E.**, Barrón, M.G., Villanueva-Cañas, J.L., Bogaerts Márquez, M., Horváth, V. and González, J. *New approaches for understanding adaptation: The role of Transposable Elements in Drosophila melanogaster*. XVI Congress of the European Society for Evolutionary Biology (ESEB). Groningen, The Netherlands. Aug. 2017.
6. Agostini, R., Postigo, A., Campos-Bermudez, V., Rius, S., **Rech, G.E.** and Vargas, W.A. *Trichoderma, a tool of agroindustrial interest for biological control of Fusarium verticillioides*. XXXI Argentinian Plant Physiology Meeting. Corrientes, Argentina. Nov. 2016.
7. **Rech, G.E.**, Sanz-Martín, J.M., Sukno, S.A., Thon, M.R. *A genome-wide survey of mutations in wild isolates of the maize pathogen Colletotrichum graminicola*. XVIII Congreso Nacional de la Sociedad Española de Fitopatología. Palencia, Spain. Sep 2016. p.p. 68.
8. Martró, E., Saludes, V., Salvatierra, K., **Rech, G.**, Sumoy, L., Artacho, A., Morillas, R.M., Berenguer, M., López-Labrador, F.X. *Assessment of the Illumina MiSeq massive parallel sequencing platform for simultaneous analysis of Hepatitis C virus resistance to all direct-acting antivirals combination regimes*. 19th Annual Meeting of the European Society for Clinical Virology, Lisbon, Portugal. Sep 2016. p.p. 79.
9. Pluvinet, R., **Rech, G.**, Sumoy, L. *Optimization of RNA isolation from small volumes of serum to enable small RNA sequencing*. 49th European Human Genetics Conference (ESHG). Barcelona, Spain. May 2016. P16.79.
10. Ramos, L., Santin, S., **Rech, G.**, Bassas, L., Mata, A., Sumoy, L., Larriba, S. *RNA sequencing analysis of human sperm samples*. 49th European Human Genetics Conference (ESHG). Barcelona, Spain. May 2016. P14.053
11. **Rech, G.E.**, Sanz Martín, J.M., Sukno, S.A, Thon, M.R. *The genome-wide mutational landscape of wild isolates of the maize pathogen Colletotrichum graminicola*. 13th European Conference on Fungal Genetics. Paris, France. Apr 2016. pp.207.
12. **Rech, G.E.**, Sanz Martín, J.M., Sukno, S.A, Thon, M.R. *Structural and gene content variation among strains of the maize anthracnose fungus Colletotrichum graminicola*. 28th Fungal Genetics Conference. Pacific Grove, Asilomar California, EEUU. Mar 2015. pp. 148.
13. Vargas, W.A., Sanz-Martín, J.M., **Rech, G.E.**, Thon, M.R., Sukno, S.A. *Genome-wide identification of nuclear effectors defines a novel family of pathogenicity factors in Colletotrichum spp. with host nuclear localization*. 28th Fungal Genetics Conference. Pacific Grove, Asilomar California, EEUU. Mar 2015. pp. 134.
14. **Rech, G.E.**, Pacheco, R., Sukno, S.A., Thon, M.R. *Structural and gene content variation among strains of the maize anthracnose fungus Colletotrichum graminicola*. 10th Annual DOE Joint Genome Institute, Genomics of Energy & Environment Meeting. Walnut Creek, California, EEUU. Mar 2015. pp.99.
15. **Rech, G.E.**, Sanz Martín, J.M., Anisimova, M., Sukno, S.A, Thon, M.R. *Patterns of natural selection in coding and noncoding DNA sequences are associated with virulence in the plant pathogen Colletotrichum graminicola*. 12th European Conference on Fungal Genetics. Sevilla, Spain. Mar 2014.
16. **Rech, G.E.**, Sanz Martín, J.M., Armijos, V.A., Vargas, W.A., González Fuentes, M., Sukno, S.A, Thon, M.R. *Comparative genomics of Colletotrichum graminicola isolates sheds light on the mechanisms of pathogenicity*. 12th European Conference on Fungal Genetics. Sevilla, Spain. Mar 2014.
17. *Selected Talk: Looking for Darwin in the plant-pathogen interactions*. Centro Hispano-Luso de Investigaciones Agrarias, University of Salamanca, Salamanca, Spain. Oct 2013.
18. *Selected Talk: A high throughput scans for positively selected genes in filamentous fungi*. MICELIO meeting: Spanish network of filamentous fungi researchers. Pamplona, Spain. Jul 2010.
19. **Rech, G.**, Pocoví, M., Collavino, G., Caruso, G., Machado C., Pacheco, G., Rago, A., Mariotti, J.A.. *Population variability of sugarcane rust (Puccinia melanocephala Sydow H & P) in the NOA*. XXXVII National Conference of Genetics. Tandil, Buenos Aires. Argentina. Sep 2008. ISSN: BAG 1666-0390 pp. S-164.
20. Pocoví M., Collavino, G., **Rech, G.**, Caruso, G., Machado Assefeh, C., Ríos, R., Mariotti, J.A. *Comparative study of the discriminatory capacity of isozyme and SSR for the establishment of genetic relationships among sugarcane varieties*. XXXVII National Conference of Genetics. Tandil, Argentina. Sep 2008. ISSN: 1666-0390 BAG pp. S-153.
21. Machado Assefeh C., Daz, M., Collavino, G., Pocoví, M., Caruso, G., **Rech, G.**, Rago, A., Mariotti, J.A. *Effectiveness of peroxidase activity quantification method for detection of resistant genotypes of sugarcane to Puccinia melanocephala Sydow H & P*. XXXVII National Conference of Genetics. Tandil, Buenos Aires Argentina. Sep 2008. ISSN: BAG 1666-0390 pp. S-146.

## TEACHING, MENTORING, EVENTS ORGANIZATION

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- Organizer of the Computational Sessions for the 2022 Long Read Sequencing Workshop. The Jackson Laboratory for Genomic Medicine, CT, USA. [www.jax.org/longread](http://www.jax.org/longread) 2021-2022
- Instructor Bioinformatics showcase sessions: Fundamental analyses of Nanopore and PacBio sequencing data. Long Read Sequencing Workshop. The Jackson Laboratory for Genomic Medicine, CT, USA. May 2022
- Instructor in the Advanced course in Phylogenomics and Population Genomics: Inference and Applications, 16th edition. Topics: High-throughput sequencing (HTS) data and Genome-wide scans for selection. Universitat de Barcelona, Spain. July 2019
- Mentor of PhD candidate María Bogaerts-Márquez (currently Postdoc at the Centre de Biologie pour la Gestion des Populations, Montpellier, France). 2017-2020
- Mentor of PhD candidate Santiago Radó (currently Bioinformatician at Sequentia Biotech, Spain). 2018-2020
- Mentor of Master student Sergio Emilio Quispe Mayta. *Genetic analysis for identification and forensic affiliation in the Bolivian population*. Universitat de Barcelona, Spain. 2018
- Instructor in the Workshop Differential Gene Expression Analysis. AdaptNET. University of Valencia, Spain. Workshop on Adaptation Bioinformatics. March 2017
- Teaching Assistant Bioinformatics and Computational Genomics. University of Salamanca, Spain. 2010-2014
- Teaching Assistant Microbiology and Genetics Department. University of Salamanca, Spain. 2010-2014
- Teaching Assistant Physics. National University of Salta, Argentina. 2008-2009
- Teaching Assistant Genetics. National University of Salta, Argentina. 2006-2008
- Mentor of high school scholarship students. Ministry of Education of Salta, Argentina. 2006-2007
- Mentor of College freshmen students (CILEU 2008). National University of Salta, Argentina. 2008
- Teaching Assistant Introduction to Biology. National University of Salta, Argentina. 2004-2005

## SCIENCE OUTREACH

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- *Public Debate* about Planetary Health. Festa de la Ciència 2019. Barcelona. 2019
- *PRBB Biojunior*. Participation as voluntary in the 2017 and 2018 editions. 2017-2018
- *PRBB Open Day*. Participation as voluntary in the activity: "Melanogaster, catch the fly!": Europe's leading citizen science network on adaptation genomics. 2016
- Blog post at *Methods.blog*, the official blog of Methods in Ecology and Evolution: *Getting Serious About Transposable Elements* (<https://methodsblog.wordpress.com/2017/06/26/transposable-elements/>). 2017

## LANGUAGES

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- Spanish Native speaker
- English Professional proficiency
- Catalan Professional working proficiency