CURRICULUM VITAE ABREVIADO (CVA)

Part A. PERSONAL INFORMATION

First name	David		
Family name	Cánovas López		
e-mail		URL Web	
Open Researcher and Contributor ID (ORCID) (*)			

(*) Mandatory

A.1. Current position

Position	Catedrático de Universidad		
Initial date	2025		
Institution	UNIVERSITY OF SEVILLE		
Department/Center	Dept. Genetics	Faculty of Biology	
Country	Spain	Phone number	
Key words	Fungal genetics, conidiation, fungal development, fungal reproduction		

A.2. Previous positions (research activity interuptions, indicate total months)

Period	Position/Institution/Country/Interruption cause
2021	Six months sabbatical, Dept. of Biosystems Science and Engineering, ETH, Switzerland
2015-2017	Visiting professor at BOKU-Vienna, Austria
2008-2012	'Ramón y Cajal' researcher, University of Sevilla, Spain
2007	Post-doctoral fellow. Plant pathogen and fungal morphogenesis. National Center for Biotechnology (CNB-CSIC). Madrid. Spain
2003-2006	Post-doctoral fellow. Transcriptional regulation in a fungal human pathogen. Univ. Melbourne. Australia
1999-2003	Post-doctoral fellow. Environmental microbiology. National Center for Biotechnology (CNB-CSIC). Madrid. Spain

A.3. Education

PhD, Licensed, Graduate	University/Country	Year
Bachelor in Pharmacology	University of Seville, Spain	1994
PhD, Cellular and Molecular Biology	University of Seville, Spain	1999

Part B. CV SUMMARY *(max. 5000 characters, including spaces)*

I started my lab in 2008 in the Dept of Genetics (University of Sevilla) under a "Ramón y Cajal" contract after postdoctoral stays in the National Center for Biotechnology CNB-CSIC (1999-2003 and 2007) and the University of Melbourne, Australia (2003-2006). I was awarded with the prestigious Marie Sklodowska-Curie Outgoing Fellowships to receive training in fungal genetics. Additionally, I was a visiting scholar at BOKU-Vienna (Austria) running a Lise Meitner grant from the Austrian FWF resulting in the first fungal nitric oxide synthesis route published. Recently I have received training in mathematical modeling and programming including R, MATLAB and Python (Pandas, Numpy, Matplolib, Sklearn). In 2021 I did a sabbatical in the Dept. of Biosystems Science and Engineering (ETH-Zürich), where I started training in Systems Biology. During my sabbatical we evolved the Opto-T7RNAP, a split T7 RNA polymerase coupled with an improved blue light-inducible VIVID system from *Neurospora crassa*, to obtain 20 variants in *E. coli* with diverse light sensitivities. I applied unsupervised machine learning techniques to time-series expression data sets obtained by robotic-guided

fluorometry with the aim of characterizing and classifying the 20 mutant variants. We are now preparing the second revised version of the ms (NCOMMS-22-53318A. bioRxiv: https://doi.org/10.1101/2022.11.14.516313). Last year I developed computational methods to analyze ribosome profiles for a project employing ribosome profiling to study the transduction responses to changes in the availability of carbon sources. I also developed an innovative computational strategy by employing mathematical modeling to obtain quantitative fungal growth features in high-throughput formats, which has revealed new insights into fungicide resistance in *Aspergilllus fumigatus* (I am currently preparing the manuscript for submission). To continue my training in systems biology, this spring I am planning to do a second sabbatical in the lab of Prof. T. Hwa in the Dept. of Physics at UC San Diego (USA). This stay is funded by the Senior Modality of the Program for mobility stays of professors and researchers of Ministry of Science, Innovation and Universities (ref PRX23/00359). The main aim of the stay is to learn how to apply quantitative microbiology to our projects with the overall goal to attain quantitative, predictive understanding of living systems. A similar approach will be applied in Task 3 of our grant proposal.

I have been the PI of five grants funded by the MINECO, and have also secured funding from the regional governments (Comunidad de Madrid and Junta de Andalucía), DOE-Joint Genome Institute (USA) and the Austrian FWF. I had a contract with industry (Abengoa-ABNT). In addition to my research publications, I have two patents to produce compounds of biotechnological interest using bacterial supernatants. I have supervised six PhDs of which three have already finished (all with Cum Laude), and 10+ Master students.

I am a seasoned expert in fungal genetics, with expertise in signaling, fungal development, and morphogenesis. Part of this work is highlighted in our recent review in *Microbiology and Molecular Biology Reviews* (revised version in preparation). I have participated in several international consortia focused on the characterization of fungal genomes, resulting in publications in high-impact journals such as *Current Biology*, *Genome Biology*, and *Studies in Mycology*. Currently, we are involved in two additional consortia: one focusing on the *fumigati* section and another covering the genome sequences of approximately 300 *Aspergillus* species. I also led one such consortium, funded by the DOE-Joint Genome Institute, which employed whole-genome sequencing (WGS) to characterize evolved populations of *Aspergillus*. Additionally, I contributed to a consortium investigating the role of DNA methylation in fungal development using early-divergent fungi (*Lax et al., Nature Communications, 2024*). My lab maintains active collaborations with research groups at UPV (Spain), the University of Macau (Macau), Institut Pasteur (France), BOKU-Vienna (Austria), and the University of Wisconsin-Madison (USA).

At the international level I participate actively in the research community life. As examples, I belong to the Editorial Boards of Studies in Mycology, Frontiers in Microbiology, Fungal Genetics & Biology, and the new journals Frontiers in Fungal Biology, and Fungal Biology and Biotechnology. I am also Associate Editor of Microbial Cell Factories and Biotechnology for Biofuels and Bioproducts. I am also a Faculty Member of F1000prime-section for Microbiology (currently H1 Connect). I was member of the *Aspergillus* Genomes Research Policy Committee (2014-24) that is in charge of managing the main *Aspergillus* genomes in public repository, and organizing the annual *Aspergillus* Conference.

Part C. RELEVANT MERITS *(sorted by typology)*

C.1. Publications (ten selected publications out of 22, not including two manuscripts in revision, in the last ten years)

¶ denotes co-first authors

* denotes co-corresponding authors

1. Steenwyk JL, Knowles S, Bastos RW, **Cánovas D** (12/20), Goldman GH and Rokas A. (2024) Evolutionary origin and population diversity of a cryptic hybrid pathogen. ***Nat Comm*** Sep 28;15(1):8412***.***
2. Cea-Sánchez S, Martín-Villanueva S, Gutiérrez G, **Cánovas D*,** Corrochano LM*. (2024) VE-1 regulation of MAPK signaling controls sexual development in *Neurospora crassa*.

mBio. Sep 16;15(10):e0226424..

3. Lax C, Mondo S, Osorio-Concepción M, **Cánovas D (17/24)**, Corrochano L, Nicolás F, Garre V. (2024) Symmetric and asymmetric DNA N6-adenine methylation regulates different biological responses in Mucorales. ***Nat Comm***. Jul 18;15(1):6066.
4. Cea-Sánchez S, Corrochano-Luque M, Gutiérrez G, Glass LN, **Cánovas D*,** Corrochano LM* (2022) Transcriptional regulation by the velvet protein VE-1 during asexual development in the fungus *Neurospora crassa.* ***mBio.*** Aug 30;13(4):e0150522.
5. **Cánovas, D.*** (2022) The fungal protein Mes1 is required for morphogenesis and virulence in the dimorphic phytopathogen *Ustilago maydis* ***J. Fungi***. 8(8): 759.
6. Franco-Cano A, Marcos AT, Strauss J and **Cánovas D.*** (2021) Evidence for an arginine-dependent route for the synthesis of NO in the model filamentous fungus *Aspergillus nidulans.* ***Environ. Microbiol****.* 23(11):6924-6939.
7. Álvarez-Escribano I, Sasse C, Bok JW, **Cánovas D* (16/16)** 2019. Genome sequencing of evolved aspergilli populations reveals robust genomes, transversions in *A. flavus*, and sexual aberrancy in non-homologous end-joining mutants. ***BMC Biology*** Nov 11;17(1), 88.
8. Ojeda-López M, Chen W, Eagle CE, Gutiérrez G, Jia WL, Swilaiman SS, Huang Z, Park H-S, Yu J-H, **Cánovas D*** and Dyer PS* (2018). Evolution of asexual and sexual reproduction in the aspergilli. ***Stu. Mycol.*** 91:37-59.
9. Marcos AT, Ramos MS, Carmona L, Marcos JF, Strauss J and **Cánovas D*** (2106) Nitric oxide synthesis by nitrate reductase is regulated during development in *Aspergillus.* ***Mol. Microbiol.*** 99(1):15-33.
10. **Cánovas D***, Marcos AT, Gacek A, Ramos MS, Gutiérrez G, Reyes-Domínguez Y and Strauss J. (2014) The histone acetyltransferase GcnE (GCN5) plays a central role in the regulation of *Aspergillus* asexual development. ***Genetics*** 197(4):1175-1189

C.2. Congress.

Invited talks:

1 Nitric oxide (NO) is a morphogenetic signal in fungi. The 8th International *Aspergillus* Meeting. 2011. Asilomar. USA.

2 Genome projects for *A. nidulans* and Zygomycetes. Eurofung Big Data Meeting. 2016. Berlin. Germany.

3 Genome wide consequences of the deletion of the Aspergilli non-homologous end joining (NHEJ) DNA repair mechanism. The 14th International *Aspergillus* Meeting. 2017. Asilomar. USA.

4 Role of the urea cycle in the synthesis of nitric oxide. 29th Fungal Genetics Conference. 2017. Asilomar. USA.

5 Regulation of asexual and sexual development by the velvet complex in *Neurospora crassa*. Neurospora 2021. Navasota. USA.

6 Organelle-dependent synthesis of nitric oxide in fungi. European Conference on Fungal Genetics 16. 2023. Innsbruck, Austria.

Conference organization:

1 Local Organizing Committee of the European Conference on Fungal Genetics (2014).

2 Organizing Committee of the International *Aspergillus* Meeting (Asperfest) from 2015 to 2024.

3 Chair of Plenary Session 3 – Metabolism and Development, in the 16th European Conference on Fungal Genetics. 2023. Innsbruck, Austria.

C.3. Research projects.

1 **Project**. Transcriptional regulation of sexual development and fertility by velvet proteins in the fungus *Neurospora crassa*. PIs: David Cánovas and Luis Corrochano. PID2021-128001OB-I00. MICINN (2022-2025).

2 **Project**. New strategies based on protein synthesis for an optimized fungal-based circular economy. PIs: David Cánovas and Jesús de la Cruz. TED2021-129601B-I00. MICINN (2022-2024).

3 **Project**. Regulation of transcription by light: mechanism of fungal photoadaptation. PI: Luis Corrochano. P20_00622. Junta de Andalucia (Regional government).

4 **Project**. Regulation of VE-1 degradation, nuclear entry, and complex formation during development and carotenoid biosynthesis in *Neurospora crassa*. PIs: David Cánovas and Luis Corrochano. RTI2018-098636-B-I00. MICINN (2019-2021).

5 **Project**. The regulation of the regulator: stability and localization of velvet during conidiation and carotenogenesis in *Neurospora*. PIs: David Cánovas and Luis Corrochano. BIO2015-67148-R. MINECO (2016-2018).

6 **Project**. Nitric oxide signalling controlling fungal reproduction. PI: David Cánovas. FWF Lise Meitner grant M01693-B22 (2015-2017).

7 **Project**. Global genomic consequences of the deletion of the Aspergilli non-homologous end joining DNA repair mechanism employed as a genetic tool world-wide. Coordinator: David Cánovas. 1401 (CSP2014). DOE-Joint Genome Institute.

C.4. Contracts, technological or transfer merits, Include patents and other industrial or intellectual property activities (contracts, licenses, agreements, etc.) in which you have collaborated. Indicate: a) the order of signature of authors; b) reference; c) title; d) priority countries; e) date; f) Entity and companies that exploit the patent or similar information, if any.

Contract. Regulation of hydrolytic genes in Myceliophthora termophyla. IP: David Cánovas. ITC-20111060. Abengoa BioEnergía Nuevas Tecnologías (ABNT) – CDTI (2012 – 2014).

Patent. Escobar-Niño A, Sánchez-Barrinuevo L, **Cánovas D,** Mellado E, González-Benjumea A, López-López O, Maya Castilla I, Fernández-Bolaños Guzmán JM (P201400374) Biotransformaciones de azúcares y polifenoles naturales utilizando cepas microbianas de los géneros *Terribacillus*, *Bacillus, Enterobacter* y *Pseudomonas* para producir compuestos de interés en la industria farmacéutica y alimentaria. European. 5th May 2014. Univ. de Sevilla

Patent. Mellado E, Escobar-Niño A, **Cánovas D,** Luna D (P201300039) Cepa microbiana *Terribacillus sp.* AE2B122 con capacidad para llevar a cabo reacciones de transesterificación y usos de la misma. 11th January 2013. Spain. Univ. de Sevilla y Univ. de Córdoba.