CURRICULUM VITAE ABREVIADO (CVA)

***IMPORTANT* – The Curriculum Vitae cannot exceed 4 pages. Instructions to fill this document are available in the website.**

Part A. PERSONAL INFORMATION

First name	Iñaki		
Family name	Comas Espadas		
Gender (*)	Male	Birth date (dd/mm/yyyy)	05/05/1979
Social Security, Passport, ID number	24360711P		
e-mail	icomas@ibv.csic.es	tgu.ibv.csic.es	
Open Researcher and Contributor ID (ORCID) (*)		0000-0001-5504-9408	

(*) Mandatory

A.1. Current position

Position	Profesor de Investigación		
Initial date	01/01/2022		
Institution	Consejor Superior de Investigaciones Científicas		
Department/Center	Unidad de Genómcia de la Tuberculosis	Instituto De Biomedicina de Valencia	
Country	España	Teleph. number	963393773
Key words	Tuberculosis, microbial genomics, evolutionary biology, public health		

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

Period	Position/Institution/Country/Interruption cause
22/02/2021-31/12/2022	Investigador Científico
01/03/2016-21/02/2021	Científico Titular CSIC
01/01/2013-29/02/2016	Ramón y Cajal FISABIO
01/09/2011-31/08/2013	Marie Curie Postdoctoral Contract FISABIO
25/03/2008-31/08/2011	Career Development Fellowship Medical Research Council
01/01/2003-11/01/2008	FPU PhD researcher

A.3. Education

Year	*University*	*Degree*	*Title*
2002	*Valencia*	*First degree*	*Biology*
		Masters (if appropriate)	
2008		*PhD*	*Biology*

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

Dr. Comas received his PhD in Biological Sciences from the University of Valencia in 2008. He was a postdoctoral researcher at the National Institute of Medical Research (NIMR-Medical Research council, London 2008-2011). Then he moved back to Spain to FISABIO (2011-2016) first with a Marie Curie Il Fellowship and later with a Ramón y Cajal position. He joined the IBV-CSIC in March 2016 as Científico titular where he is the PI of the Tuberculosis Genomics Unit. Since 2022 he is Profesor de Investigación CSIC. Iñaki Comas has a HI of 35, with more than 140 publications many of those in high impact journals (>10 IF) reflected in 3632 citations in the last five years (Scopus ID 57204252102)

Main research lines. The TGU aims at using genomics to dissect the pathogen disease mechanisms of infection and transmission. Most of our work is the result of multidisciplinary collaborations. During 2020 and 2021 we have led the SARS-CoV-2 sequencing efforts in Spain. **Range of research topics.** Our studies are leading to breakthrough insights in our understanding of antigenic variation (Nat Genet. 2010), drug resistance and diagnostics (Nat Genet. 2012, Com Biology 2022, The Lancet Microbe 2021, PNAS 2022), evolution with the human host (Nat Genet. 2013, Current Biology 2015, PNAS 2022), identification of genomic determinants of virulence (Sci Adv 2019, 2019, Nat Com 2019) and on transmission (eLife 2022, PloS Medicine 2019, Bioinformatics 2019, BMC Biology 2020, Nat Com 2019, Nat Com 2021). We are also studying SARS-CoV-2 evolution in Spain including the first (Nature Genetics) and second wave (Nature). Finally we work on drug resistance in *H. pylori* as part of the international consortium led by NIC-NIH.

Excellence in TB research. Among many contributions we were the first i. to identify compensatory mutations with clinical relevance; ii. *M. tuberculosis* epitopes are show no immune evasion; iii. co-evolution of pathogen and host using genomics; iv. subclinical TB transmission; v. role of past epidemics in current TB settings; vi evolutionary trajectories to identify novel regions under selective pressure; vi large scale culture-free genomic epidemiology and vi. Spain genomic surveillance of SARS-CoV-2

PTI Salud Global. As of January 2021 Iñaki Comas is co-coordinator of the CSIC Global Health Platform coordinating 110 CSIC research groups on infectious diseases with a budget of 57 milliones EU (2021-2023).

Projects. We have secured almost 8 million funding since 2016 including ERC Starting Grant and Consolidator Grant, La Caixa, National (MINECO SAF, Explora, Network, Equipment) , Regional (GVA Consolidables, Prometeo), Fondo COVID-19 Instituto de Salud Carlos III ,CSIC-COVID, and La Caixa.

Public health impact, knowledge transfer and capacity building. At the local level we have established a network our TB work has contributed to Valencia Region TB control helping on diagnosing difficult cases and outbreaks (60 reports). At the translational level we use genomics approaches for surveillance and diagnosis in high-burden countries and implement capacity building through courses/training. Our research and knowledge has contributed to the first catalogue of diagnostic drug resistance mutations of the WHO (co-authors) showing the transferability of our research and global impact. **SARS-CoV-2**. Iñaki Comas is also part of the Valencia Expert group on COVID-19 vaccines (ProVaVac) as well as advisor for SARS-CoV-2 variants risk assessment for the Spanish Health Ministry.

Societal impact. Iñaki Comas has been intensely communicating risk of SARS-CoV-2 variants to the general audience through news outlets 2020-2021: 225 printed press, 41 radio, 54 TV, 1307 digital media. An article on SARS-CoV-2 transmission in The Conversation had 300,000 audience.

International recognition. The group is recognized as a world expert on TB genomics. We participate in the WHO Seq &Treat consortia as advisor to develop genomics for drug resistance surveillance and diagnostics. Iñaki Comas is part of the European Society for Mycobacteriology Board and organizer of the ESM2019 meeting in Valencia (285 attendees), TB Science (3300 attendees) and the PTI Salud Global (250 attendees). Iñaki Comas is regularly invited to national and international conferences and centres. Iñaki Comas is reviewer for major funding agencies (H2020, ERC, CNRS, Welcome Trust, Medical Research Council) and publications (Science, Nature, Nature Genetics/microbiology/medicine, PNAS, Lancet ID).

Excellence on training phD researchers and Unit. Out students hold grants from FPU, FPI, CONACYT, Generalitat Valenciana, EMBO short term and multiple travel (5), talks (4), poster awards (3) showing the excellence in training and research environment of our unit. Our international connections also contributes to their training and recognition what helps for the development of their careers. Finished PhD students hold positions as Ramón y Cajal, Margarita Salas and Postdoctoral SwissTPH.

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

C.1. Publications *(see instructions)*

(selected based on impact/citations/relevance from a total of 140, 1 Spectrum Journal accepted IF 9; Lancet Global Health under review IF 38.9, Lancet Microbe under review IF 84)

Cancino-Muñoz I, López MG,; Valencia TB Working Group; **Comas I.** Population-based sequencing of *Mycobacterium tuberculosis* reveals how current population dynamics are shaped by past epidemics. **Elife. 2022** 11:e76605. doi: 10.7554/eLife.76605. IF: 8.14

Chiner-Oms Á, López MG, Moreno-Molina M, Furió V, **Comas I.** Gene evolutionary trajectories in *Mycobacterium tuberculosis* reveal temporal signs of selection. **Proc Natl Acad Sci U S A. 2022** Apr 26;119(17):e2113600119. doi: 10.1073/pnas.2113600119. IF: 12.779

López MG, Chiner-Oms Á, et al. **Comas I.** The first wave of the COVID-19 epidemic in Spain was associated with early introductions and fast spread of a dominating genetic variant. **Nat Genet. 2021** Oct;53(10):1405-1414. IF 38.33

Furió V, …**Comas I.** An evolutionary functional genomics approach identifies novel candidate regions involved in isoniazid resistance in Mycobacterium tuberculosis. **Commun Biol. 2021** Nov 24;4(1):1322. IF 6.268

Moreno-Molina M, … **Comas I.** Genomic analyses of Mycobacterium tuberculosis from human lung resections reveal a high frequency of polyclonal infections. **Nat Commun. 2021** May 11;12(1):2716. IF: 17.69

Hodcroft EB, ..,**Comas I**, González-Candelas F; SeqCOVID-SPAIN consortium, Stadler T, Neher RA. Spread of a SARS-CoV-2 variant through Europe in the summer of 2020. **Nature. 2021** Jul;595(7869):707-712. IF 49.962

Goig G…**Comas I.** Whole-genome sequencing of Mycobacterium tuberculosis directly from clinical samples for high-resolution genomic epidemiology and drug resistance surveillance: an observational study. **The Lancet Microbe 2020**. IF: 86.208

Xu Y*, Cancino-Muñoz* I……Colijn C*, **Comas I***. High-resolution mapping of tuberculosis transmission: Whole genome sequencing and phylogenetic modelling of a cohort from Valencia Region, Spain. **Plos Medicine 2019** * Contributed equally IF 11.048

Chiner-Oms A,……, **Comas I.** Genome-wide mutational biases fuel transcriptional diversity in the Mycobacterium tuberculosis complex. **Nat Com. 2019**. Sep 5;10(1):3994. IF 11.878

Meehan CJ, …39 authors… **Comas I***, Van Rie A* . Whole genome sequencing of Mycobacterium tuberculosis: current standards and open issues. **Nature Reviews Microbiology 2019** Sep;17(9):533-545.***contributed equally** IF 34.648

Chiner-Oms A, Sánchez-Busó L, Corander J, Gagneux S, Harris S, Young D, González-Candelas F, **Comas I.** "Genomic determinants of the emergence and spread of the Mycobacterium tuberculosis complex" **Science Advances, 2019**:eaaw3307). IF 12.804

Comas, I. and 15 others (2015). Population genomics of Mycobacterium tuberculosis in Ethiopia contradicts the virgin soil hypothesis for human tuberculosis in Sub-Saharan Africa. Curr. Biolo. 25(24), 3260-3266. **(1st author and Corresponding).** IF 8.983

Comas, I. and 16 others (2013). Out-of-Africa migration and Neolithic coexpansion of Mycobacterium tuberculosis with modern humans. Nat Genet, 45(10), 1176–**1182 (1st author and Corresponding).** IF 29.648

Comas, Iñaki… Gagneux, S. (2012). Whole-genome sequencing of rifampicin-resistant Mycobacterium tuberculosis strains identifies compensatory mutations in RNA polymerase genes. Nature Genetics, 44(1), 106–110. IF 35.209

Comas, Iñaki, … Gagneux, S. (2010). Human T cell epitopes of Mycobacterium tuberculosis are evolutionarily hyperconserved. Nature genetics, 42(6), 498–503. IF 36.377

C.2. Congress, indicating the modality of their participation (invited conference, oral presentation, poster)

Invited conference. Fudan University, Shanghai **11/10/2017 China** -SHANGAI Current and future perspectives on the use of whole genome sequencing to understand the evolution and epidemiology of Mycobacterium tuberculosis

Invited conference. Institute of Tropical Medicine **(ITM) 26/04/2018** Belgium The genomic landscape of Mycobacterium tuberculosis complex across evolutionary timescales.

Invited conference. Pasteur Course on TB 09/10/2018 Shenzhen China The genomic landscape of Mycobacterium tuberculosis complex across evolutionary timescales.

Invited conference. Anniversary of the St Petersburg Pasteur Institute 03/12/2018 St Petersburgh Russia. Evolution of Mycobacterium tuberculosis: from within host evolution to global migration patterns.

Invited conference. HMRG European HIV seminars 22/06/2019 UCD Dublin. Whole Genome Sequencing for TB treatment and control: a game changer?

Invited conference. 17th European AIDS Conference. 8/09/ 2019 Basel. Whole Genome Sequencing for TB treatment and control: a game changer

Invited conference. 6th Research, Development, and Innovation Symposium on Bacterial and Fungal Infections Brasil 05/10/2020 Whole genome sequencing to understand drug resistance, epidemiology and evolution of M. tuberculosis Iñaki Comas

Invited conference. Congreso Nacional Multidisciplinar Covid-19 de las Sociedades Científicas de España Consorcio SeqCOVID: una perspectiva genómica de la pandemia en España COMUNICACIÓN DE CONGRESO-CONFERENCIA INVITADA II 12/04/2021

Invited conference. MESA REDONDA II Simposio del Observatorio de la Sanidad. Las lecciones de la Covid-19 13/09/2021del Val, Margarita; López-Collazo, Eduardo; Comas, Iñaki **Invited conference.** Mesa redonda: Lecciones de la Covid-19, ¿qué ha aprendido la ciencia sobre el virus?

Invited conference. Amsterdam TB Center 13/12/2021 Genomic diversity and evolution of Mycobacterium tuberculosis: from biology to global tuberculosis control

London School of Hygiene and Tropical Medicine Seminars 06/05/2021 Evolution of the Mycobacterium tuberculosis complex: from biology to global tuberculosis control Iñaki Comas

Invited conference. European Society of Mycobacteriology. ESM 42nd Annual Meeting. Bolonia 26/06/2022 TB and COVID-19: two sides of the same coin?

Invited conference. 24 Ciclo de Seminarios Severo Ochoa "Avances en Biología Molecular" Madrid. 16/09/2022 Genomic approaches for global health pathogens: from biology to infection

Invited conference. Genomic and Molecular Epidemiology of Tuberculosis: A Focus on Southeast Asia Bangkok, Thailand 26/10/2022 Recent major adavances in genomics of TB

C.3. Research projects

(shown selected, in addition also IP: Explora 2017, GVA consolidables 2017, RyC-2013, CIBER 2022-2023**)**

Referencia: Plataforma Temática Interdisciplinar Salud Global (CSIC) Título: PTI Salud Global IP: Iñaki Comas y Margarita del Val. Agencia: Ministerio de Ciencia fondos REC_EU Periodo: 2021-2022 Cantidad**: 51.721.000 EU**

Referencia: PTI Salud Global SGL2103008 Título: Vigilancia en tiempo real del SARS-CoV-2 IP: Santiago Elena Fito y Mireia Coscolla Agencia: Ministerio de Ciencia fondos REC_EU Periodo: 2021-2022 Cantidad al grupo de Iñaki Comas**: 1.162.658.72** Euros

Referencia: TB-TARGET Título: TB-TARGET : TB-TARGET A multidisciplinary approach to understand host and pathogen interactions to develop new strategies to target tuberculosis IP: Margarida Saraiva (i3S Porto) – **IP WP3-4:** Iñaki Comas Agencia: La Caixa Research Grant Periodo: 2021-2024 Cantidad: **998,404 EU (330,000 to Iñaki comas)**

Referencia: ERC Consolidator Grant Título: TB-RECONNECT IP: Iñaki Comas. Agencia: European Research Council. Periodo: 2021-2025 Cantidad: **2,723,027 euros**

Referencia: PID2019-104477RB-I00 Título:Prediciendo genotipos exitosos de Mycobacterium tuberculosis combinando genomica de poblaciones, aproximaciones funcionales y modelos de infeccion IP: Iñaki Comas. Agencia: Ministerio de Ciencia. Periodo: 2020-2023 Cantidad: **302,500 euros**

Referencia: COV20/00140 Título:Addressing unknowns of COVID-19 transmission and infection combining pathogen genomics and epidemiology to inform public health interventions IP: Iñaki Comas. Agencia: Instituto de Salud Carlos III. Periodo: 2020-2021 (12 meses) Cantidad: **1,750,000 euros**

Referencia: 202020E085 Título:Proyecto intramural CSIC asociado a PTI Salud Global Addressing unknowns of COVID-19 transmission and infection combining pathogen genomics and epidemiology to inform public health interventions IP: Iñaki Comas. Agencia: CSIC. Periodo: 2020-2011 (12 meses) Cantidad: **747,000 euros**

Referencia: PROMETEO/2020/012 Título:USO DE ANTIBIÓTICOS, MICROBIOTA Y RESISTENCIAS: IMPACTO EN LA SALUD DE LA POBLACIÓN INFANTIL DE LA COMUNIDAD VALENCIANA (NeoHealth) IP: Mari C. Collado (Iñaki Comas, IP de paquete de trabajo). Agencia: Generalitat Valenciana Periodo: 2020-2023 **Cantidad: 390,000 euros**

Reference: EQC2018-004423-P : Adecuación a nivel bioseguridad tipo 2 de animalario, unidad de microbiología y cultivos celulares del IBV PI: Iñaki Comas. Funding body: MINECO Start: January 01/01/2018 – 31/12/2019. **Amount: 449,199 euros.** Origin: National

Reference: TB-MULTIDRUG SAF2016-77346-R : Tuberculosis multirresistente: de la biología al diagnóstico PI: Iñaki Comas. Funding body: MINECO Start: 2017. **Amount: 242,000 euros**

Reference: MycoNet BFU2016-81742-REDT:Red temática en biología de sistemas de micobacterias PI: Iñaki Comas. Funding: MINECO Start: 2015. **Amount: 20.000 euros**

Reference: TB-Accelerate : Integrating genomics, epidemiology and evolution to accelerate tuberculosis eradication PI: Iñaki Comas. Funding body: European Research Council Start: Julio 2015. **Amount: 1.671.875 euros**

Reference: SAF2013-43521-R :Transformando las nuevas tecnologías de secuenciación en una herramienta para la epidemiologia y diagnostico de la tuberculosis: del laboratorio a la clinica PI: Iñaki Comas. Funding body: MINECO. Periodo: 2014-2017 **Amount: 193,600 euros**

Reference: 272086 : High throughput sequencing to reveal the causes and consequences of Mycobacterium tuberculosis genomic variation PI: Iñaki Comas, Francisco Silva Funding body: European Comission. Periodo: 2011-2013 **Amount: 166,565 euros**

C.4. Contracts, technological or transfer merits

Reference: Provider of sequencing/analysis services. Institutions: Antwerp Tropical Medicine (2019 – 2995 EUR), Vall D'Hebron Hospital (2022 – 47001 EUR), IATA-CSIC (2021-present: 5594,45 EUR).